

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 2, 2002, 12:05:30 : Search time 26 Seconds
(without alignments)
389.870 Million cell updates/sec

Title: US-09-101-518A-2

Perfect score: 2151

Sequence: 1 MELKKYGPGRAGTIVIGGA.....SSRRDSWSFTSEASVSGL 415

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1891	87.9	368	4	US-08-709-838-2
2	1891	87.9	368	4	US-08-829-839-2
3	640	29.8	374	3	US-08-982-493-6
4	635	29.5	372	1	US-08-202-056-5
5	635	29.5	372	1	US-08-076-093A-6
6	635	29.5	372	1	US-08-701-265-6
7	635	29.5	372	2	US-08-284-586-6
8	635	29.5	372	2	US-08-805-478-6
9	635	29.5	372	2	US-08-802-627A-6
10	635	29.5	372	2	US-08-801-238-6
11	635	29.5	372	2	US-08-801-228-6
12	635	29.5	372	3	US-09-104-226-6
13	635	29.5	372	3	US-08-982-493-8
14	633	29.4	355	1	US-07-759-568-1
15	633	29.4	355	1	US-08-450-333A-8
16	633	29.4	355	2	US-08-390-000A-5
17	633	29.4	355	4	US-08-446-669-8
18	633	29.4	355	5	PCT-US95-00476-8
19	633	29.4	360	1	US-08-202-056-7
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21	605.5	28.1	350	1	US-08-076-093A-2
22	605.5	28.1	350	1	US-08-450-333A-7
23	605.5	28.1	350	1	US-08-410-453A-1
24	605.5	28.1	350	1	US-08-701-265-2
25	605.5	28.1	350	1	US-08-410-454A-1
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27	605.5	28.1	350	2	US-08-410-456A-1

28	605.5	28.1	350	2	US-08-805-478-2	Sequence 2, Appl1
29	605.5	28.1	350	2	US-08-802-627A-2	Sequence 2, Appl1
30	605.5	28.1	350	2	US-08-801-238-2	Sequence 2, Appl1
31	605.5	28.1	350	2	US-08-801-228-2	Sequence 2, Appl1
32	605.5	28.1	350	2	US-09-104-296-2	Sequence 2, Appl1
33	605.5	28.1	350	4	US-08-446-669-7	Sequence 7, Appl1
34	605.5	28.1	350	3	PCT-US95-00476-7	Sequence 7, Appl1
35	589.5	27.4	410	1	US-08-153-848-7	Sequence 7, Appl1
36	589.5	27.4	410	3	US-09-299-843A-7	Sequence 7, Appl1
37	589.5	27.4	410	4	US-09-088-337B-7	Sequence 7, Appl1
38	589.5	27.4	410	5	PCT-US93-11153-7	Sequence 7, Appl1
39	586	27.2	358	1	US-08-153-848-19	Sequence 19, Appl1
40	586	27.2	358	3	US-09-299-843A-19	Sequence 19, Appl1
41	586	27.2	358	4	US-09-088-337B-19	Sequence 19, Appl1
42	586	27.2	358	5	PCT-US93-11153-19	Sequence 19, Appl1
43	586	27.2	378	1	US-08-153-848-15	Sequence 15, Appl1
44	586	27.2	378	3	US-09-299-843A-15	Sequence 15, Appl1
45	586	27.2	378	4	US-09-251-545-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-08-709-838-2
; Sequence 2, Application US/08709838
; Patent No. 6140654
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Marcel
; APPLICANT: Moser, Bernhard
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,838
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: TK196-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-709-838-2

Query Match      87.9%  Score 1891; DB 4; Length 368;
Best Local Similarity 99.7%; Pred. No. 2.3e-148;
Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 51 QVSDHQVUNDAEVAALLENFSSSYDGENESDSCCTSPCCPDGSLNDRAPLPLYSLL 110
DB 4 EVSDHQVUNDAEVAALLENFSSSYDGENESDSCCTSPCCPDGSLNDRAPLPLYSLL 63
OY 111 FLGLILGNCAVAALVLSRTALSSDTFLHLAVADTLLVLTPLMANVDAVQWFGSGL 170

|||||
Db 64 FLGLGNGAVALLSRTALSTDTFLHLAVADTLVLPLMAVDAAYQWFGSGL 123
QY 171 CKVAGALNINIFYAGALLLACISFDRIYNIYATOLYRGPARVTLCLAWGICLLFA 230
Db 124 CKVAGALNINIFYAGALLLACISFDRIYNIYATOLYRGPARVTLCLAWGICLLFA 183
QY 231 LPDFLFLSAHNDERLNATHCOYNPQVGTALRVQLVAGFLPLLVMAVCYAHITLAVLL 290
Db 184 LPDFLFLSAHNDERLNATHCOYNPQVGTALRVQLVAGFLPLLVMAVCYAHITLAVLL 243
QY 291 VSRGGRRLRAMLVVVVYVAFALCPTPHLVVLDLMDGLALANCGRESVYDAKSVT 350
Db 244 VSRGGRRLRAMLVVVVYVAFALCPTPHLVVLDLMDGLALANCGRESVYDAKSVT 303
QY 351 SGLGYMHCCINPLLYAFVGVKFRERMMMLLRGCPNORGLOROPSSSRDSSNSETSEA 410
Db 304 SGLGYMHCCINPLLYAFVGVKFRERMMMLLRGCPNORGLOROPSSSRDSSNSETSEA 363
QY 411 SYSGL 415
Db 364 SYSGL 368

RESULT 2

US-08-829-839-2
; Sequence 2, Application US/08829839
; Patent No. 6184358

GENERAL INFORMATION:

APPLICANT: Loetscher, Marcel
APPLICANT: Moser, Bernhard
APPLICANT: Qin, Shixin
APPLICANT: Mackay, Charles R.
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
TITLE OF INVENTION: ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829, 839
FILING DATE: 31-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709, 838
FILING DATE: 10-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TK196-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-829-839-2

Query Match 87.9%; Score 1891; DB 4; Length 368;
Best Local Similarity 99.7%; Pred. No. 2,3e-148;
Mismatches 1; Indels 0; Gaps 0;

QY 51 QVSDHQVLNDAEVALLENFSSSYDYGENESDSCCTSPCCPDFSLNPDRAFLPALYSLL 110
Db 4 EVSDHQVLNDAEVALLENFSSSYDYGENESDSCCTSPCCPDFSLNPDRAFLPALYSLL 63
QY 111 FLGLGNGAVALLSRTALSTDTFLHLAVADTLVLPLMAVDAAYQWFGSGL 170
Db 64 FLGLGNGAVALLSRTALSTDTFLHLAVADTLVLPLMAVDAAYQWFGSGL 123
QY 171 CKVAGALNINIFYAGALLLACISFDRIYNIYATOLYRGPARVTLCLAWGICLLFA 230
Db 124 CKVAGALNINIFYAGALLLACISFDRIYNIYATOLYRGPARVTLCLAWGICLLFA 183
QY 231 LPDFLFLSAHNDERLNATHCOYNPQVGTALRVQLVAGFLPLLVMAVCYAHITLAVLL 290
Db 184 LPDFLFLSAHNDERLNATHCOYNPQVGTALRVQLVAGFLPLLVMAVCYAHITLAVLL 243
QY 291 VSRGGRRLRAMLVVVVYVAFALCPTPHLVVLDLMDGLALANCGRESVYDAKSVT 350
Db 244 VSRGGRRLRAMLVVVVYVAFALCPTPHLVVLDLMDGLALANCGRESVYDAKSVT 303
QY 351 SGLGYMHCCINPLLYAFVGVKFRERMMMLLRGCPNORGLOROPSSSRDSSNSETSEA 410
Db 304 SGLGYMHCCINPLLYAFVGVKFRERMMMLLRGCPNORGLOROPSSSRDSSNSETSEA 363
QY 411 SYSGL 415
Db 364 SYSGL 368

RESULT 3

US-08-982-493-6
; Sequence 6, Application US/08982493
; Patent No. 6110695

GENERAL INFORMATION:

APPLICANT: Gunn, Michael D
APPLICANT: Williams, Lewis T
APPLICANT: Cyster, Jason G
TITLE OF INVENTION: Modulating B Lymphocyte Chemokine /
TITLE OF INVENTION: Receptor Interactions
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA

ZIP: 94010

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982, 493
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCSET98-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-982-493-6

Query Match 29.8%; Score 640; DB 3; Length 374;

Best Local Similarity 40.9%; Pred. No. 2.5e-45;
Matches 143; Conservative 54; Mismatches 139; Indels 14; Gaps 6;

QY 70 FSSSDYDGENESDSCCTSPCCPODLSINFDRAFLPALYSLLFLGLGGAVALLSRR 129
Db YSNSTSEIPLQSNFST---VEGPLLTSEKAFVMPVAVSLIFLGMGNILVILIERR 82
QY 130 TALSTDFELHLAAVDLLVLTPLMAVDAVOMVFGSLCKVAGALENINPYAGALL 189
Db HTRSTEFELFLAAVDLLVLTPLFAVAGSVGWLGFLCKYIALKINFTCSLLV 142
QY 190 ACISDRYLNIYHATQLYRRGPARTLTCLAVWGLCLFLPDLFLSA---HNDERLN 246
Db ACIAVDRLAIYHAAVYRRRLSHITCTAIWLAGFLALPELLFAKVGQPHNDSL- 201
QY 247 ATHCOYNFQVORT---ALRYLOLVAGFLPLLYMAICYAHILAVL-VSGQRRLRAM 301
Db 202 -PQCTFSENEAETAMFTSRFLYHIGFLPLMLVMGVCYGVVHRLLOAQRRPQOKAV 260
QY 302 RLWVVVVAFAFCWTPYHLVLTPLMDLGALARNCGRESRYDAKSVTSGLYMHCCLN 361
Db 261 RVAITVTSIFFLCWSPIYHIVFLDTERLKAVNSSCELSGYLSVAITLCEFLGLAHCCLN 320
QY 362 PLLAVGVKFRERMMMLRLGCPNQRGLQRPSSRRDSMSSETSAS 411
Db 321 PMLYFAGVKFRSDLSRLTLKLGCGAGPAST-CQLFPMNRKSSLSSEENAT 369

RESULT 4
US-08-202-056-5
Sequence 5, Application US/08202056
Patent No. 5440021

GENERAL INFORMATION:

APPLICANT: Chuntharapal, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202.056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-202-056-5

Query Match 29.5%; Score 635; DB 1; Length 372;
Best Local Similarity 40.8%; Pred. No. 6.5e-45;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

QY 67 LENFSSSY---DYGENESD-SCTSPCCPO---DLSINFDRAFLPALYSLLFLGLGNG 119
Db 11 LENLEDLFWELDRDYNNTSLVENHLCPATGEPMLASKAFVPAVAYSLIFLIGVIGAV 70
QY 120 AVAAVLSRRLSTDFELHLAAVDLLVLTPLMAVDAVOMVFGSLCKVAGALFN 179
Db 71 LVLTIERHRRQRTSEFLFLHAAVDLLVLTPLFAVAGSVGWLGFLCKYIALK 130
QY 180 INEYGAALLACISPRYNIYHATQLYRRGPARTLTCLAVWGLCLFLPDLFLSA--- 237
Db 131 VNFYCSSLLACIAVDRLAIYHAAVYRRRLSHITCTAIWLAGFLALPELLFAK 190
QY 238 -SAHDERLNATHCOYNFQVORT---ALRYLOLVAGFLPLLYMAICYAHILAVL-LV 291
Db 191 SOGHNNNSL--PQCTFSENEAETAMFTSRFLYHIGFLPLMLVMGVCYGVVHRLRQA 248
QY 292 SNGQRRLRAMRLVVVVAFAFCWTPYHLVLTPLMDLGALARNCGRESRYDAKSVTS 351
Db 249 QRPPQOKAVRVAITVTSIFFLCWSPIYHIVFLDTERLKAVDNCKLGSIPVAITWCE 308
QY 352 GLGYMHCCNLPLLYAVGVKFRERMMMLRLGCPNQRGLQRPSSRRDSMSSETSAS 411
Db 309 FLGLAHCCNLPLMLYTFAGVKFRSDLSRLTLKLGCTGPASPACOLPPSWR-SSLSEENAT 367

RESULT 5
US-08-076-093A-6
Sequence 6, Application US/08076093A
Patent No. 5543503

GENERAL INFORMATION:

APPLICANT: Chuntharapal, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PFA Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076.093A
FILING DATE: 11-Jun-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids

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; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-076-093A-6

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Query Match	29.5%:	Score 635:	DB 1:	Length 372:
Best Local Similarity	40.8%:	Pred. No. 6.5e-45:		
Matches 147; Conservative	50:	Mismatches 145:	Indels 18:	Gaps 8

[illegible]

RESULT 6
US-08-701-265-6
Sequence 6, Application US/08701265
Patent No. 5776457
GENERAL INFORMATION:
APPLICANT: Chuntarapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4a Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,265
FILING DATE: 22-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/2225-5530
TELEFAX: 415/252-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-701-265-6

[illegible]

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1      RESULT 7
2      US-08-284-586-6
3      : Sequence 6, Application US/08284586
4      : Patent No. 5840856
5      : GENERAL INFORMATION:
6      : APPLICANT: Chuntharapai, Anan
7      : APPLICANT: Lee, James
8      : APPLICANT: Hebert, Caroline
9      : APPLICANT: jin kim, K.
10     : TITLE OF INVENTION: Antibodies to Human PPA
11     : NUMBER OF SEQUENCES: 6
12     : CORRESPONDENCE ADDRESSES:
13     : ADDRESSEE: Genentech, Inc.
14     : STREET: 460 Point San Bruno Blvd
15     : CITY: South San Francisco
16     : STATE: California
17     : COUNTRY: USA
18     : ZIP: 94080
19     : COMPUTER READABLE FORM:
20     : MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
21     : COMPUTER: IBM PC compatible
22     : OPERATING SYSTEM: PC-DOS/MS-DOS
23     : SOFTWARE: Winpatin (genentech)
24     : CURRENT APPLICATION DATA:
25     : APPLICATION NUMBER: US/08/284,586
26     : FILING DATE:
27     : CLASSIFICATION: 424
28     : PRIOR APPLICATION DATA:
29     : APPLICATION NUMBER: US/08/076,093A
30     : FILING DATE: 11-Jun-1993
31     : APPLICATION NUMBER: 07/810782
32     : FILING DATE: 19-DEC-1991
33     : PRIOR APPLICATION DATA:
34     : APPLICATION NUMBER: 07/677211

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; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino acid
; TOPOLOGY: Linear
; US-08-284-586-6

Query Match
Best Local Similarity 40.8%; Score 635; DB 2; Length 372;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

Oy 67 LENFSSSY---DYGENESP-SCCTSPPCPO---DFSINDFRAFLPALYSLLFLGLGNG 119
Db 11 LENEDELFEWELDRDLYNNTSLVENHLCPTATEGPLMAFKAVFVPAVYSLIFLGVIGNV 70
Oy 120 AVAAVLLSRRLSSDTPFLHLAVADTLVLTPLMAVDAVQWFGSGCKVAGALFN 179
Db 71 LVLVILERRQRSSSTETFLFLAVADLLVFLPPRAVAGSGVWLGFLLCTVTYALAK 130
Oy 180 INFVAGALLLACISFDRIYINIVHATQLYRGRPARVTLTCLAWGICLLFALPDFTFL-- 237
Db 131 VNFYCSLLACIADVDRYLAIVHAAVYHRRRLSHITCGTLMVGLFLALPEILFAVY 190
Oy 238 -SAHNDERLNATHCOYNPOVGRT----ALRVQLVAGFLPLLVMAVYAHILAVL-LV 291
Db 191 SOGHNNNSL--PRCTFSQENOAETHAMFTSRFLYHVAAGFLPLLVGMWCYGVVHRLROA 248
Oy 292 SRGQRRLRAMRLVVVVVAFALCMTPYHLVLDLMDGALARNGRSRDVAKSVTS 351
Db 249 QRRPORQAKAVRAIIVTSTFFLCWSPYHIVFLDTLARKAVDNTCKLNGSLPVALTWCE 308
Oy 352 GIGYMHCCNPLLIYAFVGVKFERMMMLLRGCPNORGLOROPSSSRDSSWSETSEAS 411
Db 309 FLGLAHCCNPLMYTFAGVKFRSDLSRLTLKIGCTGPASLCQLFPWMRR-SLSSESENA 367

RESULT 8
US-08-805-478-6
; Sequence 6, Application US/08805478
; Patent No. 5874543
; GENERAL INFORMATION:
; APPLICANT: Chuncharapal, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: ANTIBODIES TO PFAA RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE: 25-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-805-478-6

Query Match
Best Local Similarity 40.8%; Score 635; DB 2; Length 372;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

Oy 67 LENFSSSY---DYGENESP-SCCTSPPCPO---DFSINDFRAFLPALYSLLFLGLGNG 119
Db 11 LENEDELFEWELDRDLYNNTSLVENHLCPTATEGPLMAFKAVFVPAVYSLIFLGVIGNV 70
Oy 120 AVAAVLLSRRLSSDTPFLHLAVADTLVLTPLMAVDAVQWFGSGCKVAGALFN 179
Db 71 LVLVILERRQRSSSTETFLFLAVADLLVFLPPRAVAGSGVWLGFLLCTVTYALAK 130
Oy 180 INFVAGALLLACISFDRIYINIVHATQLYRGRPARVTLTCLAWGICLLFALPDFTFL-- 237
Db 131 VNFYCSLLACIADVDRYLAIVHAAVYHRRRLSHITCGTLMVGLFLALPEILFAVY 190
Oy 238 -SAHNDERLNATHCOYNPOVGRT----ALRVQLVAGFLPLLVMAVYAHILAVL-LV 291
Db 191 SOGHNNNSL--PRCTFSQENOAETHAMFTSRFLYHVAAGFLPLLVGMWCYGVVHRLROA 248
Oy 292 SRGQRRLRAMRLVVVVVAFALCMTPYHLVLDLMDGALARNGRSRDVAKSVTS 351
Db 249 QRRPORQAKAVRAIIVTSTFFLCWSPYHIVFLDTLARKAVDNTCKLNGSLPVALTWCE 308
Oy 352 GIGYMHCCNPLLIYAFVGVKFERMMMLLRGCPNORGLOROPSSSRDSSWSETSEAS 411
Db 309 FLGLAHCCNPLMYTFAGVKFRSDLSRLTLKIGCTGPASLCQLFPWMRR-SLSSESENA 367

RESULT 9
US-08-802-627A-6
; Sequence 6, Application US/08802627A
; Patent No. 5892017
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PFAA RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802.627A
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-802-627A-6
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Query Match 29.5%; Score 635; DB 2; Length 372;

Best Local Similarity 40.8%; Pred. No. 6.5e-45; Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

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QY 67 LENFSSSY---DYGENESD-SCTSPPCPO---DFSINFDRAFLPALYSILFLGLGNG 119
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Db 11 LENTLEDLFWELDRLDNYNTSLVENHLCPTBGPMLASFRKAVVPVAYSLIFLGLGNG 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 AYAAYLSRRLASTDTFLHLAVADTLVTLPLMAVDAAVQWFGSLCKVAGALFN 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 LVLVILERRHQRSSSTETFLHLAVADTLVTLPLPFAVAGSVGWLGTFLCKTVIALHK 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 180 INFYAGALLACISPRRYNIYATQLYRGRPARVTLTCLAWGCLLFAIPDFTEL-- 237
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 VNFYCSLLDLACTADRYALTAIVAHAYRHRRLSLHTGCTIWLGVFLALPELIFAKV 190
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 238 -SAHDERLNATHCOYNPQVGR---ALRVQLVAGFLPLPLVMAVCYAHILAVL-LV 291
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 SQGHNNNSL--PRCTFSQENQAEHTAMFTSRFLYHAGFLPLVVGKCYGVGVHRLRQA 248
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QY 292 SRGQRLRLMRLLVYVVAFAALCWTPIYHLVLDLIMDLGALARNCGRESRDVAKSVTS 351
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 249 ORRPOROKAVRAVAILVTSIFFLCMSPYHIVIFLDTLARKAVDNTCKLNGSLPVAITMCE 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 352 GIGYMHCCINPLLYAVGVKFRFRMMMLLRGCPNQRGLQRPSSRRDSSMSEISEAS 411
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 FLGLAHCCINPLLYTFAVGKFRSDLSRLTLTKLGCTGPASLCLQLEPSWRR--SSLSESENA 367
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RESULT 10
US-08-801-238-6

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; Sequence 6, Application US/08801238
; Patent No. 5919896
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PFAA RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
```

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-801-238-6
```

Query Match 29.5%; Score 635; DB 2; Length 372;

Best Local Similarity 40.8%; Pred. No. 6.5e-45; Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

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QY 67 LENFSSSY---DYGENESD-SCTSPPCPO---DFSINFDRAFLPALYSILFLGLGNG 119
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 LENTLEDLFWELDRLDNYNTSLVENHLCPTBGPMLASFRKAVVPVAYSLIFLGLGNG 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 AYAAYLSRRLASTDTFLHLAVADTLVTLPLMAVDAAVQWFGSLCKVAGALFN 179
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Db 71 LVLVILERRHQRSSSTETFLHLAVADTLVTLPLPFAVAGSVGWLGTFLCKTVIALHK 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 180 INFYAGALLACISPRRYNIYATQLYRGRPARVTLTCLAWGCLLFAIPDFTEL-- 237
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 VNFYCSLLDLACTADRYALTAIVAHAYRHRRLSLHTGCTIWLGVFLALPELIFAKV 190
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 238 -SAHDERLNATHCOYNPQVGR---ALRVQLVAGFLPLPLVMAVCYAHILAVL-LV 291
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 SQGHNNNSL--PRCTFSQENQAEHTAMFTSRFLYHAGFLPLVVGKCYGVGVHRLRQA 248
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QY 292 SRGQRLRLMRLLVYVVAFAALCWTPIYHLVLDLIMDLGALARNCGRESRDVAKSVTS 351
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Db 249 ORRPOROKAVRAVAILVTSIFFLCMSPYHIVIFLDTLARKAVDNTCKLNGSLPVAITMCE 308
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QY 352 GIGYMHCCINPLLYAVGVKFRFRMMMLLRGCPNQRGLQRPSSRRDSSMSEISEAS 411
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 FLGLAHCCINPLLYTFAVGKFRSDLSRLTLTKLGCTGPASLCLQLEPSWRR--SSLSESENA 367
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 11

US-08-801-228-6

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; Sequence 6, Application US/08801228
; Patent No. 5922541
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
; TITLE OF INVENTION: PFAA RECEPTOR NUCLEIC ACID
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: November 2, 2002, 12:11:20 ; Search time 49 seconds

(without alignments)
2080.365 Million cell updates/sec

Title: US-09-101-518A-2

Perfect score: 2151

Sequence: 1 MELRRYGPRLAGFYIGGA.....SSRRDSWSESEASYSGL 415

Scoring table:

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=x1h
-O=/cgn2_1/USPTO_spool/US09101518/runat_29102002_091056_29932/app_query.fasta_1.583
-DB=Issued_Patents_NA -QEXT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi
-LIST=45 -DOCLALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09101518_ECGN_1.1.13 @runat_29102002_091056_29932 -NCPU=6 -ICPU=3
-NO_XLPRX -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents.NA:*

- 1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/lna/PCRTUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1897	88.2	1670	4	US-08-709-838-1
2	1897	88.2	1670	3	US-08-829-838-1
3	640	28.8	2517	3	US-08-982-493-5
4	635	28.5	1510	1	US-07-759-568-4
5	635	29.5	1679	1	US-08-202-056-6
6	635	29.5	1679	1	US-08-076-093A-5
7	635	29.5	1679	1	US-08-701-265-5
8	635	29.5	1679	2	US-08-284-586-5
9	635	29.5	1679	2	US-08-805-478-5
10	635	29.5	1679	2	US-08-802-627A-5
11	635	29.5	1679	2	US-08-801-238-5
12	635	29.5	1679	2	US-08-801-228-5

13	635	29.5	1679	3	US-09-104-296-5	Sequence 5, Appl1
14	635	29.5 <td>1679</td> <td>5</td> <td>PCT-US94-06380-3</td> <td>Sequence 3, Appl1</td>	1679	5	PCT-US94-06380-3	Sequence 3, Appl1
15	635	29.5 <td>1748</td> <td>1</td> <td>US-08-202-056-8</td> <td>Sequence 8, Appl1</td>	1748	1	US-08-202-056-8	Sequence 8, Appl1
16	635	29.5 <td>2818</td> <td>3</td> <td>US-08-982-493-7</td> <td>Sequence 7, Appl1</td>	2818	3	US-08-982-493-7	Sequence 7, Appl1
17	635	29.5 <td>2818</td> <td>4</td> <td>US-08-628-653-1</td> <td>Sequence 1, Appl1</td>	2818	4	US-08-628-653-1	Sequence 1, Appl1
18	621.5	28.9	1200	5	PCT-US95-03032-1	Sequence 1, Appl1
19	620	28.8	1106	5	PCT-US92-02977-5	Sequence 5, Appl1
20	620	28.8	1106	5	PCT-US95-03032-4	Sequence 4, Appl1
21	615	28.6	1373	5	PCT-US92-02977-6	Sequence 6, Appl1
22	615	28.6	1373	5	PCT-US95-03032-3	Sequence 3, Appl1
23	609	28.3	1176	5	PCT-US95-03032-2	Sequence 2, Appl1
24	609	28.3	1933	1	US-08-076-093A-1	Sequence 1, Appl1
25	609	28.3	1933	1	US-08-410-451-1	Sequence 1, Appl1
26	609	28.3	1933	1	US-08-410-455-1	Sequence 1, Appl1
27	609	28.3	1933	1	US-08-410-455-1	Sequence 1, Appl1
28	609	28.3	1933	1	US-08-410-453A-2	Sequence 2, Appl1
29	609	28.3	1933	1	US-08-701-265-1	Sequence 1, Appl1
30	609	28.3	1933	1	US-08-410-454A-2	Sequence 2, Appl1
31	609	28.3	1933	2	US-08-284-586-1	Sequence 1, Appl1
32	609	28.3	1933	2	US-08-410-455A-2	Sequence 2, Appl1
33	609	28.3	1933	2	US-08-805-478-1	Sequence 1, Appl1
34	609	28.3	1933	2	US-08-802-627A-1	Sequence 1, Appl1
35	609	28.3	1933	2	US-08-801-238-1	Sequence 1, Appl1
36	609	28.3	1933	2	US-08-801-228-1	Sequence 1, Appl1
37	609	28.3	1933	2	US-09-104-296-1	Sequence 1, Appl1
38	609	28.3	1933	5	PCT-US94-06380-1	Sequence 1, Appl1
39	607.5	28.2	1300	5	PCT-US92-02977-1	Sequence 1, Appl1
40	605.5	28.1	1883	1	US-08-202-056-2	Sequence 2, Appl1
41	589.5	27.4	1900	1	US-08-153-843A-18	Sequence 18, Appl1
42	589.5	27.4	1900	3	US-09-299-843A-18	Sequence 18, Appl1
43	589.5	27.4	1900	4	US-09-088-337B-18	Sequence 18, Appl1
44	589.5	27.4	1900	5	PCT-US93-11153-18	Sequence 18, Appl1
45	589.5	27.4	2058	1	US-08-153-848-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-709-838-1
Sequence 1, Application US/08709838
Patent No. 6140064
GENERAL INFORMATION:
APPLICANT: Loetscher, Marcel
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,838
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TK196-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1670 base pairs


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Percent Similarity: 97.63%      Conservative: 1
Best Local Similarity: 97.36%      Mismatches: 5
Query Match: 88.19%      Indels: 4
DB: 4      Gaps: 1

US-09-101-518A-2 (1-415) x US-08-829-839-1 (1-1670)

OY 41 ThrAlaProSer-----SerProPheProSerGlnValSerAspHisGln 56
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Db ACACACCCAGCAGCCAGACAGCAGCCAGCCAGCATGCTTGAAGTGAAGCAGCA 95

OY 57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheserSerTyr 76
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db GTGCTAAATGACGCCGAGGTTGCCGCTCTGGAGAACTTCAAGCTCTTGAATAT 135

OY 77 GlyGluAsnGluSerAspSerCysGlyThrSerProProCysProGlnAsp 96
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 156 GGAGAAACGAGAGTACATCGCTTACCCTCCGCCCTCCAGAGACTTCAGCTG 215

OY 97 AsnPhesAspArgAlaPheLeuProAlaLeuTyrSerLeuPheLeuGlyLeu 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 216 AACTTGACCGGGCTTCTGCTCCAGCCCTTACAGCTCTCTTCTGCTGGGCTG 275

OY 117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgTThrAlaLeuSerThr 136
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 276 GGCAACGGCGGTGGACGCCGTGCTGAGCGCGGAGACCCCTGAGCAGACGAC 335

OY 137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeu 156
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 336 ACCCTTCCTGCTCACCCTGACCTGACAGACACCTGCTGCTGACACGCGCTG 395

OY 157 AlaValAspAlaAlaValAlaValGlnTrpValPheGlySerGlyLeuGly 176
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OY 177 LeuPheAsnIleAsnPhetYrAlaGlyAlaLeuLeuAlaCysIleSerPhe 196
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Db 456 CTCTTCAACATCAACTTTCACGAGAGAGCCCTGCTGGCCGTCATCAAGCTT 515

OY 197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgGlyProProAlaArg 216
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Db 516 TACCTGAACATGATGTTATCCACCCAGCTCTACCGCGGGGGCCCCCGGCTG 575

OY 217 LeuThrCysLeuAlaValTrpGlyLeuCysIleLeuPheAlaLeuProAsp 236
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 576 CTCACCTGCTGCTGCTGCTGGGGGCTGCTGCTCTTTGCCCCCAGACTTCA 635

OY 237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsn 256
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Db 636 CTGTGCGGCCACAGCAGAGCGGCTCAAGCGCACCCAGCCCAATCAACTTCC 695

OY 257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeu 276
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OY 277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArg 296
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 756 GTCATGCTTACTGCTATGCTCCATCTGCGCTGCTGCTGCTTCCAGGGCCAG 815

OY 297 ArgLeuArgAlaMetArgLeuValValValAlaValAlaPheAlaLeuCys 316
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 816 CGCTGCGGGCCATGCGGCTGGGTGGTGGTGGTGGCTTCCCTGCTGCTGAC 875

OY 317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeu 336
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 876 CCTTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 935

OY 337 CysGlyArgGluSerArgValAspValAlaValSerValThrSerGlyLeu 356
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 936 TGTGGCGGAAAGCGAGGTAGACGTGGCCAGATGCGCTGAGGCTGAGGCTA 995

OY 357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArg 376
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Db 996 CACTGCTGCCCAACCCGCTGCTTATGCTTCTAGGGGTCAAGTTCCGGAGCGATG 1055

OY 377 TrpMetLeuLeuAsnArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGln 396
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1056 TGGATGCTGCTTGGCCCTGGGCTGCCCAACCAAGAGAGGGCTCCAGAGCAGCAT 1115

OY 397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGly 415
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1116 TCTTCCCGCGGATTCATCTGCTGTGAGACCTCAGAGGCTCTTACTGCGCTTG 1172

RESULT 3
US-08-982-493-5
: Sequence 5, Application US/08982493
: Patent No. 6110695
: GENERAL INFORMATION:
: APPLICANT: Gunn, Michael D
: APPLICANT: Williams, Lewis T
: APPLICANT: Cyster, Jason G
: TITLE OF INVENTION: Modulating B Lymphocyte Chemokine /
: TITLE OF INVENTION: Receptor Interactions
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
: STREET: 75 DENISE DRIVE
: CITY: HILLSBOROUGH
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94010
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/982,493
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: OSMAN, RICHARD A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: UCSFT98-026
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 343-4341
: TELEFAX: (650) 343-4342
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2517 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1122
: US-08-982-493-5

Alignment Scores:
Pred. No.: 1.76e-61      Length: 2517
Score: 640.00      Matches: 143
Percent Similarity: 56.29%      Conservative: 54
Best Local Similarity: 40.86%      Mismatches: 139
Query Match: 29.75%      Indels: 14
DB: 3      Gaps: 6

US-09-101-518A-2 (1-415) x US-08-982-493-5 (1-2517)

OY 70 PheSerSerSerTyrArgGlyGluAsnGluSerAspSerCysThrSerPro 89
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 TACAGTAACAGCAGCGGATTCCTCCACAGAGACAGTAATCTTGTGCTTACA----- 126

OY 90 CysProGlnAspPheSerLeuAsnPhesAspArgAlaPheLeuProAlaLeuTyr 109
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Db 127 GTGAGAGGAGCCCTTACTGACGCTCTTAAAGCGGTATTCATGCTGTGGGCTAC 186
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OY      110 LeuPheLeuLeuGIleuLeuGLysASIGlyAlaValAlaAlaValLeuLeuSerArgArg 129
       ||||||| :||| |
Db      187 ATCTTCTCCCGGGTAGAAGGGAACATCCTGTGGTGGTAATCTGGAGAAGCAACGG 246
OY      130 ThrAlaLeuSerThrAspTrpPheLeuIleHisIleAlaValAlaAspPheTrpLeu 149
       ||||||| :||| |
Db      247 CAACTCGAGACTAACCGAGACCTTCCTGTTCCTGCAGTACCGAACCCTTGCTTA 306
OY      150 ValLeuThrLeuProLeuTrpAlaValAlaValAlaValAlaGlnTrpValPheGlySerGly 169
       ||| ||||| :||| |
Db      307 GTCATTACCTCGGCTTTTGGACAGTGGCGAGAGGCGCTGTGGTGGTGGTCTAGGAGACTTC 366
OY      170 LeucylsLysValAlaGlyAlaLeuPheAsnPIeaSnPheTrpAlaGlyAlaLeuLeuLeu 189
       ||||||| :||| |
Db      367 CTCTGCAAAAGTGTAGTGCCTGCCACAGATCAATTTCTACTGCGAGCGCTGCTGCTGG 426
OY      190 AlaAcylIleSerPheAspArgcTYrLeuAsnPIeValHisAlaThrClmLeuTyrlArg 209
       ||||||| :||| |
Db      427 GCCTGTANAGCTGNAGACCGGTACCTAGCATGCTGCATGCTGTTCAGCCCTTACCGCGCC 486
OY      210 GlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPhe 229
       ||| :||| |
Db      487 CGTGAGACTCCTCTCAATCCACATCACCTGCAGCGCATTTGGCTGGCGCTTCTCTGTC 546
OY      230 AlaleuProAspPheIlePheLeuSerAla-----HisHisaspLunArgLeuasn 246
       ||||||| :||| |
Db      547 GCCATTACCGAGACTCCCTCTTGCCAAAGTTGGGCCAACCCTCATATACAGACACTCTTA--- 603
OY      247 AlaThrHisCysGlnTryaSnPheProGlnValGlyArgThr-----AlaLeu 262
       ||| :||| |
Db      604 ---CCACAGTGCACCTCTCCACGAAAGAAAGAGCGGAACATAAGACCTGGTTCACCTCC 660
OY      263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetLarycystyr 282
       ||| ||| :||| |
Db      661 CGTTTCTCTACACCAATCGGGGGCTTCTTAATCCCATGCTGTGTGAGGAGTGATTAC 720
OY      283 AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgPheLeuArgLamet 301
       ||| :||| |
Db      721 GTGGGCGGTGCTCCAGAGCTACTGTCAGAGGCCAGCGGCCCTCTACAGCGAGAAAGCGGTC 780
OY      302 ArgLeuValValValValValAlaPheAlaLeuCysTrpTrpProThrsIleuVal 321
       ||| :||| |
Db      781 AGGTTGGCGCATTTTGAACAACAACTTTCTCTGCTGCGGCGCCCTTACCAACATTTGC 840
OY      322 ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgasncysGlylArgelUser 341
       ||| :||| |
Db      841 ATCTTCCAGATTACACTGAGAGGCTGAAGCGCTGAATAGCAGCTGCGACGTTGAGTGCGC 900
OY      342 ArgValAspValAlaLysSerValThrSerGlyLeuGlyTYrMethIscysCysLeuasn 361
       ||| :||| |
Db      901 TATCTCTCTGTGGGCATACCACTGTTGTGAATTCCTGTGGCTGGCAACAGCTGCTCATAT 960
OY      362 ProLeuLeuTyrlAlaPheValAlaGlyValLysPheArgGluArgMetTrpMetLeuLeu 381
       ||| :||| |
Db      961 CCCATGCTTTTACACTTTCGCTGGCGTAAATTTCCGACAGTACCTCTGCGCTTGTGACC 1020
OY      382 ArgLeuGlyCysProAsnglnArgGlyLeuGlnArgGlnProSerSerSerArgArgasp 401
       ||| :||| |
Db      1021 AAGCTGGGCTGTGCTGGCCCCGGCCTCCCTT---TGCCAACTTTTCCCACACTGGCGCAAG 1077
OY      402 SerSerTrpSerGlnTrpSerGluAlaSer 411
       ||||| ||||| :||| |
Db      1078 AGTAGTCTCTGTGAGTCAGAGAAATGCTACT 1107

RESULT 4
US-07-759-568-4
; Sequence 4, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional Human Interleukin-8 Receptor

```

```
? NUMBER OF SEQUENCES: 5
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: Cushman, Dardy & Cushman
? STREET: 1615 L Street, N.W.
? CITY: Washington
? STATE: D.C.
? COUNTRY: USA
? ZIP: 20036-5601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/759,568
? FILING DATE: 19910913
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Scott, Watson T.
? REGISTRATION NUMBER: 26581
? REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-861-3000
? TELEFAX: 202-822-0944
? TELEX: 6714627 cush
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1510 base pairs
? TYPE: NUCLEIC ACID
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
US-07-759-568-4

Alignment Scores:
Pred. No.:      2,84e-61          Length:    1510
Score:           635.00             Matches:   146
Percent Similarity: 53.56%         Conservative: 57
Best Local Similarity: 38.52%       Mismatches: 136
Query Match:     29.52%            Indels:    40
DB:              1                  Gaps:      8

US-09-101-518A-2 (1-415) x US-07-759-568-4 (1-1510)
QY      50 SerGlnValSerAsnHisGlnValLeuAsnAspAlaGluValAlaIleLeuLysGluAsn        69
|||:::||||: ||| :: :|||::: |::|:
Db      20 TCAAAATATTGAAGATTTCACATGTGGAGTGCACAGC-----TTTGAAAGAT        64
QY      70 Phe-----SerSetrtytAsprlyrglLygluaEngLuSerpsercys      84
|||
Db      65 TTCCTGAAAGGTGAAGATCTTAGTAATACAGTTAACACTCTACCCTCGCCCTTTTCTA      124
QY      85 cysthiserproprococyproglinaspheseriueasnspheaspargalaPheLeupro      104
|||:||||: |||::: |||::: |||::: |||:::
Db      125 CTAGATGCCGCCCATGTGAACAAGA--TCCCTGGAAATCAACAAGATAATTGTGGTC      188
QY      105 AlaLeutySerLeuLepHeLyuLeuEugLYASNGLyALALAIAlaLaVaI                124
:::||:::||||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      182 ATTAATCTATGCCCTGTATTCCTGTGTGAGCCTGCGGGAACATCGCTGATGTCGCTGC      241
QY      125 LeuleuSerAtgArgThAlaleuSerSetrthraspthrPheileuHIsLeulaVaI      144
:::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      242 ATCTATATCACAGAGGSGTGGCGCGCTCGCTSCATGATGTCTACSTGTGAACSTGACCTTG      301
QY      145 AlaaSPThrLeuLeuValLeIThrLeuProleutPrpaLavalaPaRllaAlavalGItpR      164
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      302 GCCGACCTACTCTTTGGCCCTACCTGCCCATCTGGCGGCGGCGCTCCAAGGTGAATGGCTGG      361
QY      165 ValIPegilyseRGlyLeucylsyVALalaglyAlaleuPhasnIIleaSnPhetRYAla      184
::::|||:::||||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      362 ATTTTTGGCACATTCTCTGTGCAAGGTGTCTCACTCTGGAAGAAGTCMACTTTATAGT      422
185 GlYAlaIleuLeuAlaCyIlSeSrPheaSpArGYTYReuasniIvalIHISAlatThr      204
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Db 422 GGCATCTGCTAGTGGCTGATGAGTGGACGCTTACCTGGCATTTGCTGACGACAA 481
Qy 205 GlnLeuTyrArgGlyProProAlaArgValThrLeuThr----- 218
Db 482 CGC-----ACACTGACCCAGAGCGCTACTTGGTC 511
Qy 219 -----CysLeuAlaValTrpGlyLeuCysLeuPheAlaLeuProAspPheIle 235
Db 512 AAATTCATATGCTCAAGCATCTGGGGTCTGCTCTGCTGGCCCTGCTGCTTACT 571
Qy 236 PheLeuSerAlaHisHisAspGluArgLeuAlaTrpHisCysGlnTyrAsnPro 255
Db 572 TTCCGAGAGCGCTACTCATCCATGTATACCCAGCC---TGC-----TATGAG 619
Qy 256 GlnValGly-----ArgThrAlaLeuArgValLeuGlnLeuValAla 269
Db 620 GACATGGGCAACATATACGAAACTGGCGGATGCTGTACGGATCTGCGCCAGTCTTT 679
Qy 270 GlyPheLeuProLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu 289
Db 680 GGCCTCATCTGTCACATGCTGTATCATGCTTCTGCTACGGATTACCCCTGCTACGCTG 739
Qy 290 LeuValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValVal 309
Db 740 TTTAAGGCCACATGGGCGAGAGACCGGGCATGGGGTCACTTTGCTGCTGCTC 799
Qy 310 AlaPheAlaLeuCysTyrThrProTyrHisLeuValValLeuValAspIleLeuMetCsp 329
Db 800 ATCTTCGCTGCTTGTCTGCTGCTGCTACAAACCTGCTGCTGCTGCGACCCCTCATGAGG 859
Qy 330 LeuGlnAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerVal 349
Db 860 ACCGAGGTGATCCAGAGAACTGTCAGCGCGCCAAATCACAATGACCGGCGCTTGATGCC 919
Qy 350 ThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGly 369
Db 920 ACCGAGATTCTGGGATCTTCACAGCTGCTCAACCCCGCTCATCGCCCTTCAATTGGC 979
Qy 370 ValLysPheAlaArgGlnArgMetTrpMetLeuLeuAlaArgLeuGlyCysProAsnGlnArg 389
Db 980 CAGAAGTTTCCGACAGCATCTCTCAAGATTCTACCTATACATACATGCTGATCGACGAC 1039
Qy 390 GlyLeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGlnThrSer 408
Db 1040 TCCCTGCCCAAGACAGACAGGCGCTTCTTTGTTGGCTCTTCTTCAAGGCGACACTTCC 1096

RESULT 5
US-08-202-056-6
: Sequence 6, Application US/08202056
: Patent No. 5440021
:
: GENERAL INFORMATION:
: APPLICANT: Chuntharapal, Anan
: APPLICANT: Hebert, Caroline
: APPLICANT: Kim, Kyung Jin
: APPLICANT: Lee, James
: TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
: NUMBER OF SEQUENCES: 8
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/202.056
: FILING DATE: 25-FEB-1994
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: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/677211
: FILING DATE: 29-MAR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: 706P3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-5530
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1679 bases
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-08-202-056-6
:
: Alignment Scores:
: Pred. No.: 3,366-61 Length: 1679
: Score: 635.00 Matches: 147
: Percent Similarity: 54.72% Conservative: 50
: Best Local Similarity: 40.83% Mismatches: 145
: Query Match: 29.52% Indels: 18
: DB: 1 Gaps: 8
:
: US-09-101-518a-2 (1-415) x US-08-202-056-6 (1-1679)
Qy 67 LeuGluAsnPheSerSerSerTyr-----AspTyrGlyGluAsnGluSerAsp--- 82
Db 399 CTCGAGAACCTTGAGAGACTGCTTCTGGGACACTGACAGATTGGACAACATATACGACACC 458
Qy 83 SerCysTyrSerProCysProGln-----AspPheSerLeuAsnPheAsp 99
Db 459 TCCCTGCTGGAATAATCATCTGCTGCTGCCACAGAGGGGCCCTCATGAGCTTCAAG 518
Qy 100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGlyLeuLeuGlyLysGly 119
Db 519 GCCGTGTCGTCGCCGTGGCCATCAGACCTCATCTTCTGCGGTGATCGGCAACGTC 578
Qy 120 AlaValAlaValAlaValLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
Db 579 CTGGTCTGCTGATCTCTGAGCGCGGACCGGACAGACGACGATTCACAGGACGACTTCCG 638
Qy 140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
Db 639 TTCACATGCGCGGTGGCGGACCTCTGCTGCTTCATCTTGCCTTTGGCCGTGGCGGAG 698
Qy 160 AlaAlaValAlaGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
Db 699 GGCCTGTGGGCTGGGTCCCTGGGACCTTCTCAAAACTGTGATTCCTCGCAAAA 758
Qy 180 IleAsnPheTyrAlaGlyAlaValLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
Db 759 GTCAACTTCTACTGACAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
Qy 200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
Db 819 ATTGTCCAGCGCGCTCATGCCACCGGACCGCGCGCTTCCTCATTCACATCCATCTG 878
Qy 220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu----- 237
Db 879 GGGACATCTGGCTGGTGGCTTCTCTGCTTCCAGAGATTCCTTCTCCCAAAGTC 938
Qy 238 ---SerAlaHisHisAspGluArgLeuAsnAlaTrpHisCysGlnTyrAsnProGln 256
Db 939 AGCCAAAGGCATACAAACACTCCCTG-----CCACGTGGACCTTCTTCCAAAGAAC 992
Qy 257 ValGlyArgThr-----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
Db 993 CAAGCAAGAACGATGCTGTTGACATCCGATTCCTTACATGATGCGGGGATTCCTG 1052
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Db 1233 GCCGTGACAAATACCTGCAAGCTGAATGCTCTCTCCCGTGGCCATCAGCATGTGTGAG 1292
QY 352 GtyleuGlyTyrMetHisCysCysLeuasnProLeuLeuTyrAlaPheValIys 371
Db 1293 TTCCTGGGCGCTGGCCCGCTGCTGCTCAACCCCATGCTTACACTTTCGCCGCGTGAAG 1352
QY 372 PheArgGlyuArgMetTyrMetLeuLeuArgLeuGlyCysProAsnIlnArgIleu 391
Db 1353 TTCGCCATGACCTGTCCGGGCTCTGCTGACGAGCTGGGTGACGGGCTTCCTCCG 1412
QY 392 GlnArgGlnProSerSerArgArgAspSerSerTyrSerGluThrSerGluAsp 411
Db 1413 TGCCAGCTCTTCCCTAGCTGCGGCAAG---AGCAGTCTCTGTGAGTCAAGATGCCACC 1469

RESULT 7

US-08-701-265-5
Sequence 5, Application US/08701265
Patent No. 5776457
GENERAL INFORMATION:
APPLICANT: Chuntharapal, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PFAA Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipaltn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,265
FILING DATE: 22-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 415/952-5530
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-701-265-5

Alignment Scores:

Pred. No.: 3,36e-61 Length: 1679
Score: 635.00 Matches: 147
Percent Similarity: 54.72% Conservative: 50
Best Local Similarity: 40.83% Mismatches: 145
Query Match: 29.52% Indels: 18
Gaps: 8

US-09-101-518a-2 (1-415) x US-08-701-265-5 (1-1679)
QY 67 LeuGluAsnPhSerSerSerTyr-----AsPTyGlyGluAsnGluSerAsp--- 82
Db 399 CTCGGAAACGTGAGAGACCTGTTCTGGGAACGTGACAGATTGTGACAACTATACGACACC 458
QY 83 SerCysCysThrSerProProCysProGln-----AspPheSerLeuAsnPhSer 99
Db 459 TCCCTGTGTGAAATCATCTTGCCCTGCCACAGAGGGCCCTCATGGCTTCCTTCAAG 518
QY 100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGlyLeuLeuGlyAsnGly 119
Db 519 GCCGTGTGTGCTGCCCGCTGCTACAGCCTCATCTTCTGCGGTGATTCGGCAACGTC 578
QY 120 AlaValAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
Db 579 CTGGTGTGTGATCTCTGAGCGGACCGGACGACGAGTTCACGAGACCTTCTCG 638
QY 140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuThrAlaValAsp 159
Db 639 TTCACACTGCGCGCTGGCGGACCTCTGCTGCTTCATCTTGCCTTTCGCGCGGAG 698
QY 160 AlaAlaValGlnTyrValPheGlySerGlyLeuCysValAlaGlyAlaLeuPheAsn 179
Db 699 GGCTGTGTGGCTGGGCTCTGGGACCTTCCTGTGAATACTGTGATTGCCCTGGACAA 758
QY 180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
Db 759 GTCAACTTCTACTGACGACGCTGCTGCGCTGATGCGGTGAGACCGCTACCTGGGCG 818
QY 200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
Db 819 ATTGTTCACGCGCTGCATGCTTACCGGACCGCGGCTCTCTCCATCATCATCATCTGT 878
QY 220 LeuAlaValTyrGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu----- 237
Db 879 GGGACCATGTGGCTGTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 938
QY 238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
Db 939 AGCCAAAGCCATCAACAACTCCCTG-----CCAGCTTGGACCTTCCCAAGAGAAC 992
QY 257 ValGlyArgThr-----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
Db 993 CAAGCAAGAACCATGCTGCTGCTTACCTCCGATCTCTTACCATGTGCGGATTCCTG 1052
QY 273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
Db 1053 CTGCCATGCTGTGATGGGCTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1112
QY 292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValAlaValAlaPhe 311
Db 1113 CAGCGCGGCTCAGCGGCGGAGAGGACGACGAGGCGGCTGCTGCTGCTGCTGCTGCTGCT 1172
QY 312 AlaLeuCysTyrThrProTyrHisLeuValValLeuValAlaIleLeuMetAspLeuGly 331
Db 1173 TTCCTCTGCTGTACCTCTACCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1232
QY 332 AlaLeuAlaArgAsnCysGlyArgGlnSerArgValAspValAlaIlysSerValThrSer 351
Db 1233 GCCGTGACAAATACCTGCAAGCTGAATGCTCTCCCGTGGCATCATCATCATCATCATCAT 1292
QY 352 GtyleuGlyTyrMetHisCysCysLeuasnProLeuLeuTyrAlaPheValIys 371
Db 1293 TTCCTGGGCGCTGGCCCGCTGCTGCTCAACCCCATGCTTACACTTTCGCCGCGTGAAG 1352
QY 372 PheArgGlyuArgMetTyrMetLeuLeuArgLeuGlyCysProAsnIlnArgIleu 391
Db 1353 TTCGCCATGACCTGTCCGGGCTCTGCTGACGAGCTGGGTGACGGGCTTCCTCCG 1412
QY 392 GlnArgGlnProSerSerArgArgAspSerSerTyrSerGluThrSerGluAsp 411
Db 1413 TGCCAGCTCTTCCCTAGCTGCGGCAAG---AGCAGTCTCTGTGAGTCAAGATGCCACC 1469

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RESULT 8
US-08-284-586-5
; Sequence 5, Application US/08284586
; Patent No. 5840856
;
; GENERAL INFORMATION:
; APPLICANT: Chunharapal, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PFA Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,586
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1679 nucleotides
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
; US-08-284-586-5
;
; Alignment Scores:
; Pred. No.: 3,366-61 Length: 1679
; Score: 635.00 Matches: 147
; Percent Similarity: 54.72% Conservative: 50
; Best Local Similarity: 40.83% Mismatches: 145
; Query Match: 29.52% Indels: 18
; DB: 2 Gaps: 8
;
; US-09-101-518a-2 (1-415) x US-08-284-586-5 (1-1679)
;
; QY 67 LeuGluaAnPheSerSerSerTyr-----AspTyrGlyGluAsnGluSerAsp--- 82
; ||||||||| :||| :||| :|||
; DB 399 CTCGAGAACCTGGAGACCTGTTCTGGGAACGTGGACAGATTGGACACATTAACGCACACC 458
;
; QY 83 SerCysCysThrSerProCysProGln-----AspPheSerLeuAsnPhaSp 99
; ||| :||| :||| :|||
; DB 459 TCCCTGGGTGGAATCATCTCTGCGCCCTGCCACAGAGGGGCCCTCATGGCTTCCTTCAAG 518
;
; QY 100 ArgAlaPheLeuProAlaLeuTyrSerLeuPheLeuGlyLeuLeuGlyAsnGly 119
; ||||| :||| :||| :|||
; DB 519 GCCGTGTTGTCGCCCTGAGCTACAGCCATCATCTCTCTCTGCGGTGATCGGCAACGTC 578
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QY 120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
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; QY 140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuThrAlaValAsp 159
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; DB 639 TTCACCTGGCCGCGGACCTCTGCTGCTTCATCTCATCTTCCTTGCCTGGCCGCGAG 698
;
; QY 160 AlaAlaValAlaGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyValaLeuPheAsn 179
; :||| :||| :||| :|||
; DB 699 GCGCTCTGTGGGCTGGGCTCTGGGGACCTTCCTGTGCAAACTGTGATTCCTCGACAAA 758
;
; QY 180 IleAsnPheTyrAlaGlyAlaLeuLeuAlaCysLysPheAspArgTyrLeuAsn 199
; :||| :||| :||| :|||
; DB 759 GTCACTTCTACTGACAGCAGCCTGCTCTGGCTGATCCGCGGTGAGACCGCTACCTGGCC 818
;
; QY 200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
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; DB 819 ATTGTCCACGCGCTCATGCTACCGCCACCGCCGCTCTCCATCCATCCACATCATCTGT 878
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; QY 220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheLeu----- 237
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; DB 879 GGGACCATCTGGCTGGGCTGCTCTCTGCTTGCAGAGATTCCTTCGCGCAAAAGTC 938
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; QY 238 ---SerAlaHisHisAspGlnArgLeuAsnAlaThrHisCysGlnTyrAsnPhaProGln 256
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; DB 939 AGCCAAAGCCATCACACACATCCCG-----CCAGCTGACCTTCTCCCAAGAGAAC 992
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; QY 257 ValGlyArgThr-----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
; ||| :||| :||| :|||
; DB 993 CAAGCAGAAACCCATGCTGTTACCTCCGATCTCCATCTCCATCAGATGGCGGATTCCTG 1052
;
; QY 273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
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; DB 1053 CTGCCCATGCTGTGTGGTGGCTGTGCTACGTGGGGGTATGTACACAGTTGGCGCCAGGCC 1112
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; QY 292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValAlaValAlaValAlaPhe 311
; ||| :||| :||| :|||
; DB 1113 CAGCGGCGCCCTCAGCGGAGAGAGCAGTGAAGGCGCATCTGTGTGACAGCATCTTC 1172
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; QY 312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
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; DB 1173 TTCCTGTGCTGTCACTCCATCCATCTCTCTGACACCTGCGCGAGCTGAAG 1232
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; DB 1233 GCCGTGGACATATCTGCAAGCTGAATGCTCTTCCCGTGGCATCACATGTGTGAG 1292
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; QY 352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
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; DB 1293 TTCCTGGGCTGGCCACTGCTGCTCAACCCCATGCTCTACATCTTGCGCGGCGAGAG 1352
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; QY 372 PheArgGlnArgMetTyrMetLeuLeuAlaGlyLeuGlyCysProAsnGlnArgGlyLeu 391
; ||||| :||| :||| :|||
; DB 1353 TTCCTCAGTGAACCTGTGCGGCTCTGTGACAGAGCTGGGTGACCGGCTCTCCCTG 1412
;
; QY 392 GlnArgGlnProSerSerArgArgAspSerSerTyrSerGlnThrSerGlnLaser 411
; :||| :||| :||| :|||
; DB 1413 TCCCAAGCTTCTCCCTAAGCTGCGCGCAGG---AGCAGTCTCTGAGTCAAGATGACCCACC 1469
;
;
; RESULT 9
; US-08-805-478-5
; Sequence 5, Application US/08805478
; Patent No. 5874543
;
; GENERAL INFORMATION:
; APPLICANT: Chunharapal, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: ANTIBODIES TO PFA RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
```

```

ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-805-478-5

Alignment Scores:
Pred. No.: 3,36e-61 Length: 1679
Score: 635.00 Matches: 147
Percent Similarity: 54.72% Conservative: 50
Best Local Similarity: 40.83% Mismatches: 145
Query Match: 29.52% Indels: 18
Gaps: 8

US-09-101-518a-2 (1-415) x US-08-805-478-5 (1-1679)
QY 67 LeuGluAsnPheserSerSerTyr-----AspTyrGlyGluAsnGluSerAsp--- 82
Db 399 CTCGAGAACCTGGAGACCTCTTGTGGAACTGACAGATTGGACACTATAAGCACACC 458
QY 83 SerCysCysThrSerProCysProGln-----AspPheSerLeuAsnPheser 99
Db 459 TCCCTGGTGAATAATCATCTTGTCCCTGCCACAGAGGGGCCCTCAGCCCTTCAAG 518
QY 100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuGlyAsnGly 119
Db 519 GCCGTGTTGCGCCGGCGGCTACAGCCTCATCTTCCCTCGGGCGGATGGCAGACCTC 578
QY 120 AlaValAlaValAlaLeuLeuSerArgThrAlaLeuSerSerThrAspThrPheLeu 139
Db 579 CTGGTGTGTGATCTCGAGCCGACCGGACAGCAGCACTTCACGAGACCTTCTCTG 638
QY 140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuThrAlaValAsp 159
Db 639 TTCACACCTGGCGCGGCGGACCTCTGCTGTTCATCTTGGCCGTCGCGGCGGAG 698
QY 160 AlaAlaValGlnThrValPheGlySerGlyLeuCysIysValAlaGlyAlaLeuPheAsn 179
Db 699 GCGCTGTGGGCTGGGCTGCGGAGACCTTCTCTGCAAAACTGATTCGCCCTGCACAA 758

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QY 180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
Db 759 GTCAACTTCTTACTGACGACGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 818
QY 200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
Db 819 ATTGTCCACGCCGCTCCATGCTCACCAGCCAGCCGCCCTCTCTCCATCATCATCTGCT 878
QY 220 LeuAlaValITrpglyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu----- 237
Db 879 GGGACCATCTGGCTGGTGGGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 938
QY 238 ---SerAlaHisHisAspGlnArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
Db 939 AGCCAGGCCCATCACACAACTCCTG-----CCAGCTTGACCTTCTCCACAGAGAAC 992
QY 257 ValGlyArgThr-----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
Db 993 CAGCAGAAACCGCATGCTGCTGCTCACCCTCCGATTCCTCTACCATGTGGCGGATTCCTG 1052
QY 273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
Db 1053 CTGCCCATGTGTGATGATGGCTGTGTGTACGTTGGGGGTAGTGCACAGGTGGCGCAGGCC 1112
QY 292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValAlaValAlaPhe 311
Db 1113 CAGCGGCCCTCCAGCGGCGCAGAGCACTGACAGGGGCCATCTGTTGACAACTCTTTC 1172
QY 312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAlaPheLeuMetAspLeuGly 331
Db 1173 TTCTCTGCTGTGCTACCTTACCATCATCTCTCTCTGACACCTTGGCAGGCTGGAAG 1232
QY 332 AlaLeuAlaArgAsnCysGlyArgGlnSerArgValAlaValAlaIysSerValThrSer 351
Db 1233 GCCGTGACAATATCCTGCAGAGCTGAATGCTCTCTCCCGTGGCATCATCATGTGTGAG 1292
QY 352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyAlaIys 371
Db 1293 TTCTGTGGGCTGGGCCACTGCTGCTCAACCCAGCTCACTTCTGCTGCTGCTGCTGAG 1352
QY 372 PheArgGluArgMetTrpMetLeuLeuLeuLeuGlyCysProAsnGlnArgGlyLeu 391
Db 1353 TTCCGCAATGACCTTCCGCGGCTCTGCTGACAGAGCTGGGCTGTACGGCGCTCCCTG 1412
QY 392 GlnArgGlnProSerSerArgArgAspSerSerTrpSerGlnThrSerGlnAlaSer 411
Db 1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTGAGTACAGAGATCCACC 1469

RESULT 10
US-08-802-627A-5
Sequence 5, Application US/08802627A
Patent No. 5892017
GENERAL INFORMATION:
APPLICANT: Lee, James
TITLE OF INVENTION: NUCLEIC ACID ENCODING PFAA RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,627A
FILING DATE: 19-Feb-1997

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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2PID2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-802-627A-5

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Alignment Scores:
Pred. No.: 3,366-61 Length: 1679
Score: 635.00 Matches: 147
Percent Similarity: 54.72% Conservatave: 50
Best Local Similarity: 40.83% Mismatches: 145
Query Match: 29.52% Indels: 18
DB: 2 Gaps: 8

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US-09-101-518A-2 (1-415) x US-08-802-627A-5 (1-1679)

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OY 67 LeuGIuAsnPhSeSerSerTyR-----AspTYRgLyGIuAsnGluSerAsp--- 82
Db 399 CTCGAGAACCTGAGACCTGTTGGGAACCTGACACATGTGCAACATATACGACACC 458
OY 83 SerCySgYThSerProCySProGln-----AspPhSeSerLeuAsnPhSeasp 99
Db 459 TCCTGGGTGGAAATCATCTGCTGCGCCGACAGAGGGGCCCTCATGGCCCTTCAAG 518
OY 100 ArgAlaPheLeuProAlaLeuTySerLeuLeuPheLeuGlyLeuLeuGlyAsnGly 119
Db 519 GCCGCTGTCGTCGCCGCGCCACACCTCATCTCTCTGCGGTATGCGCAACGTC 578
OY 120 AlaValAlaAlaValLeuLeuSerArgArgThraAlaLeuSerSerThraSphrPheLeu 139
Db 579 CTGTGCTGTGATCTGTGAGCGGACCGACGACGACGAGATTTCACGAGACCTCTG 638
OY 140 LeuHISLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuThrAlaValAsp 159
Db 639 TTCACCTGGCGCGTGGACCTGCTGCTGCTCATCTTGCCTTTGCGCGTGGCGGAG 698
OY 160 AlaAlaValAlaValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
Db 699 GGCTGTGCGGTGGTCTGCGGACCTTCCTGCAAAACGTGATGTCCTCGACAA 758
OY 180 IleAsnPheTyAlaGlyAlaLeuLeuLeuAlaCysLLeSerPheAspArgTyRLeuAsn 199
Db 759 GTCACTTCTACTGACAGACCTGCTGCGCTGCATGCGCGTGGACCGTACCTGGCC 818
OY 200 IleValHISAlaThrGlnLeuTyArgArgGlyProProAlaArgValThrLeuThrCys 219
Db 819 ATGTGCAAGCGCGTCAATGCTACCGCACCGCGCTCTTCATCCATCCATCATCTGT 878
OY 220 LeuAlaValTTPGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu----- 237
Db 879 GGGACCATCTGCGTGGTGGCTTCTCTGCTTGCCTTGCACAGATTTCTTCCGCAAGTC 938
OY 238 ---SerAlaHISHisAspGluArgLeuAsnAlaThrHIScysGlnTyRAsnPhProGln 256

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Db 939 AGCCAGGCCATCACACAACTCCCTG-----CCAGCTTGCACCTTCTCCCAAGAAC 992
OY 257 VALGlyArgThr-----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
Db 993 CAGCAGAAACGATGCTGCTGACCTCCGATTCCTTCCATTCAGGTCGGGATTCCTG 1052
OY 273 LeuProLeuLeuValMetAlaTyrcysTyraLanHisIleLeuAlaValLeu---LeuVal 291
Db 1053 CTGCGCATGCTGTGATGGCGGTGCTACAGTGGGGGATGATGACAGATGTGGCCAGGCC 1112
OY 292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValAlaValAlaValAlaPhe 311
Db 1113 CAGCGCGCCCTCACCGGACAGAGCAGTCAAGGTGGCCATCTGTCAGAACGATCTTC 1172
OY 312 AlaLeuCysTTPThrProTyHISLeuValValLeuValAlaSPHLeuMetAspLeuGly 331
Db 1173 TTCCTGTGTGTCACCTTACATGTCATCTTCTGGACACCTTGGCGGCGCTGAG 1232
OY 332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
Db 1233 GCCGTGGACATACCTGCAAGCTGAATGCTCTCCCGTGGCATCACCATGTGTGAG 1292
OY 352 GlyLeuGlyTyRMetHIScysCysLeuAsnProLeuLeuTyRAlaAlaPheValGlyValys 371
Db 1293 TTCCTGGGCGCTGGCCACCTGCTGCTCAACCCCATGCTTCACTTCCGCGCGCTGAG 1352
OY 372 PheArgGluArgMetTTPMetLeuLeuArgLeuGlyCysProAsnGluArgGlyLeu 391
Db 1353 TTCGCGAGTACCTGTGCGGCTGCTGACGAGGTGGGTGACCGGCCCTGCTCCCTG 1412
OY 392 GlnArgGlnProSerSerSerArgArgAspSerSerTTPSerGluThrSerGluLaser 411
Db 1413 TGCACGCTCTTCCCTACGCTGGCGCAGG---ACCACCTCTCTGATCAGAGATCCAC 1469

RESULT 11
US-08-801-238-5
; Sequence 5, Application US/08801238
; Patent No. 5919896
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: P74A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID1

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-801-238-5

Alignment Scores:
Pred. No.: 3,366-61
Score: 635.00
Percent Similarity: 54.72%
Best Local Similarity: 40.83%
Query Match: 29,52%
Gaps: 8

US-09-101-518a-2 (1-415) x US-08-801-238-5 (1-1679)

OY 67 LeuGIuAsnPhSeSerSerTyT-----AspTYrGlyGluAsnGluSerAsp--- 82
Db 399 CTGAGAACTGGAGACCTGTCTGGGAAGTGGACAGATTGGACAATGAACAGCACCC 458
OY 83 SerCysCysThrSerProProCysProGln-----AspPheSerLeuAsnPhSeAsp 99
Db 459 TCCCTGGTGGAAAATCATCTGTGCGCCACAGAGGGCCCTCATGGCCCTTCGCAAG 518
OY 100 ArgAlaPheLeuProAlaLeuTySerLeuLeuPheLeuGlyLeuLeuGlyAsnGly 119
Db 519 GCCGCTTCGTCGCCGCGGCTGACAGCCCTCATCTCTGCGCTGATTCGCAACGTC 578
OY 120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
Db 579 CTGGTCTGCTGATCGACGCGGACGCGACAGACAGCATTCACAGGAGAGACTTCCTG 638
OY 140 LeuHisLeuAlaValAlaAspThrLeuValLeuThrLeuProLeuThrAlaValAsp 159
Db 639 TTCACACCTGGCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 698
OY 160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
Db 699 GGCCTGTGGCGGTGGGCTCTGCGGACCTTCCTGTGAAACGTGATTCCTCCGCAANA 758
OY 180 IleAsnPheTyAlaGlyAlaLeuLeuLeuAlaCysLysSerPheAspArgTyLeuAsn 199
Db 759 GTCACTTCTACTGCGAGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 818
OY 200 IleValHisAlaThrGlnLeuTyArgArgGlyProProAlaArgValThrLeuThrCys 219
Db 819 ATTGTCCAGCGCGTCCATGCCACCGCCGCCCTCTCTCCATCCATCCATCCATCCATCT 878
OY 220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu----- 237
Db 879 GGGACCATCTGGCTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 938
OY 238 ---SerAlaHisHisAspGlnArgLeuAsnAlaThrHisCysGlnTrpAsnPhProGln 256
Db 939 AGCCAGGCGCATCACACAACTCCCTG-----CCACGTTGCACCTTCTCCCAAGAGAAC 992
OY 257 ValGlyArgThr-----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
Db 993 CAAAGAGAAAGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1052
OY 273 LeuProLeuLeuValMetAlaTyCysTyAlaHisIleLeuAlaValLeu---LeuVal 291
Db 1053 CTGGCCATGCTGGTGGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1112
OY 292 SerAlaGlyGlnArgArgLeuArgAlaMetArgLeuValValValValAlaPhe 311
Db 1113 CAGCGGCGCCCTCAGCGGAGAGAGAGTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1172

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OY 312 AlaLeuCysTrpThrProTyRHisLeuValValLeuValAlaPheLeuMetAspLeuGly 331
Db 1173 TTCCTCTGCTGGTACACCTTACCACTGTCATCTTCTGACACCTTGGCGAGGCTGAAG 1232
OY 332 AlaLeuAlaArgAsnGlyArgGlnSerArgValAspValAlaLysSerValThrSer 351
Db 1233 GCGGTGGACAAATACCTGCAAGCTGAATGGCTCTCCCGGTGGCCATTCACATGCTGAG 1292
OY 352 GlyLeuGlyTyRMetHisCysCysLysAsnProLeuLeuTyRAlaPheValGlyValLys 371
Db 1293 TTCCTGGCGCTGGCCCACTGCTGCTCAACCCCATCTCTACACTTCCGCGCGTGAAG 1352
OY 372 PheArgGlnArgMetThrPheLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
Db 1353 TTCGCGAGTACCTGTCGCGGCTCTGACAGAACTGGCTGTACCGGCGCTGCTCTG 1412
OY 392 GlnArgGlnProSerSerSerArgArgAspSerSerTyRSerGlnThrSerGlnAlaSer 411
Db 1413 TGGCAGCTCTTCCCTGATGCGGCGAGG---AGCAGTCTCTGAGTCAAGATGCCACC 1469

RESULT 12
US-08-801-228-5
; Sequence 5, Application US/08801228
; Patent No. 5922541
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,228
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1679 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-801-228-5

Alignment Scores:

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Pred. No.:	3,366-61	length:	1679
Score:	655.00	Matches:	147
Percent Similarity:	55.72%	Conservative:	50
Best Local Similarity:	40.83%	Mismatches:	145
Query Match:	29.52%	Indels:	18
DB:	2	Gaps:	8

US-09-101-518A-2 (1-415) x US-08-801-228-5 (1-1679)

QY	67	LeuGluIAspHeuSerSerSerTyr-----AspTyrGlyGlnAsnGlySerAsp---	82
Db	399	CTCGAGAAACCTGGAGGACCGCTTCTGGGAACGTGCAGACAGATTGGACAACATTATACGACACC	458
QY	83	SeTcysCysThrSerProProCysProGln-----AspPheSerLeuAsnPheAsp	99
Db	459	TCCCTGGTGGAAATATCATCTCTCCCTGGCACAGAGAGGGCCCTCATGAGCTCTTCTAAG	518
QY	100	ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGlyLeuLeuGlyAsnGly	119
Db	519	GCCGTGTCCTGGCCCGTGGCCATACACCCATCTTCCTGGGGGTATGGCAACATC	578
QY	120	AlaValAlaAlaValLeuLeuSerArgTrpAlaLeuSerSerTyrAspThrPheLeu	139
Db	579	CTGGTCTGGTGAATCTCTGGAGCGGACCGGACAGACAGAGTTCACAGGACCTTCTCG	638
QY	140	LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTPrAlaValAsp	159
Db	639	TTCACCTGGCCGCTGGCGCCACCTCTGCTGTCATCTTCCCTTTGGCCGTGGCCAG	698
QY	160	AlaAlaValGlnTrpValPheGlySerGlyLeuCysGlyValAlaGlyAlaLeuPheAsn	179
Db	699	GCGCTGTGGGTGGCTGGCTGGGAGCTTCCTGTGAATAACGTGATGGCCCTGCACAA	758
QY	180	IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn	199
Db	759	GTCACACTTCTACGACAGACACCTGCTCTGGCTGATGCCGTGGACCGCTACTGGCC	818
QY	200	IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys	219
Db	819	ATTGTCCACCCGCTCATGCGCTCCGCCACCGCCGCTCTCTTCATCCATCCATCCGT	878
QY	220	LeuAlaValThrGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu-----	237
Db	879	GGGACCATCTGGCTGGTGGCTTCCTTCGGCTGGCCAGAAATCTCTGGCCAAAGTC	938
QY	238	---SerIAsHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln	256
Db	939	AGCCAGACGCATGCACAAACACTCCG-----CCACGTGCACCTTCTCCCAAGAGAAC	992
QY	257	ValGlyArgThr-----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu	272
Db	993	CAGACGAACAAACGATCGCTGGTTCACCTCCGATTCCTTACATGATGGAGATTCTCG	1052
QY	273	LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal	291
Db	1053	CTGGCCCAATGGTGGATGGCTGGCTCTACGTTGGGGGTATGCCACAGGTGGCGCAGCC	1112
QY	292	SerArgGlyGlnArgGluLeuArgAlaMetArgLeuValValValValAlaPhe	311
Db	1113	CAGGGGGCCCTCAGCGCGAGGAAGGACAGGTGGGATCTCTGTATACAAAGCATTTCT	1172
QY	312	AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly	331
Db	1173	TTCCTGTGCTGGTACCCCTACATCGATCTTCCTGGACACCTGGCGAGGTGAAG	1232
QY	332	AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer	351
Db	1233	GCGCTGGACAATGCTGCAGAGCTGAATGGCTCTCCCGCTGGCCATGCACATGTGTAG	1292
QY	352	GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuTyrAlaPheValGlyAlaLys	371
Db	1293	TTCCTGGGCTGGCCCACTCTCCCTCAACCCCATAGCTCTTACACTTTTGCCGGCGTGAAG	1352

Oy	372	Phearglunargmetrmpelmeleluarleglylcysproalnglnarglyleu	391
		:	
Dd	1353	TTCGGCAGTACCTGTGCGGGCTCTGACGAACCTGGCTGACCGCCCTCCCTCG	1412
		:	
Oy	392	GlnarginproserSerargatgaspberSerTrpsergluthSerqlualaser	411
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RESULT 13
US-09-104

; sequence 3, Application US/091042396
; Patent No. 6087475

APPLICANT: Lee, J

TITLE OF INVENTION: PF4A Receptors

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech Inc

STREET: 1 DNA way
CITY: South San Francisco

COUNTRY: USA

COMPUTER READ
MEDICINE

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: MINIFLUX (GENERIC)
;
; CURRENT APPLICATION DATA:

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FILING DATE: 24-June-1998

PRIOR APPLICATION NUMBER

;; FILING DATE: 22-AUG-1990
;; PRIOR APPLICATION DATA:

FILING DATE: 06-JUN-1996

APPLICATION NUMBER: 08/076093

APPL.ICATION NUMBER: 07/810782

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 34,659

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/725-5530

TELEFAX: 413/952-9881
TELEX: 910/371-7168

SEQUENCE CHARACTERISTICS:

TYPE: Nucleic Acid

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;          TOPOLOGY:  Linear
ITS-09-104-296-5

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Alignment Scores:

Score: 635.00

Best Local Similarity: 40.83%

DB: 3

03-09-101-3104-2 (1-413) X 03-09-104-290-3 (1-10/9)

[illegible]

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Qy 100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGlyLeuLeuGlyAsnGly 119
Db 519 GCCGTGTTGCGCGCGGCTACAGCCTCATCTTCCTCGGGCGGTATGGCAACCTC 578
Qy 120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
Db 579 CTGCTGCTGGTACTGACAGCGGACCGGACAGACACGACGATCCACAGGAGACCTTCTG 638
Qy 140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
Db 639 TTCACACCTGGCGCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 698
Qy 160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysValAlaGlyAlaLeuPheAsn 179
Db 699 GGCCTGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTG 758
Qy 180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
Db 759 GTCAACTTCTACTGACAGCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 818
Qy 200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
Db 819 ATTGTCCACGCGGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 878
Qy 220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu----- 237
Db 879 GGGACCATGTCGCGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 938
Qy 238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
Db 939 AGCCAGAGCCCTCAACCACTCCCTG-----CCAGCTGACACTCTCTCCCAAGAGAAC 992
Qy 257 ValGlyArgThr-----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
Db 993 CAAGCAGAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1052
Qy 273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
Db 1053 CTGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1112
Qy 292 SerArgGlyGlnArgGlyLeuArgAlaMetArgLeuValValAlaValAlaPhe 311
Db 1113 CAGGCGGCGCTCAGCGGAGAGAGATCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1172
Qy 312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAlaPheLeuMetAspLeuGly 331
Db 1173 TTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1232
Qy 332 AlaLeuAlaArgAsnGlyArgGlnSerArgValAspValAlaIleValSerValThrSer 351
Db 1233 GCCGTGACATACCTGCAAGCTATGCTCTCTCCCGGCGGCTGCAATGCTGCTGCTGCTG 1292
Qy 352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValIys 371
Db 1293 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1352
Qy 372 PheArgGlyGlnArgMetTrpMetLeuLeuArgGlyGlyCysProAsnGlnArgGlyLeu 391
Db 1353 TTCGCGAGTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1412
Qy 392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGlnThrSerGlyAlaSer 411
Db 1413 TGCACAGCTTCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1469

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RESULT 14
 PCT-US94-06380-3
 ; Sequence 3, Application PC/TUS9406380

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; GENERAL INFORMATION:
; APPLICANT: Chuntcharapal, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: K. Jin Kim
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY DISORDERS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1679 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US94-06380-3

Alignment Scores:
Pred. No.: 3,36e-61 Length: 1679
Score: 635.00 Matches: 147
Percent Similarity: 54.72% Conservative: 50
Best Local Similarity: 40.83% Mismatches: 145
Query Match: 29.52% Indels: 18
DB: 5 Gaps: 8

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Db 399 CTCGAGAACCTGGAGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAGACACC 458
Qy 83 SerCysCysThrSerProProCysProGln-----AspPheSerLeuAsnPheasp 99
Db 459 TTCCTGGTGGAAATCATCTCTGCTGCTGCCACAGAGGGGCCCTTCATGGCTCTTCAAG 518
Qy 100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGlyLeuLeuGlyAsnGly 119
Db 519 GCCGTGTTGCGCGGCTACAGCCTCATCTTCCTCGGGCGGTATGGCAACCTC 578
Qy 120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
Db 579 CTGCTGCTGGTACTGACAGCGGACCGGACAGACGACGATCCACAGGAGACCTTCTG 638
Qy 140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
Db 639 TTCACACCTGGCGCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 698

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      ::::::::::::::::::::
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Qy 200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
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Qy 220 LeuAlaValTrrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu----- 237
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Db 879 GGCACCATCTGCTGGTGGCTCTCTCTGCTGCGACAGATTCCTTGGCCAAAGTTC 938
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Db 993 CAGAGAGAAAGCATGCTGCTGCTACCTCCGATTCCTCTACCATGTGGCGGATTCCTG 1052
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Qy 273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
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Db 1053 CTGCCCATGCTGTGTGATGGCTGTGTACGTGGGGGTAGTGACAGATTTGGCGCAGGCC 1112
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Qy 292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValAlaValAlaAlaPhe 311
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Db 1113 CAGGGGCGCCCTCAGCGGACAGAGCATGAGGTGGCCATCTGTGTACAAAGCATCTTC 1172
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Qy 312 AlaLeuCysTrrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspGly 331
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Db 1173 TTCCTCTGCTGTGATGCTTACCATCTCTCATCTCTGACACCTGCGCAGGCTGTGAAG 1232
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Qy 332 AlaLeuAlaArgAsnCysGlyArgGlnSerArgValAspValAlaIleValSerValThrSer 351
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Db 1413 TGCAGGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAAGAAATGCCACC 1469
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      SOFTWARE: patin (Genentech)
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/202,056
      FILING DATE: 25-FEB-1994
      CLASSIFICATION: 436
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 07/677211
      FILING DATE: 29-MAR-1991
      ATTORNEY/AGENT INFORMATION:
      NAME: Love, Richard B.
      REGISTRATION NUMBER: 34,659
      REFERENCE/DOCKET NUMBER: 706P3
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 415/225-5530
      TELEFAX: 415/952-9881
      TELEX: 910/371-7168
      INFORMATION FOR SEQ ID NO: 8:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 1748 bases
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      US-08-202-056-8

Alignment Scores:
Pred. No.: 3,58e-61 Length: 1748
Score: 635.00 Matches: 146
Percent Similarity: 53.56% Conservative: 57
Best Local Similarity: 38.52% Mismatches: 136
Query Match: 29.52% Gaps: 40
DB: 1

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Qy 70 Phe-----SerSerSerTyrAspTrrpGlyGlnAsnGlnSerAspSerCys 84
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Qy 125 LeuLeuSerArgArgThrAlaLeuSerSerThrArgPheLeuLeuHisLeuAlaVal 144
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Qy 145 AlaAspThrLeuLeuValLeuLeuThrLeuProLeuTrrpAlaValAspAlaAlaValGlnTrp 164
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Db 388 ATTTTGGACATTCCTGTGCAAGGTGGTCTACCTCTGCAAGAGATCACTTCTATAGT 447
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Qy 185 GlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThr 204
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Db 448 GGCATCTGCTACTGCGCTGTGATGCTGAGCCGTTACCTGGGCCATTGTCCATGCCACA 507
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Qy 205 GlnLeuTyrArgArgGlyProProAlaArgValThrLeuThr----- 218
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Db 508 CGC-----ACACTGACCCAGAAAGCGCTACTGTGCTC 537
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Db 598 TTCCGAAGACCGGTACTCATCAATGTTAGCCAGCC--TGC-----TATGAG 645
Oy 256 GlnValGly-----ArgThrAlaLeuArgValLeuGlnLeuValAla 269
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Db 646 GACATGGGCAACAAATACAGCAAACTGGGGGATGCTGTACGATCCTGGCCCACTCCTT 705
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Db 766 TTTAAGGCCACATGGGGCAGAGCACCGGCCATGCGGGTCATCTTGTCTGTCCTC 825
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Db 826 ATCTTCCTGCTTGTGCTGGCTGACCAACCTGCTGCTGCTGCGAGACACCTCATGAGG 885
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Job time : 73 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2002, 06:28:13 : Search time 66 Seconds
(without alignments)
698.419 Million cell updates/sec

Title: US-09-101-518A-2

Perfect score: 2151

Sequence: 1 MELRKYPGRGLAGTVIGGAA.....SSRRDSSWSETSASYSGL 415

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :

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- 2: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
- 6: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
- 7: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
- 8: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
- 9: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
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- 13: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
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- 21: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDSL1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2142	99.6	415	18	AAW19780
2	2136	99.3	472	22	AAW19780
3	1909	88.7	378	20	AAW50129
4	1891	87.9	368	19	AAW54371
5	1891	87.9	368	21	AAW50614
6	1891	87.9	368	22	AAW50614
7	1885	87.6	368	21	AAW50648
8	1626.5	75.6	367	19	AAW59999
9	640	29.8	374	20	AAW50643
10	637.5	29.6	399	22	ABG13609
11	637.5	29.6	399	22	ABW12024

12	635	29.5	372	13	AAW27793	New platelet facto
13	635	29.5	372	16	AAW92239	Chemokine superfam
14	635	29.5	372	16	AAW68813	Human lymphocyte p
15	635	29.5	372	20	AAW50644	Human Burkitt's ly
16	635	29.5	372	21	AAW50627	Human G protein-co
17	635	29.5	372	22	AAW80124	Human CXCR5 protei
18	635	29.5	378	22	ABW11873	Human Burkitt lymph
19	633	29.4	355	14	AAW33420	Human IL-8 recepto
20	633	29.4	355	17	AAW09990	Human IL-8 recepto
21	633	29.4	360	13	AAW28273	Sequence in a low
22	633	29.4	360	16	AAW80758	Interleukin 8 rece
23	633	29.4	372	21	AAW80121	Human CXCR2 protei
24	633	29.4	372	21	AAW90661	Human mutant G pro
25	626.5	29.1	1064	16	AAW70124	IL-8 type 2-GFP 1
26	618	28.7	360	16	AAW80953	Recombinant high a
27	615.5	28.6	355	13	AAW28272	Sequence in a high
28	615.5	28.6	355	16	AAW80950	Recombinant high a
29	615	28.6	358	16	AAW80952	Recombinant high a
30	605.5	28.1	350	16	AAW68811	Interleukin-8 rece
31	605.5	28.1	350	16	AAW80756	Interleukin-8 rece
32	605.5	28.1	350	16	AAW80951	Interleukin 8 rece
33	605.5	28.1	350	17	AAW09989	Recombinant high a
34	605.5	28.1	350	22	AAW80120	Human IL-8 recepto
35	605.5	28.1	1060	16	AAW70123	IL-8 type 1-GFP 1
36	600.5	27.9	350	13	AAW27791	Interleukin-8 rece
37	589.5	27.4	410	15	AAW53743	Putative seven tra
38	589.5	27.4	410	19	AAW48723	Polypeptide sequen
39	589.5	27.4	410	21	AAW21687	Genomic clone of 7
40	588.5	27.4	569	22	ABG12373	Novel human diagno
41	586	27.2	358	15	AAW53745	Partial sequence o
42	586	27.2	358	21	AAW21689	Human 7TM receptor
43	586	27.2	378	19	AAW48724	Human V31 seven tr
44	586	27.2	378	21	AAW21688	Human 7TM receptor
45	586	27.2	378	21	AAW90629	Human G protein-co

ALIGNMENTS

RESULT 1
AAW19780 standard; Protein: 415 AA.

AAW19780:
28-SEP-1997 (first entry)

Human G-protein chemokine receptor HSATU68.

HSATU68: G-protein chemokine receptor; 7-transmembrane receptor;
signal transduction; therapy; diagnosis; agonist; antagonist;
antibody.

Hom sapiens.
W09725340-A1.

17-JUL-1997.

11-JAN-1996; 96WO-US00499.

11-JAN-1996; 96WO-US00499.

(HUMA-) HUMAN GENOME SCI INC.

L1 Y;
WPI: 1997-372810/34.
N-PSDB: AAT72800.

DNA encoding new isolated human G-protein chemokine receptor - used
to develop products for treating, e.g. autoimmune diseases, chronic
infections, allergy, malignancy, inflammation or shock

XX Claim 13; Fig 1a-d; 54pp; English.
PS A newly identified human 7-transmembrane receptor (AAW19780) has been
XX putatively identified as a chemokine receptor or HSATU68. Its amino
CC designated G-protein chemokine receptor or HSATU68. From an
CC acid sequence was deduced from a cDNA clone (AA72800) obtd. from an
CC activated T-cell library. The protein shows 39.31% identity and
CC 58.405% similarity to human interleukin-8 receptor. Recombinant
CC HSATU68 can be expressed in prokaryotic or eukaryotic host cells
CC and used to raise antibodies or to screen for agonists or
CC antagonists useful in the treatment of conditions associated with
CC chemokine receptor under- or overexpression. Gene therapy can be
CC used to express HSATU68 in vivo as a means of treating conditions
CC related to receptor underexpression.
XX
XX Sequence 415 AA:
SQ
Query Match 99.6%; Score 2142; DB 18; Length 415;
Best Local Similarity 99.8%; Pred. No. 1.2e-236;
Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MELRYGPGRLAGTYIGGAOSKSDTKKEFLPGLYTAPSSPPPSQVSDHQV LND 60
Db 1 MELRYGPGRLAGTYIGGAOSKSDTKKEFLPGLYTAPSSPPPSQVSDHQV LND 60
QY 61 AEVAALLENFSSSYDYGGENESDSCCTSPPCQDFSLNEDRAFLPALYSILFLGLGNGA 120
Db 61 AEVAALLENFSSSYDYGGENESDSCCTSPPCQDFSLNEDRAFLPALYSILFLGLGNGA 120
QY 121 VAAVLISRTALSTDTFELHLAVADTLVTLPLMAVDAVQWVFGSGLCKVAGALENI 180
Db 121 VAAVLISRTALSTDTFELHLAVADTLVTLPLMAVDAVQWVFGSGLCKVAGALENI 180
QY 181 NFYAGALLIACISFDRYLIYHATOLYRRGPARVTLCTLAWGICLLEFALDFTFLSH 240
Db 181 NFYAGALLIACISFDRYLIYHATOLYRRGPARVTLCTLAWGICLLEFALDFTFLSH 240
QY 241 HDERLNATHCOYNFPOVGRFALRVQLVAGFLPLLYMAVCYAHILAVLVSRGORRLRA 300
Db 241 HDERLNATHCOYNFPOVGRFALRVQLVAGFLPLLYMAVCYAHILAVLVSRGORRLRA 300
QY 301 MRLVVVVVVAFAALCWTPTLHVLDLMDLGLARNCGRESRYDVAKSVTSGIGYWHCCL 360
Db 301 MRLVVVVVVAFAALCWTPTLHVLDLMDLGLARNCGRESRYDVAKSVTSGIGYWHCCL 360
QY 361 NPLLYAFVGVKFRERMMILLRLGCPNORGLOROPSSSRDSSWSSETSEASTSGL 415
Db 361 NPLLYAFVGVKFRERMMILLRLGCPNORGLOROPSSSRDSSWSSETSEASTSGL 415
RESULT 2
AA675628
ID AAG75628 standard; Protein: 472 AA.
XX
AC AAG75628;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:6192.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
RV colorectal carcinoma; chromosome 8.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.

PR 03-NOV-1999; 99US-0163280.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
XX
DR N-PSDB; AAH35033.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX Claim 11; Page 7873-7875; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 472 AA:
Query Match 99.3%; Score 2136; DB 22; Length 472;
Best Local Similarity 99.5%; Pred. No. 6.9e-236;
Matches 413; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MELRYGPGRLAGTYIGGAOSKSDTKKEFLPGLYTAPSSPPPSQVSDHQV LND 60
Db 58 MELRYGPGRLAGTYIGGAOSKSDTKKEFLPGLYTAPSSPPPSQVSDHQV LND 117
QY 61 AEVAALLENFSSSYDYGGENESDSCCTSPPCQDFSLNEDRAFLPALYSILFLGLGNGA 120
Db 118 AEVAALLENFSSSYDYGGENESDSCCTSPPCQDFSLNEDRAFLPALYSILFLGLGNGA 177
QY 121 VAAVLISRTALSTDTFELHLAVADTLVTLPLMAVDAVQWVFGSGLCKVAGALENI 180
Db 178 VAAVLISRTALSTDTFELHLAVADTLVTLPLMAVDAVQWVFGSGLCKVAGALENI 237
QY 181 NFYAGALLIACISFDRYLIYHATOLYRRGPARVTLCTLAWGICLLEFALDFTFLSH 240
Db 238 NFYAGALLIACISFDRYLIYHATOLYRRGPARVTLCTLAWGICLLEFALDFTFLSH 297
QY 241 HDERLNATHCOYNFPOVGRFALRVQLVAGFLPLLYMAVCYAHILAVLVSRGORRLRA 300
Db 298 HDERLNATHCOYNFPOVGRFALRVQLVAGFLPLLYMAVCYAHILAVLVSRGORRLRA 357
QY 301 MRLVVVVVVAFAALCWTPTLHVLDLMDLGLARNCGRESRYDVAKSVTSGIGYWHCCL 360
Db 358 MRLVVVVVVAFAALCWTPTLHVLDLMDLGLARNCGRESRYDVAKSVTSGIGYWHCCL 417
QY 361 NPLLYAFVGVKFRERMMILLRLGCPNORGLOROPSSSRDSSWSSETSEASTSGL 415
Db 418 NPLLYAFVGVKFRERMMILLRLGCPNORGLOROPSSSRDSSWSSETSEASTSGL 472
RESULT 3
AA550129
ID AA550129 standard; Protein: 378 AA.
XX

AC AAY50129;
 XX
 DT 31-JAN-2000 (first entry)
 XX
 DE Human chemokine receptor CXCR3b.
 XX
 KW Chemokine receptor; CXCR3b; splice variant; N-terminus; CXCR3a;
 KW seven transmembrane; G-protein coupled; CXCR3; IP10; MIP; T-lymphocyte;
 KW recruitment; selective; activated; T-cell; neutrophil; inflammation;
 KW tissue distribution; therapy; rheumatoid arthritis; psoriasis;
 KW multiple sclerosis; transplantation; atherosclerosis; restenosis;
 KW cytokine; delayed type hypersensitivity reaction.
 OS Homo sapiens.
 XX
 PN MO9950299-A1.
 XX
 PD 07-OCT-1999.
 XX
 PE 26-MAR-1999; 99MO-SE00501.
 XX
 PR 30-MAR-1998; 98SE-0001098.
 XX
 PA (ASTR) ASTRA PHARM LTD.
 PA (ASTR) ASTRA AB.
 XX
 PI Delaney S;
 XX
 DR WPI: 1999-633638/54.
 DR N-PSDB: AA232713.
 XX
 PT New polynucleotide encoding a variant chemokine receptor
 PS Claim 6: Fig 4: 18pp: English.
 XX
 CC This sequence represents human chemokine receptor CXCR3b, a splice
 CC variant of chemokine receptor CXCR3 (also referred to as CXCR3a).
 CC Chemokines are a family of small cytokines which bring about the
 CC recruitment of leukocytes during inflammation. The CXCR3 chemokines
 CC mostly attract neutrophils, while the CC chemokines are less selective.
 CC All chemokine receptors are seven transmembrane G-protein coupled
 CC receptors and most are receptors for a number of chemokines, CXCR3a
 CC being a receptor for the CXCR3 chemokines IP10 and MIP. CXCR3a is
 CC expressed in activated, but not in resting T-lymphocytes, and may
 CC therefore play an important role in the selective recruitment of
 CC T-cells which occurs in T-cell mediated inflammatory conditions.
 CC CXCR3b may have an altered pattern of tissue distribution and
 CC function in the inflammatory process. Cells expressing the active
 CC CXCR3b are useful for identifying ligands, especially agonists and
 CC antagonists, of a chemokine receptor. In addition, the receptor
 CC facilitates identification of chemokines responsible for mediating
 CC inflammation reactions via interaction with CXCR3b. The modulation
 CC of inflammatory responses is of therapeutic benefit in many conditions
 CC such as rheumatoid arthritis, psoriasis, multiple sclerosis,
 CC transplantation, delayed type hypersensitivity reactions, atherosclerosis
 CC and restenosis.
 CC
 XX
 SQ Sequence 378 AA:
 Query Match 88.7%; Score 1909; DB 20; Length 378;
 Best Local Similarity 97.4%; Pred. No. 5,6e-210;
 Matches 370; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

DB 119 MAVDAAVQVWFSSGLCKVAGALFNINFYAGALLLACISFDRLNIYHATOLYRRGPPARV 178
 QY 216 TLTLCLAWGICLLFALPDPFTFLSAHNDERLNATHCOVNFPOVGTALRVQLVAGFLPL 275
 DB 179 TLTLCLAWGICLLFALPDPFTFLSAHNDERLNATHCOVNFPOVGTALRVQLVAGFLPL 238
 QY 276 LVNAVCCYAHILAVILVSRGGRRLRAMRLVYVVVAFALCWTPTYLVVLDLMDGLAR 335
 DB 239 LVNAVCCYAHILAVILVSRGGRRLRAMRLVYVVVAFALCWTPTYLVVLDLMDGLAR 298
 QY 336 NCGRESRVDAKSVTSGLYGHCCCLNPLLYAFVGVKFEREMMLLRGCPNDRGLQROP 395
 DB 299 NCGRESRVDAKSVTSGLYGHCCCLNPLLYAFVGVKFEREMMLLRGCPNDRGLQROP 358
 QY 396 SSSRRDSSMSETSEASVSGL 415
 DB 359 SSSRRDSSMSETSEASVSGL 378
 RESULT 4
 ID AAM54371 standard; Protein: 368 AA.
 XX
 AC AAM54371;
 XX
 DT 14-AUG-1998 (first entry)
 XX
 DE Human IP-10/MIP receptor CXCR3 protein.
 XX
 KW chemokine receptor; cellular signal; treatment; T cell; antitumour;
 KW antiviral; inflammatory disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 22
 FT /note= "N-linked glycosylation site"
 FT Modified-site 32
 FT /note= "N-linked glycosylation site"
 FT Domain 59..79
 FT /note= "TM1 transmembrane domain"
 FT Domain 91..111
 FT /note= "TM2 transmembrane domain"
 FT Domain 127..147
 FT /note= "TM3 transmembrane domain"
 FT Domain 170..190
 FT /note= "TM4 transmembrane domain"
 FT Modified-site 199
 FT /note= "N-linked glycosylation site"
 FT Domain 224..244
 FT /note= "TM5 transmembrane domain"
 FT Domain 257..277
 FT /note= "TM6 transmembrane domain"
 FT Domain 302..322
 FT /note= "TM7 transmembrane domain"
 XX
 PN MO9811218-A1.
 XX
 PD 19-MAR-1998.
 XX
 PE 10-SEP-1997; 97MO-US15915.
 XX
 PR 31-MAR-1997; 97US-0829839.
 PR 10-SEP-1996; 96US-0709838.
 XX
 PA (KOCH-) KOCHER INST THEODOR.
 PA (LEUK-) LEUKOSITE INC.
 XX
 PI Loetscher M, Mackay CR, Moser B, Qin S;
 DR WPI: 1998-207381/18.
 DR N-PSDB: AAV26557.
 XX

PT DNA encoding CXK chemokine receptor 3 - inhibitors and promoters of
PT which, are useful for treatment of inflammation or in anti-tumour or
PT anti-viral therapy
XX
XX
PS Claim 7, Fig 2: 137pp: English.
XX
XX The mammalian CXK chemokine receptor 3 (CXCR3) protein can selectively
CC bind one or more chemokines and can mediate cellular signalling and/or a
CC cellular response in response. Inhibitors and promoters of mammalian
CC CXCR3 can be detected and identified using host cells expressing CXCR3.
CC CXCR3 inhibitors can be used for treatment of inflammatory diseases which
CC are T cell mediated. CXCR3 promoters are useful for antitumour or
CC antiviral therapy.
XX
XX
SQ Sequence 368 AA:
Query Match 87.9%; Score 1891; DB 19; Length 368;
Best Local Similarity 99.7%; Pred. No. 6.3e-208;
Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 51 QVSDHQVLNDAEVAALLLENFSSSYDYGENESDSCCTSPPCPODFSINFDRAPALATYSL 110
:|||||
DB 4 EVSDHQVLNDAEVAALLLENFSSSYDYGENESDSCCTSPPCPODFSINFDRAPALATYSL 63
QY 111 FLGLGNGAVAAVLLSRRTALSTDTFLHLAVDTLLVTLPLMAVDAVQWVEGSG 170
|||||
DB 64 FLGLGNGAVAAVLLSRRTALSTDTFLHLAVDTLLVTLPLMAVDAVQWVEGSG 123
QY 171 CKVAGALFNINFAVALLLACISFDRYLNVHATOLYRRGPPARVTLTCLAVNGLCILFA 230
|||||
DB 124 CKVAGALFNINFAVALLLACISFDRYLNVHATOLYRRGPPARVTLTCLAVNGLCILFA 183
QY 231 LPDFIFLSAHHDERLNATHCOYNEPOVGRTALRVQLVAGFLPLVMAYCYAHIIAVLL 290
184 LPDFIFLSAHHDERLNATHCOYNEPOVGRTALRVQLVAGFLPLVMAYCYAHIIAVLL 243
DB 291 VSRGQRRLRAMRLVYVVVVAFAFCWTPYHLVYLVLDIMDGALARNCGRSRDVAKSVT 350
244 VSRGQRRLRAMRLVYVVVVAFAFCWTPYHLVYLVLDIMDGALARNCGRSRDVAKSVT 303
QY 351 SGLGYMHCCNPLLYAFVGVKFRERMMMLLRLGCPNORGLOROPSSSRDSSMSSETSEA 410
|||||
DB 304 SGLGYMHCCNPLLYAFVGVKFRERMMMLLRLGCPNORGLOROPSSSRDSSMSSETSEA 363
QY 411 SYSGL 415
|||||
DB 364 SYSGL 368
RESULT 5
AAAY90614
ID AAAY90614 standard; Protein; 368 AA.
XX
XX
AC AAAY90614;
XX
DT 21-AUG--2000 (first entry)
XX
DE Human G protein-coupled receptor GPR9.
XX
KM G protein-coupled receptor; GPCR; constitutively active;
KM intracellular loop 3; transmembrane domain 6; drug screening;
KM agonist; antagonist.
XX
XX Homo sapiens.
XX OS
XX PN WO200022129-A1.
PD 20-APR--2000.
XX
XX 12-OCT--1999; 99WO-US23938.
XX PF
XX 13-OCT--1998; 98US-0170496.
XX PR
XX

PA (AREN-) ARENA PHARM INC.
XX Behan DP, Chalmers DT, Liaw CW;
XX
XX WPI; 2000-329165/28.
DR N-PSDB; AAA30593.
XX
XX Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents -
XX
XX Example 1; Page 116-117; 341pp: English.
XX
XX The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAAY90643-
CC AAAY90677 and AAAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC and AAA30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC or Ala, and is preferably Lys. When the endogenous residue at this
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC The 15 amino acid stretch between the substituted amino acid and the Pro
CC may be endogenous, non-endogenous, or a mixture of endogenous and
CC non-endogenous residues. The constitutively active GPCRs are useful for
CC identifying antagonists, agonists and partial agonists for use as
CC pharmaceutical agents. The mutant proteins are also useful in research
CC settings for elucidating the roles of the receptors in normal and
CC diseased conditions. Antagonists for a particular GPCR are useful for
CC treating diseases and disorders associated with that receptor. Because
CC the novel mutant GPCRs are constitutively active, they can be used
CC directly for screening of compounds without the need for endogenous
CC ligands. The present sequence represents a human wild-type GPCR referred
CC to in an exemplification of the invention.
XX
XX
SQ Sequence 368 AA:
Query Match 87.9%; Score 1891; DB 21; Length 368;
Best Local Similarity 99.7%; Pred. No. 6.3e-208;
Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 51 QVSDHQVLNDAEVAALLLENFSSSYDYGENESDSCCTSPPCPODFSINFDRAPALATYSL 110
:|||||
DB 4 EVSDHQVLNDAEVAALLLENFSSSYDYGENESDSCCTSPPCPODFSINFDRAPALATYSL 63
QY 111 FLGLGNGAVAAVLLSRRTALSTDTFLHLAVDTLLVTLPLMAVDAVQWVEGSG 170
|||||
DB 64 FLGLGNGAVAAVLLSRRTALSTDTFLHLAVDTLLVTLPLMAVDAVQWVEGSG 123
QY 171 CKVAGALFNINFAVALLLACISFDRYLNVHATOLYRRGPPARVTLTCLAVNGLCILFA 230
124 CKVAGALFNINFAVALLLACISFDRYLNVHATOLYRRGPPARVTLTCLAVNGLCILFA 183
DB 231 LPDFIFLSAHHDERLNATHCOYNEPOVGRTALRVQLVAGFLPLVMAYCYAHIIAVLL 290
184 LPDFIFLSAHHDERLNATHCOYNEPOVGRTALRVQLVAGFLPLVMAYCYAHIIAVLL 243
QY 291 VSRGQRRLRAMRLVYVVVVAFAFCWTPYHLVYLVLDIMDGALARNCGRSRDVAKSVT 350
244 VSRGQRRLRAMRLVYVVVVAFAFCWTPYHLVYLVLDIMDGALARNCGRSRDVAKSVT 303
QY 351 SGLGYMHCCNPLLYAFVGVKFRERMMMLLRLGCPNORGLOROPSSSRDSSMSSETSEA 410
|||||
DB 304 SGLGYMHCCNPLLYAFVGVKFRERMMMLLRLGCPNORGLOROPSSSRDSSMSSETSEA 363
QY 411 SYSGL 415
|||||
DB 364 SYSGL 368
RESULT 6

AAG80122
ID AAG80122 standard; Protein; 368 AA.
XX
AC AAG80122;
XX
DT 17-JAN-2002 (first entry)
XX
DE Human CXCR3 protein.
XX
KM Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KM Inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KM Chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KM antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KM antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200172830-A2.
XX
PD 04-OCT-2001.
XX
PE 02-APR-2001; 2001WO-EP03708.
XX
PR 31-MAR-2000; 2000DE-1016013.
XX
PA (IPEP-) IPE PHARM GMBH.
XX (FORS/) FORSMANN U.
XX
PI Forssmann W, Adermann K, Heltland A, Spodsborg N;
DR WPI; 2001-626256/72.
XX
PT Diagnostic agent containing two or more receptor-specific ligands,
PT useful for detecting tumors, inflammation etc., also therapeutic use of
PT ligand inhibitors
XX
PS Disclosure; Page 12; 26pp; German.
XX
CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiasthmatic,
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CR), which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention.
XX
SQ Sequence 368 AA;
XX
Query Match 87.9%; Score 1891; DB 22; Length 368;
Best Local Similarity 99.7%; Pred. No. 6.3e-208;
Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 231 LPDFIFLSAHHDERLNATHCQYNEPOVGRPTALRYQLVAGFLPLLYMAYCYAHITLAVLL 290
|||||
DB 184 LPDFIFLSAHHDERLNATHCQYNEPOVGRPTALRYQLVAGFLPLLYMAYCYAHITLAVLL 243
QY 291 VSRGQRRRLRAMLVVVVVVAFAICWTPYHLVLDIIMDIGALARNCGRSRVDVAKSVT 350
|||||
DB 244 VSRGQRRRLRAMLVVVVVVAFAICWTPYHLVLDIIMDIGALARNCGRSRVDVAKSVT 303
QY 351 SGLGYMHCCCLNPLLYAFVGVKFRFRMMMLLRLGCPNORGLQRPSSRRDSSMSSETSEA 410
|||||
DB 304 SGLGYMHCCCLNPLLYAFVGVKFRFRMMMLLRLGCPNORGLQRPSSRRDSSMSSETSEA 363
QY 411 SYSGL 415
|||||
DB 364 SYSGL 368

RESULT 7
AAY90648
ID AAY90648 standard; Protein; 368 AA.
XX
AC AAY90648;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human mutant G protein-coupled receptor GPR9 (M254K).
XX
KM G protein-coupled receptor; GPCR; constitutively active;
KM Intracellular loop 3; transmembrane domain 6; drug screening;
KM agonist; antagonist; mutant; mutein.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO200022129-A1.
XX
PD 20-APR-2000.
XX
PE 12-OCT-1999; 99WO-US23938.
XX
PR 13-OCT-1998; 98US-0170496.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Behan DP, Chalmers DT, Liaw CW;
XX
DR WPI; 2000-329165/28.
XX N-PSDB; AAA30714.
XX
PT Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
XX agents
XX
PS Example 2; Page 224-225; 341pp; English.
XX
CC The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC and AAA30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC or Ala, and is preferably Lys. When the endogenous residue at this
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC The 15 amino acid stretch between the substituted amino acid and the Pro
CC may be endogenous, non-endogenous, or a mixture of endogenous and
CC non-endogenous residues. The constitutively active GPCRs are useful for
CC identifying antagonists, agonists and partial agonists for use as
CC pharmaceutical agents. The mutant proteins are also useful in research
CC settings for elucidating the roles of the receptors in normal and
CC diseased conditions. Antagonists for a particular GPCR are useful for

ID AAY06643 standard; Protein: 374 AA.
XX
AC AAY06643;
XX
DT 26-OCT-1999 (first entry)
XX
DE Mouse Burkitt's lymphoma receptor 1 (BLR1).
XX
KW Burkitt's lymphoma receptor 1; BLR1; mouse;
KW B lymphocyte chemottractant; BLC; chemokine; ligand;
KW drug screening; leukaemia; autoimmune disease; therapy.
XX
OS Mus musculus.
XX
PN MO9928468-A1.
XX
PD 10-JUN-1999.
XX
PF 02-DEC-1998; 98WO-US25561.
XX
PR 02-DEC-1997; 97US-0982493.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Cyster JG, Gunn MD, Williams LT;
XX
DR WPI: 1999-493764/41.
DR N-PSDB: AAX87709.
XX
PT Modulating interaction of a Burkitt's lymphoma Receptor 1
XX polypeptide and ligand, useful in drug screens
XX
PS Claim 1; Page 35; 42pp; English.
XX
CC This sequence represents mouse Burkitt's lymphoma receptor 1
CC (BLR1). The invention relates to methods for modulating the
CC interaction of BLR1 with its ligand, B lymphocyte chemottractant
CC (BLC, see AAY06641). The methods comprise combining BLR1 and BLC
CC polypeptides with a candidate modulator agent under conditions
CC whereby, but for the presence of the agent, the polypeptides engage
CC in a first interaction, and determining a second interaction of the
CC polypeptides in the presence of the agent, wherein a difference
CC between the first and second interactions indicates that the agent
CC modulates the interaction of the polypeptides. The modulator is
CC preferably an antagonist, especially dominant negative, form of
CC BLC. BLC and BLC agonists and antagonists may be useful for
CC treating viral (e.g. HIV) infections, lymphoma, B lineage
CC leukaemia, and autoimmune diseases such as rheumatoid arthritis,
CC thyroiditis and diabetes.
XX
SO Sequence 374 AA;
Query Match 29.8%; Score 640; DB 20; Length 374;
Best Local Similarity 40.9%; Pred. NO. 2.4e-64;
Matches 143; Conservative 54; Mismatches 139; Indels 14; Gaps 6;
OY 70 FSSSDYGENSDSCCTSPCPCQDPSLNFRAFLPALYSLLFLGLLGAAYAVLSRR 129
DB 26 YSNSEIRLPDQSNFCST---VEGPIITSEKAVMPVAVSLIFLDMGNTLVILRRR 82
OY 130 TALSTDTFLHLAAVADTLVLTPLMAVDAVQVWFGSGLCCKVAGALFNINFGALLL 189
DB 83 HTRSTETFLFLAAVADLLVLFILPFAVAGSVGVLGFLPCKTYIALHKINFYCSSLLV 142
OY 190 ACISDRLNLYHATQLRRGPRPARVTLTCLAVWGLCULFALPDITFLSA---HHDERLN 246
DB 143 ACIAVDRLAIVHAHVAVRRRLSIHTCTAIVLAGEFLFALPELLFAKVGQPHNNDSL- 201
OY 247 ATHCOYNFPOYGRT-----ALRVQLVAGFLPLPLVMAVCYAHILAVL-VSRGQRLRAM 301
DB 202 -PQCFISQENAEETAMWTSRFLYHIGGFLPLMLVGMGCVGVVRLLOAQRRPQOKAV 260
OY 302 RLVVVVVAFALCWPTPHLVVLVLDILMDLGALEARNCGRSVDVAKSVTSGLGMHCCLN 361

DB 261 RVALIWTSEIFLCWSPYHIVIEFLDTERLKAVNSCELSGYLSVAITLCEFLAHCCLN 320
OY 362 PLLXAFVGVKFRERMMMLLRGCPNQRLQRPSSRRDSSMSERSEAS 411
DB 321 PMLYTFAGVKKFRSDLSRLTLTKLGCAGPAST-CQLPFPNKRKSSISEENAT 369
RESULT 10
ABG13609
ID ABG13609 standard; Protein: 399 AA.
XX
AC ABG13609;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #13600.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB: AAS77796.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity
XX
PS Claim 20; SEQ ID NO 43968; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
SO Sequence 399 AA;
Query Match 29.6%; Score 637.5; DB 22; Length 399;
Best Local Similarity 37.3%; Pred. NO. 5.2e-64;
Matches 154; Conservative 57; Mismatches 145; Indels 57; Gaps 10;

QY 17 GGAASQSKTSQKSDITKEFLPGLYTAAPSSPP-PSQVSDHQVLMNDAEVALLENF----- 70
DB 20 GGVLYQVKS-----PATQSGFKFTSKMEDFNMESDS-----FEDFWKGBD 58
QY 71 SSSYDGENESDSCCTSPCPDQFSLNFDRAFLPALYSLLFLGLGNCANAAVLISRT 130
DB 59 LSNYSSTLPFPFLDAAACEPE-SLEIKRYFVVIYALVFLSLGNSLVMVILYSRV 117
QY 131 ALSSTDFPLHLAVADTLVLFLPLAVDAVQWVGSGLCVAGALFNINFYAGALLA 190
DB 118 GRSVDVYILNLAADLFLALFLPTAASKVNGWIFGTLCKVYSLSLKKNYSGILLIA 177
QY 191 CTSFDRYLNIVAHATOLYRGRPARVLT-----CLAVGCLLFLALPDFIFLSAH 241
DB 178 CTSVDRYLAIVAHTR-----TLTQKRYLVKFCISLIGSLALLPVLFFRRVY 227
QY 242 DERLNATHQVNPQVVG-----RTALRVQLVAGFLPLVMAVCYAHITAVLVSRQ 295
DB 228 SSNVSPA-C---YEDMGNTANWRMLRLTLPOSFGFIYBLTLMFCYGTLETLFRKAHNG 283
QY 296 RRLRAMRLVAVVAVAFALCWPTPYHLVLDIIMDICALARNGGRSRYVAVKSVTSGLY 355
DB 284 QKRRAMRVFAVVLFLFLCWLPLYNVLADTLMKROYIOETCERNRHIDRALDATEIIGI 343
QY 356 MHCCLNPLLYAENVGVKFRERMMMLLRGCPNQROGLOROPSSRRDSVMSSETS 408
DB 344 LHSCLNPLIYAFIYGOKFRHGLKILIAHGLISKDSLPRKSRSPVSGSSGHS 396

RESULT 11

ABBI2024
ID ABBI2024 standard; peptide; 399 AA.

ABBI2024;
XX

DT 11-JAN-2002 (first entry)
XX

Human IL-8R B homologue, SEQ ID NO:2394.
XX

Human; cytokine; cell proliferation; cell differentiation; growth factor;
haematopoiesis regulation; tissue growth; immunomodulator; activin;
inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
proliferation; metastasis; cancer; tumour; haematopoietic disorder;
myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
chronic inflammatory condition; proliferative retinopathy;
atherosclerosis; coronary heart disease; arterial ischaemia;
bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antihistaminic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotrophic; cardiant; virucide; antibacterial;
antifungal; vulnerary; antitumor.

OS Homo sapiens.
XX

PN WO200157188-A2.
XX

PD 09-AUG-2001.
XX

PF 05-FEB-2001; 2001WO-US03800.
XX

PR 03-FEB-2000; 2000US-0496914.
XX
PR 27-APR-2000; 2000US-0560875.
XX

PA (HYSE-) HYSEQ INC.
XX

PI Tang YF, Liu C, Dimaenac RT;
XX

DR WPI; 2001-457740/49.
XX

XX N-PSDB; ABA09268.
XX

PT Human proteins and DNA encoding sequences useful for preventing,

PT treating or ameliorating a medical condition in a mammalian subject
PR e.g. arthritis and cancer -
PS Claim 20; Page 298; 1963pp; English.

XX Sequences ABBI0981-ABBI2330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention.

XX Sequence 399 AA:

Query Match 29.6%; Score 637.5; DB 22; Length 399;
Best local similarity 37.3%; Pred. No. 5,2e-64;
Matches 154; Conservative 57; Mismatches 145; Indels 57; Gaps 10;

QY 17 GGAASQSKTSQKSDITKEFLPGLYTAAPSSPP-PSQVSDHQVLMNDAEVALLENF----- 70
DB 20 GGVLYQVKS-----PATQSGFKFTSKMEDFNMESDS-----FEDFWKGBD 58
QY 71 SSSYDGENESDSCCTSPCPDQFSLNFDRAFLPALYSLLFLGLGNCANAAVLISRT 130
DB 59 LSNYSSTLPFPFLDAAACEPE-SLEIKRYFVVIYALVFLSLGNSLVMVILYSRV 117
QY 131 ALSSTDFPLHLAVADTLVLFLPLAVDAVQWVGSGLCVAGALFNINFYAGALLA 190
DB 118 GRSVDVYILNLAADLFLALFLPTAASKVNGWIFGTLCKVYSLSLKKNYSGILLIA 177
QY 191 CTSFDRYLNIVAHATOLYRGRPARVLT-----CLAVGCLLFLALPDFIFLSAH 241
DB 178 CTSVDRYLAIVAHTR-----TLTQKRYLVKFCISLIGSLALLPVLFFRRVY 227
QY 242 DERLNATHQVNPQVVG-----RTALRVQLVAGFLPLVMAVCYAHITAVLVSRQ 295
DB 228 SSNVSPA-C---YEDMGNTANWRMLRLTLPOSFGFIYBLTLMFCYGTLETLFRKAHNG 283
QY 296 RRLRAMRLVAVVAVAFALCWPTPYHLVLDIIMDICALARNGGRSRYVAVKSVTSGLY 355
DB 284 QKRRAMRVFAVVLFLFLCWLPLYNVLADTLMKROYIOETCERNRHIDRALDATEIIGI 343

CC treating viral (e.g. HIV) infections, lymphoma, B lineage
CC leukemia, and autoimmune diseases such as rheumatoid arthritis
CC thyroiditis and diabetes.

SQ Sequence 372 AA;

Query Match	Score	DB	Length
29.58	635	20	372

	Matches	147	Conservative	50	Mismatches	145	Indels	18	Gaps	8	
QY	67	LENNSSSY	---	DYGNESD	-SCTSPQPCQ	---	DSLNDRAFLPALYSLLFLGLG	119			
Db	11	LENEDLEWELDRDNDNDSTL	VENHNLCPATEG	PLMASTKAVEVPA	PAVSLILGLV	IGNV	70				
QY	120	AAVAALLSRPTALSTDP	FFLLHVAADFLVLT	PLPMDA	VAQVWFGSLCK	KGALFN	179				
Db	71	LVLVILEHNRQTRSTET	FFFLHVAADLLVLT	FPNVAEGSVGNV	LGTFLCKTYAL	TLAK	130				
QY	180	INFYAGALLLACISF	DRYLNITVHATOLY	RGRPARVTLTCL	LAWGLCLFALP	DFIYL	237				
Db	131	VNFVCSLLLACIAND	RYLATIYHAAV	HRHRLLS	IHITCGITWLV	GLFALPELIF	FAVY	190			
QY	238	-SAHHDEFLNAT	HCQYNF	POYGR	---	ALRYQLVAGFL	FLPLVMA	YAHILAVL	-LV	291	
Db	191	SGCHNNNSL	-	PRCTFSG	ENQNAET	HAMFTSR	FLYHVAGFL	PLMLVGM	CVGVHRL	BOA	248
QY	292	SRGRRLRAMRLV	VVVVVA	FALCWRPHYL	LVLDLMDL	GLALRNCGR	SRDVA	KSVTS	351		
Db	249	QRBPOROKAV	RAVALLV	YSIFELC	MSPRYHIV	LDPLARLKA	VNDNCK	LKNGSL	PRVAITMKE	308	
QY	352	GLGVNHCCUNFL	FAVGVFR	FRERMMML	LLRLRG	CNQGLO	QAPSSSR	DDSSMS	ETSEAS	411	
Db	309	FLGLAHCCUNFL	TEFACV	KFRSDRL	SLRLTLK	GGCPAS	LSLOLP	SWMR	-SSLSEBNT	367	

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Db 189 EVLGNDAKMKRVVILRLPHTEGIVPLFVLMFCYGTFLTRFKAHMGOKHRAMRVFAVV 248
QY 309 VAFALCMWPHVHVVYVDLMDGALARNGRESRDVAKSVTSGLGYMCCINPLLYAFV 368
Db 249 LFLCLMPLRYNLVLAADLMTFRQVIOQESCRNNNGRALDAVEILLGFLHSCINPLIYAFI 308
QY 369 GVKFRERMMMLLRGCPNQRGLQROPSSSRDSSMSETS 408
Db 309 GGNFRHGFGLKIAMHGVSKFELARHRTSYTSSSVNVS 348

RESULT 10
S42096
Interleukin-6 receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
R:Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
A:Accession: S42096
A:Description: Molecular cloning of the rat IL6 receptor.
A:Reference number: S42096
A:Accession: S42096
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-356 <GOB>
A:Cross-references: EMBL:X77797
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.6%; Score 593.5; DB 2; Length 356;
Best Local Similarity 38.1%; Pred. No. 1.2e-44;
Matches 135; Conservative 60; Mismatches 136; Indels 23; Gaps 8;

QY 67 LENES----STDGENESDSCCTSPCCODESLNFDRAFLPALYSLEFLGLGNGAVA 122
Db 11 LEDFSGDIDSNFSSDPPFLSDACP--SANLDINRAVYVIVYVLLSLVGNLSLV 69
QY 123 AVLSRPTALSTDFELHLAVADTLVTLPLMAVDAVQVFGSLCKVAGALENIF 182
Db 70 LVILNRSTCSTVDYVLLNLALADLFLPALTLPLVMASKVNGMFSSFLCKVSEFLOETIF 129
QY 183 YAGALLACISFDRLYNIVHATQ--LYRGRPARVTLTCLAVWGICLFLALDPFIFLSAH 240
Db 130 YSSVLLACISMDRYLAIVHATSTLIQK--HLVKFCITMPLSLVSLDFIFLRT 185
QY 241 HDERLNATHCOYFPQV-----RTALRVQLVAGFLLPLLVMAVCVAHIIAVLVSRG 294
Db 186 VKANSTVVCYEN---IGNNTSKMRVRLILPQTYGFLPLIMFCYGFTRTLFKAHM 242
QY 295 QRLRAMLVVVVAVFALCMWPHVHVVYVDLMDGALARNGRESRDVAKSVTSGLG 354
Db 243 GOKHRAMRVFAVVVFLCLMPLRYNLVLAADLMTFRQVIOQESCRNNNGRALDAVEILLGFLHSCINPLIYAFI 299
QY 355 YMHCCINPLLYAFVGVKFRERMMMLLRGCPNQRGLQROPSSSRDSSMSETS 408
Db 300 FLHSCINPLIYAFIIGQKFRHGLKIAMHGVSKFELARHRTSYTSSSVNVS 353

RESULT 11
B55735
Lymphocyte-specific G protein-coupled receptor EB11 - human
N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
A:Accession: B55735; S52443
A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically tra
A:Reference number: S52443
A:Accession: S52443
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 21-378 <BUR>
A:Cross-references: EMBL:X84702
C:Genetics:
A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7
A:Cross-references: GDB:342065; OMIM:600242
A:Map position: 17q12-17q21.2
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

A:Cross-references: GB:L31581; NID:9468319; PIDN:AAA74231.1; PID:9468320
R:Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically tra
A:Reference number: S52443
A:Accession: S52443
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 21-378 <BUR>
A:Cross-references: EMBL:X84702
C:Genetics:
A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7
A:Cross-references: GDB:342065; OMIM:600242
A:Map position: 17q12-17q21.2
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 27.2%; Score 586; DB 2; Length 378;
Best Local Similarity 38.4%; Pred. No. 5.9e-44;
Matches 133; Conservative 62; Mismatches 139; Indels 12; Gaps 7;

QY 75 DY-GENES--DSCCTSPCCODESLNFDRAFLPALYSLEFLGLGNGAVAVALSRRTAL 132
Db 31 DYIGDNTVDYTLFESLCKKDVNRKAMFLPIMYSIIQFVGLGVLVLYIFKRLK 90
QY 133 SSTDFELHLAVADTLVTLPLMAVDAVQVFGSLCKVAGALENIFYAGALLACI 192
Db 91 YMDYVLLNLAVADLLETLPLFMAYSAKSWVGVHFKLIFAIYKMSFFSGMILLICI 150
QY 193 SFDRYLNIVHATQVYRGPARV---TLTCLAVWGICLFLALDPFIFLSAHDERLNT 248
Db 151 SIDRYVAIVQANSAHNN--RARVLLISKLSYGVITLAVLSIPELLYDLQRSSEQAM 208
QY 249 HCQYNEPQV--GRTALRVQLVAGFLLPLLVMAVCVAHIIAVLVSRGORRLRAMRLVVV 307
Db 209 RCLITEHEAEFTIQVQAMVIGFLVPLLMASFICYLVIITLLQARNFRNKAIKVIYAV 268
QY 308 VVAFALCMWPHVHVVYVDLMDGALARNGRESRDVAKSVTSGLGYMCCINPLLYAF 367
Db 269 VVVFYFQPLRYGVAVLAQVAVNNTTSTPCELSKOLINIVDYVYSIACVCCNPFLYAF 328
QY 368 VVKFRERMMMLLRGCPNQRGLQROPSSSR--RDSMSETSAS 411
Db 329 IGKFRNDLFKFLKDGCLSQDQL--RQWSSCHIRRSSVSEAFET 373

RESULT 12
G00048
fusin (LESTRA) - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 26-Aug-1999
R:Tatsumi, M.
submitted to GenBank, July 1996
A:Accession: G00048
A:Reference number: H00048
A:Status: Preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-352 <TAT>
A:Cross-references: GB:D86579; NID:91468948; PID:91468949
C:Superfamily: vertebrate rhodopsin

Query Match 27.1%; Score 582.5; DB 2; Length 352;
Best Local Similarity 35.4%; Pred. No. 1.1e-43;
Matches 123; Conservative 70; Mismatches 137; Indels 17; Gaps 5;

QY 68 ENFSSSYDVGENESDSCCTSPCCODESLNFDRAFLPALYSLEFLGLGNGAVAVALS 127
Db 10 DNTTERMGSDVDS---IKEPCFRENAHFNRIPLTYITFLIGVNGSLVILWGY 65
QY 128 RRTALSTDTFLLHLAVADTLVTLPLMAVDAVQVFGSLCKVAGALENIFYAGAL 187
Db 66 OKKIRSMTDKRYRLHLSVADLVYITLPLFMAVDAVANMRYGNFLCAKRVHYITVNLSSVL 125

[illegible]

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match	26.8%;	Score 576.5;	DB 2;	Length 352;
Best Local Similarity	35.0%;	Pred. No. 3.8e-43;		
Matches 121; Conservative	70;	Mismatches 140;	Indels 15;	Gaps 4;

QY	68	ENFSSSDYGENESDSCCTPPCCDFSLNFDRAFLPALYSLLFLGLLGNCAVAAYLLS	127
		10 DNYTEMGSDGYD----MKPECFREBNAPNIFLPTJYSIIFLGTJGNGVLTVLLMGY	65
QY	128	RTALSSDTFLHLAAADPLDLVLTPRLMAVDAAYQWVGSGLCKAGALFNINFYACAL	187
Db	66	QKRLSMWDKYRLHLVAADLLFVITLPEMAVDAVAMWYGNELCKAAHYLYVNLYSYL	125
QY	188	LLACISDGRYLNIVHAQOLYLRGRGPARVLTCTCAVGLCLLFALPDFTLSAHNDRLNA	247
Db	126	ILAFISIDRYATLVAHNDSORPKRLAEKVYUWGVIPALLTLTPDFT--ANVSEADRR	183
QY	248	THCQYNPF--QVGRFALVLDLVAGFLLPLLYMAVYCAHLAVLVSROGRRLRARLVVV	306
Db	184	YICDRFYPNDLWVVPFOHIMGLIPGLYILSCYCIILSKSHSGKQKRAKLTIVY	243
QY	307	VVVAFALOWFPHYLVLVDILMDGALARNCGRESRYDAKSVTSGLGMYMCCLPPLLYA	366
Db	244	LILAFPCWLTPYUIGISIDSFLILETIKQCSERENTVHKMISITELARFHCCLNPILYA	303
QY	367	FVGVKFRERMMILL-----LRLGCPNORGLQORPSSRRDSSW	404
Db	304	FLGAKFTSAQHALTYSVRGSSSLKILSKGRGSHSVSESSSSP	349

RESULT 14
A48921

Interleukin-8 receptor type B - mouse

N; Alternate names: G-protein coupled receptor Gpcr16

Species: *Mus musculus* (house mouse)

```

C; Date: 20-Feb-1995 #sequence_revisio
140001 153577 140040

```

Accession: A48921; A53677; 149348; 155421; H48909; 153774

Reviews 18 410-413 1893
D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.

A:Tit+]: The murine homolog of the human

A:Reference number: A48921: MUTD:94117014

A: Accession: A48921

A; molecule type: DNA

A;Residues: 1-359 <

A;Cross-references: GB:L23637; NID:g435093; PIDN:AAA39305.1; PID:g435094

R; Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.

J. Biol. Chem. 269, 18263-18266, 1994

AA;Title: The N terminus of interleukin-8

Accession: AF33677
Reference number: A53677; MUID:94308043

not shown; not compared with noncontingent treatment

A: Molecule type: DNA

A: Residues: 1-359 <SI1Z>

A:Cross-references: GB:L26549

A;Note: sequence extracted from NCBI backbone (NCBIP:149812)

R; Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.

J. Immunol. 155, 2158-2164, 1995

A;Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.

A;Reference number: I49348; MUID:95363183

A;Accession: 149348

A;status: preliminary

A; molecule type: DNA

A: Cross-references:

References: EMBL:U01207, NID:9950174, FIDN:AC02239.1, FID:9950174; B021C C B : Gerard N P : von Mexl] = Guldenband C : Kojakowski I. F

Chem	269	29355-29358	1994
Biol			

Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression

A:Reference number: 155421; MUID:950507666

A;Accession: I55421

A;Status: preliminary

A:molecule type: DNA

A;Residues: 1-359 <RE2>

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OM protein - protein search, using sw model

Run on: November 2, 2002, 06:53:33 ; Search time 26 Seconds
(without alignments)
618.024 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRRYGPGRAGTIVIGGA.....SSRRDSWSETSSEASYSGL 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1891	87.9	368	1	P49682 homo sapien
2	1626.5	75.6	367	1	CCR3_HUMAN
3	641	29.8	374	1	CCR3_MOUSE
4	640	29.8	374	1	CCR5_MOUSE
5	635	29.5	372	1	CCR5_HUMAN
6	633	29.4	360	1	CCR5_MOUSE
7	629.5	29.3	353	1	CCR5_HUMAN
8	622	28.9	353	1	CCR5_MOUSE
9	615.5	28.6	355	1	CCR5_MOUSE
10	615	28.6	358	1	CCR5_MOUSE
11	614	28.5	353	1	CCR5_MOUSE
12	612.5	28.5	350	1	CCR5_MOUSE
13	606	28.2	360	1	CCR5_MOUSE
14	605.5	28.1	350	1	CCR5_MOUSE
15	605	28.1	359	1	CCR5_MOUSE
16	600	27.9	350	1	CCR5_MOUSE
17	590	27.4	356	1	CCR5_MOUSE
18	586	27.2	378	1	CCR5_MOUSE
19	584	27.2	359	1	CCR5_MOUSE
20	582.5	27.1	352	1	CCR5_MOUSE
21	577.5	26.8	352	1	CCR5_MOUSE
22	577	26.8	353	1	CCR5_MOUSE
23	576.5	26.8	352	1	CCR5_MOUSE
24	573	26.6	359	1	CCR5_MOUSE
25	571	26.5	353	1	CCR5_MOUSE
26	568.5	26.4	352	1	CCR5_MOUSE
27	567.5	26.4	352	1	CCR5_MOUSE
28	567.5	26.4	378	1	CCR5_MOUSE
29	566.5	26.3	378	1	CCR5_MOUSE
30	565.5	26.3	349	1	CCR5_MOUSE
31	563.5	26.2	374	1	CCR5_MOUSE
32	559	26.0	382	1	CCR5_MOUSE
33	552.5	25.7	349	1	CCR5_MOUSE

ALIGNMENTS

34	551.5	25.6	360	1	CCR4_HUMAN	P51679 homo sapien
35	549.5	25.5	361	1	CCR4_MOUSE	O91121 mus musculus
36	548.5	25.5	384	1	CCR4_HUMAN	O00590 homo sapien
37	548	25.5	360	1	CCR4_MOUSE	P51680 mus musculus
38	547.5	25.5	367	1	CCR4_MOUSE	O54689 mus musculus
39	539.5	25.1	362	1	CCR4_HUMAN	P46092 homo sapien
40	535	24.9	373	1	CCR2_MOUSE	O55197 rattus norv
41	534.5	24.8	374	1	CCR2_HUMAN	P41597 homo sapien
42	528	24.5	360	1	CCR2_MOUSE	O18793 macaca mula
43	528	24.5	373	1	CCR2_MOUSE	P51683 mus musculus
44	520	24.2	352	1	CCR5_MOUSE	P79436 macaca mula
45	519.5	24.2	352	1	CCR5_MOUSE	P56493 cercopithec

RESULT 1
ID CCR3_HUMAN STANDARD: PRT: 368 AA.
AC P49682; O15185; Created
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-X-C chemokine receptor type 3 (CXCR-3) (CXCR-3) (CD183 antigen).
GN CXCR3 OR GPR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=97188912; PubMed=9064356;
RA Loetscher M., Gerber B., Loetscher P., Jones S.A., Piali L., Clark-Lewis I., Baggiolini M., Moser B.;
RA "Chemokine receptor specific for IP10 and MIP-1 structure, function, and expression in activated T-lymphocytes.";
RT J. Exp. Med. 184:963-969(1996).
RL [2]
RN SEQUENCE FROM N.A.
RP Gutierrez J., Varona R., Zaballero A., Lind P., Marquez G.;
RL Submitted (Sep-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RX SEQUENCE OF 5-368 FROM N.A.
RX MEDLINE=96115583; PubMed=8666380;
RA Marchese A., Helber M., Nguyen T., Heng H.H.O., Saidi V.R., Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R., O'Dowd B.F., Docherty J.M.;
RA "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10, and GPR14, encoding receptors related to interleukin 8, neuropeptide Y, and somatostatin receptors.";
RT Genomics 29:335-344(1995).
RL [4]
RN LIGAND BINDING.
RC TISSUE=Retal astrocytes;
RX MEDLINE=98290735; PubMed=9625760;
RA Cole K.E., Strick C.A., Paradis T.J., Osborne K.T., Loetscher M., Glaque R.P., Lin W., Boyd J.G., Moser B., Wood D.E., Sahagan B.G., Neve K.;
RA "Interferon-inducible T cell alpha chemottractant (I-TAC): A novel non-ELR CXC chemokine with potent activity on activated T cells through selective high affinity binding to CXCR3.";
RT J. Exp. Med. 187:2009-2021(1998).
RL [5]
RN FUNCTION: RECEPTOR FOR SCYB9/MIG, SCYB10/IMP10 AND SCYB11/ITAC.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD183 entry.
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/650534941.g.htm".
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CC EMBL: X95876; CA65126.1; -
 CC EMBL: Z79783; CAB02143.1; ALT_INIT.
 CC EMBL: U32674; AAC50505.1; -
 CC GCRDB: GCR_1341; -
 CC GCRDB: GCR_1972; -
 CC MIM: 600894; -
 DR InterPro: IPR004070; CXCchemok_receptor3.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR01532; CXCCKMKINER3.
 DR PRINTS: PR00237; GPCRHOODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; glycoprotein; Antigen.
 FT DOMAIN 1 53
 FT TRANSMEM 4 80
 FT DOMAIN 81 89
 FT TRANSMEM 110 110
 FT DOMAIN 111 125
 FT TRANSMEM 126 147
 FT DOMAIN 148 169
 FT TRANSMEM 170 189
 FT DOMAIN 190 212
 FT TRANSMEM 213 233
 FT DOMAIN 234 255
 FT TRANSMEM 256 277
 FT DOMAIN 278 298
 FT TRANSMEM 299 321
 FT DOMAIN 322 368
 FT DISULFID 124 203
 FT CARBOHYD 22 22
 FT CARBOHYD 32 32
 FT CONFLICT 75 75
 FT A -> R (IN REF. 2).
 SQ SEQUENCE 368 AA; 40659 MW; F08A3B44B2BAD04 CRC64;

Query Match
 Best Local Similarity 99.7%; Score 1891; DB 1; Length 368;
 Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 51 OVSDFQVNDAAEVAALLLENSSSYDYGENESDSCCTSPCPODFSLNFPDRAFLPALYSLL 110
 DB 4 EYSDQVNDAAEVAALLLENSSSYDYGENESDSCCTSPCPODFSLNFPDRAFLPALYSLL 63
 OY 111 FLGLGNGAANAVALLSRRTALSTDTFLHLAVADTLVLTPLMAVDAVQWFGSGL 170
 DB 64 FLGLGNGAANAVALLSRRTALSTDTFLHLAVADTLVLTPLMAVDAVQWFGSGL 123
 OY 171 CKVAGALFNINFAAGALLACTSFDYRLNVAHTQLYRGPPARVLTCLAVAGLCLLFA 220
 DB 124 CKVAGALFNINFAAGALLACTSFDYRLNVAHTQLYRGPPARVLTCLAVAGLCLLFA 183
 OY 231 LPDFIFLSAHHDERLNATHCOYNEPOVGRALRVLDVAGFLLPLVMAVCYAHILLAVLL 290
 DB 184 LPDFIFLSAHHDERLNATHCOYNEPOVGRALRVLDVAGFLLPLVMAVCYAHILLAVLL 243
 OY 291 VSRGQRRLRMLRVVVVVAFAICWTPYHLVVLVDILMDGALARNCGRESRVDAKSVY 350
 DB 244 VSRGQRRLRMLRVVVVVAFAICWTPYHLVVLVDILMDGALARNCGRESRVDAKSVY 303
 OY 351 SGLGYHNCCLNPLLYAFVGVKKFEREMMLLRGCPNKGLOKOPSSSRDSSWSETSEA 410
 DB 304 SGLGYHNCCLNPLLYAFVGVKKFEREMMLLRGCPNKGLOKOPSSSRDSSWSETSEA 363
 OY 411 SYSGL 415
 DB 364 SYSGL 368

RESULT 2
 CCR3_MOUSE
 ID CCR3_MOUSE STANDARD: PRT; 367 AA.
 AC 088410;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-X-C chemokine receptor type 3 (CXCR-3) (CXCR-3).
 GN CXCR3 OR CMKAR3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP MEDLINE=98318636; PubMed=9653165;
 RA Soto H., Wang W., Strieter R.M., Copeland N.G., Glibert D.J.,
 RA Jenkins N.A., Hedrick J., Zlotnik A.;
 RT "The CC chemokine 6ckine binds the CX-C chemokine receptor CXCR3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8205-8210(1998).
 CC -!- FUNCTION: RECEPTOR FOR SCYB9/MIG, SCYB10/INP10 AND SCYB11/ITAC (BY SIMILARITY). BINDS TO SCYB21.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL: AF045146; AAC40163.1; -
 DR MGI: 1277207; Cmkar3.
 DR InterPro: IPR004070; CXCchemok_receptor3.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR01532; CXCCKMKINER3.
 DR PRINTS: PR00237; GPCRHOODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; glycoprotein.
 FT DOMAIN 1 52
 FT TRANSMEM 53 79
 FT DOMAIN 80 88
 FT TRANSMEM 89 109
 FT DOMAIN 110 124
 FT TRANSMEM 125 146
 FT DOMAIN 147 168
 FT TRANSMEM 169 188
 FT DOMAIN 189 211
 FT TRANSMEM 212 232
 FT DOMAIN 233 254
 FT TRANSMEM 255 276
 FT DOMAIN 277 297
 FT TRANSMEM 298 320
 FT DOMAIN 321 367
 FT DISULFID 123 202
 FT CARBOHYD 22 22
 FT CARBOHYD 32 32
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 367 AA; 41016 MW; 029FBB778E3CD4EA CRC64;

Query Match
 Best Local Similarity 86.0%; Score 1626.5; DB 1; Length 367;
 Matches 314; Conservative 22; Mismatches 28; Indels 1; Gaps 1;

OY 51 OVSDFQVNDAAEVAALLLENSSSYDYGENESDSCCTSPCPODFSLNFPDRAFLPALYSLL 110
 DB 4 EYSEQVNDAAEVAALLLENSSSYDYGENESD- FSDSPCPODFSLNFPDRAFLPALYSLL 62
 OY 111 FLGLGNGAANAVALLSRRTALSTDTFLHLAVADTLVLTPLMAVDAVQWFGSGL 170

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Db 63 FLGLGNGAAVAALISQRTALSTDFLLHLAVADVLLVTLPLMAVDAQAQVFGGL 122
Qy 171 CKVGALEFNINFGALLLACISFDRYLINIVAHQLYRRGPARTITCLAWGICLLFA 230
Db 123 CKVGALEFNINFGAFLACISFDRYLISIVAHQLYRRDPVRALCIYVWGICLLFA 182
Qy 221 LPDFELSAHDERLNATHQCYNFPQVGRTRALVQLVAGFLPLLVMAVCYAHILAVLL 290
Db 183 LPDFELYSANTDQRLNATHQCYNFPQVGRTRALVQLVAGFLPLLVMAVCYAHILAVLL 242
Qy 291 VSRGQRRLAMRLVVVVVVAFAALCWTPTVHLVVDILMDLGLALANCGRESFVDAKSVT 350
Db 243 VSRGQRRLAMRLVVVVVVAFAALCWTPTVHLVVDILMDVGLANCGRSHVDAKSVT 302
Qy 351 SGLGYMHCCLPPLLYAFGVAFREMMMLRLCGPNRGDROGROSSRDSMSSETSEA 410
Db 303 SGMGYMHCCLPPLLYAFGVAFREMMMLFRLGRSDQGRGPORSSSRSSMSSETSEA 362
Qy 411 SYSGL 415
Db 363 SYLGL 367

RESULT 3
CCRS_RAT STANDARD: PRT: 374 AA.
AC P34997;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-X-C chemokine receptor type 5 (CXCR-5) (CXCR-5) (Burkitt's lymphoma
GN BLR1 OR CXCR5.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen; PubMed=8386678;
RX MEDLINE=93238948;
RA Koda M., Vanetti M., Wang X., Schaefer M., Hoell V.;
RT "Cloning of a novel putative G-protein-coupled receptor (NLR) which
RT is expressed in neuronal and lymphatic tissue.";
RL FEBS Lett. 321:173-178(1993)..
CC -1- FUNCTION: CITOKINE RECEPTOR THAT BINDS TO B LYMPHOCYTE
CC CHEMOTACTICANT (BLC) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURONAL AND LYMPHATIC TISSUE.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X71463; CAAS0582.1; -.
DR PIR: S32785; S32785.
DR GCRDB: GCR 0648; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; B-cell.
FT DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).
FT TRANSDOM 58 78 1 (POTENTIAL).
FT DOMAIN 79 90 CYTOPLASMIC (POTENTIAL).
FT TRANSDOM 91 111 2 (POTENTIAL).
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FT DOMAIN 112 126 EXTRACELLULAR (POTENTIAL).
FT TRANSDOM 127 147 3 (POTENTIAL).
FT DOMAIN 148 169 CYTOPLASMIC (POTENTIAL).
FT TRANSDOM 170 190 4 (POTENTIAL).
FT DOMAIN 191 221 EXTRACELLULAR (POTENTIAL).
FT TRANSDOM 222 242 5 (POTENTIAL).
FT DOMAIN 243 261 CYTOPLASMIC (POTENTIAL).
FT TRANSDOM 262 282 6 (POTENTIAL).
FT TRANSDOM 283 306 EXTRACELLULAR (POTENTIAL).
FT TRANSDOM 307 327 7 (POTENTIAL).
FT DOMAIN 328 374 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 124 204 POTENTIAL.
SQ SEQUENCE 374 AA; 42012 MW; D87A3AC816207319 CRC64;

Query Match 29.8%; Score 641; DB 1; Length 374;
Best Local Similarity 41.7%; Pred. No. 2,1e-37;
Matches 146; Conservative 50; Mismatches 140; Indels 14; Gaps 6;

Qy 70 FSSSYDYGNEEDSCCTSPCPQDESLNDRAPLALYSLLFLGLGNGAAVAALISR 129
Db 26 YSNSTFPLQDSIFCSTE--EGPLTSTKTFMPVAASLYFLGMMGNILVTLIERHR 82
Qy 130 TALSTDFELHLAAVADTLVTLPLMAVDAVQVFGSLCKVAGALPNINFGALL 189
Db 83 HRSSTFELFLHAAVDLLVFLPFAVAGSGVGLGFLCKYIALHKINFYCSLL 142
Qy 190 ACISFDRYLINIVAHQLYRRGPARTITCLAWGICLLFALPDFE--LSAHHDERLN 246
Db 143 ACIAVDRLAIYAHAAVYRRRLSHITPCSTIWLGLFALPELLFAKVQPHNNESL- 201
Qy 247 AHQCYNFPQVGT---ALRVQLVAGFLPLLVMAVCYAHILAVLL-VSRGQRRLAM 301
Db 202 -PQCFISQENAEETRAWFRSLYHTGFLPLPLVMAVGVVHRLQAQRPRQKAV 260
Qy 302 RLVVVVVVAFAALCWTPTVHLVVDILMDLGLALANCGRESRDVAKSVSGLYMHCCLN 361
Db 261 RAILVLTSTFLCWSPIYHIVIFLDILERAKAVNSCELSGYSVAITLCEFLGIAHCCLN 320
Qy 362 PLLYAFGVKFRERMMMLRLCGPNRGDROGROSSRDSMSSETSEA 411
Db 321 PALYFAGVKKFRSDLSRLTLKGCAGPASTL-CQLPPGMKSSLSSEENAT 369

RESULT 4
CCRS_MOUSE STANDARD: PRT: 374 AA.
AC Q04683;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-X-C chemokine receptor type 5 (CXCR-5) (CXCR-5) (Burkitt's lymphoma
GN BLR1 OR CXCR5 OR GPCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C; TISSUE=Liver;
RX MEDLINE=94009211; PubMed=8405054;
RA Kaiser E., Foerster R., Wolf I., Epensperger C., Kuehl W.M., Lipp M.;
RT "The G protein-coupled receptor BLR1 is involved in murine B cell
RT differentiation and is also expressed in neuronal tissues.";
RL Eur. J. Immunol. 23:2532-2539(1993).
RN 12
RP SEQUENCE OF 151-269 FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=94116980; PubMed=8288218;
RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
RA Copeland N.G., Jenkins N.A.;
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Query Match	Best Local Similarity	Score 615.5; DB 1; Length 355;
Matches 136; Conservative 58; Mismatches 130; Indels 29; Gaps 5;		
69 NFSSSYDGENESDSCSTPPCPODFS-----LNFDRAPLPALYSILFLGLGNGAVA 122		

```

Db      7  NMTDLMTFNEDEDFANATGMPPEYKERYSCVLVYQGLNKYYVVVVVIALVEFLLSLIGNSLYM 66
Qy      123  AVLLSRRTALSTSTDFELLHLAVADTLVLVTLPLMAVDAVQWEGSGICKVAGALENINE 182
      1  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      67  LVILYSRSRSRSTVYLTNLINAMADLLFALTPIMAWSEKKEGIFSTPLCKVSLVKEVNE 126
Qy      183  YAGALLIACISFDRRLNTVYHATQLYRRQPPAVYLT-----CLAVMGLCLLFLAPD 233
      1  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      127  YSGILLIACISYDRRLATVYHATR-----TLTKQRHLVKEFLCIGLIMLSLTLSPF 176
Qy      234  FTF---LSAHNDEERNATHCQYNEFPQVGRFALRVQLVAGFLPLPLMAWCVYAHILAVL 290
      1  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      177  FLFRQVYFSPNNSSPCYEDLGHNTRYK -WRMYLRILPHFGFILLPLVWFLCYGFLTRLKF 235
Qy      291  VSRGGRFLRLAMELVVVVVAFAFCWTFPHLVVLDIIMDLGALARNCRGSRVDVAKSVT 350
Db      236  QAHMQGKHRAHMEVFAVYVILFCLCWPLYNVLADTLKRTFHVIGETCCQRNDIDRALDAT 295
Qy      351  SGLGTWHECCNLPLTAFPGVKFREMMMLLRGLCPNQRGIGORQDPSSSRDSS 403
      1  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      296  EILGLHLSCLNDIYAFIGQNRNGLKMLAARGLSKFELTRHRVTSYSSS 348

RESULT 10
IL8B_RABIT
ID      IL8B_RABIT      STANDARD:      PRT:      358 AA.
AC      P35344:
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (GRO/MSA
      receptor).
GN      IL8RB OR CXCR2.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ALBINO; TISSUE=Blood;
RX      MEDLINE=94230294; PubMed=8175642;
RA      Prado G.N., Thomas K.M., Suzuki H., Larosa G.J., Wilkinson N.C.,
      Folco E., Navarro J.;
      "Molecular characterization of a novel rabbit interleukin-8 receptor
      isotype.";
RT      J. Biol. Chem. 269:12391-12394(1994).
RL      J. Biol. Chem. 269:12391-12394(1994).
CC      -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
      NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
      CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
      G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
      MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
      MGSa (GRO).
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEUTROPHILS.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
      -----
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      or send an email to license@isb-sib.ch).
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DR      EMBL: L24445; AAA31378.1; -.
DR      PIR: A53752; A53752.
DR      GCRDB: GCR_0861; -.
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      InterPro: IPR000832; GPCR_secretin.
DR      Pfam: PF00001; 7tm.1; 1.
DR      PRINTS: PR00237; GPCRHHODPSN.
DR      PROSITE: PS00237; G-PROTEIN_RECPEP_F1_1; 1.
DR      PROSITE: PS50262; G-PROTEIN_RECPEP_F1_2; 1.

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KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Chemotaxis.
 FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 47 73 1 (POTENTIAL).
 FT DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 2 (POTENTIAL).
 FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 140 3 (POTENTIAL).
 FT DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 181 4 (POTENTIAL).
 FT DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 229 5 (POTENTIAL).
 FT DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 250 271 6 (POTENTIAL).
 FT DOMAIN 272 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 313 7 (POTENTIAL).
 FT DOMAIN 314 358 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 117 194 BY SIMILARITY.
 SQ SEQUENCE 358 AA; 40632 MW; 6899716944D6126A CRC64;

Query Match 28.6%; Score 615; DB 1; Length 358;
 Best Local Similarity 39.7%; Pred. No. 1.2e-35;
 Matches 141; Conservative 55; Mismatches 139; Indels 20; Gaps 6;

OY 68 ENFS-----SSYDGENESDSCCTSPCPDPSLNFDRAPLALYSLLFLGLGNG 119
 DB 7 ENVSIEDPFGDSNYSYSDLPPTLLDSAPCRSE-SLEPNSVVLITYLLVLSLNGS 65
 OY 120 AYAVALLSRRALSSDTDFLLHAAVDTLVTLPLMAVDAVQVFGSGCLKVAGALFN 179
 DB 66 LVMLVILYSRSCSYTDVYLLNLALADLLEFATTLPIWASKVHGWFQPLCKVYSVME 125
 OY 180 INFYAGALLACISDRYINITYHATQ--LYRRGPPARVTLGLAVGCLLALPDFTL 237
 DB 126 VNFYSGILLACISVDRLAIYHATRTMIOKR--HLVFICLSIMVGSLSLIPLLFR 182
 OY 238 SAHDERLNATHCOY-----NFPQVGRFALRVOLVAGFLPLLVMAVCYAHILAVLVSR 293
 DB 183 NAIFPP--NSSVVCYEDMGNSTAKRMYRIIPQTFGFLPLLVMLFCYVFLRLTFOAH 240
 OY 294 GQRRLAMRLVVVVVAVAFALCPTPHLVVLDLMDGLARNCGRESRVDAKSVTSGL 353
 DB 241 MGQKRAMRVIRAVVLIFLCLWLPYNLVLTDTLMKTHVIOGTCERNIDALALATELL 300
 OY 354 GYMHCCLPLLYAFYGVFREMMMLRLGCPNORGLOROPSSSRDSSMSETS 408
 DB 301 GFLHSCLPDIYAFIGOKFRYGLRLKILAAHGLISKEFLAKESRPSFVASSGNTS 355

RESULT 11
 IL8B_GORGO STANDARD: PRT; 353 AA.
 AC Q28422;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE High affinity Interleukin-8 receptor B (IL-8R B) (CXCR-2) (Fragment).
 GN IL8B OR CXCR2.
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
 OX NCBI_TaxID=9595;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96175151; Pubmed=9110929;
 RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
 RA Lopez-Larrea C.;
 RT "Characterization of Interleukin-8 receptors in non-human primates.";
 RT Immunogenetics 43:261-267(1996).
 CC -I- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR

CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: X91114; CA662564.1; -
 DR HSP; P34996; 1DDP.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR InterPro: IPR000832; GPCR_secretln.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT NON_TER 1 1
 FT DOMAIN <1 45 1 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 46 72 1 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 73 81 2 (POTENTIAL).
 FT TRANSMEM 82 102 2 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 103 117 3 (POTENTIAL).
 FT TRANSMEM 118 139 3 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 140 160 4 (POTENTIAL).
 FT TRANSMEM 161 180 4 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 181 205 5 (POTENTIAL).
 FT TRANSMEM 206 228 5 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 229 248 6 (POTENTIAL).
 FT TRANSMEM 249 270 6 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 271 291 7 (POTENTIAL).
 FT TRANSMEM 292 312 7 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 313 >353 7 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 116 193 BY SIMILARITY.
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 353 353
 SQ SEQUENCE 353 AA; 39919 MW; 1PF04E31A7E825E4 CRC64;

Query Match 28.5%; Score 614; DB 1; Length 353;
 Best Local Similarity 39.3%; Pred. No. 1.4e-35;
 Matches 138; Conservative 52; Mismatches 131; Indels 30; Gaps 6;

OY 72 SSYDGENESDSCCTSPCPDPSLNFDRAPLALYSLLFLGLGNGAVALLSRRTA 131
 DB 18 SNVSISALPPEFLLDASPCPE-SLEINKYFYIYIALVFLSLGNSLYIILYSRG 76
 OY 132 LSSTDFLLHAAVDTLVTLPLMAVDAVQVFGSGCLKVAGALFNINFYAGALLAC 191
 DB 77 RSVTDVYLLNLADLLEFATTLPIWASKVNGMIFGTCCKVYSLLKEVNFYSGILLAC 136
 OY 192 ISFDRLNIVHATQLYRRGPPARVILT-----CLAVWGICLLFALPDFTPLSAHND 242
 DB 137 ISVDRLAVIYHATR-----TLTKRYLVKFCISIWGSLSLDALPVLVLFRTIYP 186
 OY 243 ERLNATHCOYNPQV-----RTALRVOLVAGFLPLLVMAVCYAHILAVLVSRGR 296
 DB 187 SNVSPV-C--YEDMGNNTANRMYRIIPQSGFIVPLIMLFCYVFLRLTFOAHMGQ 242
 OY 297 RLAMRLVVVVVAVAFALCPTPHLVVLDLMDGLARNCGRESRVDAKSVTSGLGYM 356
 DB 243 KHRAMRVIRAVVLIFLCLWLPYNLVLTDTLMKTHVIOGTCERNHINDALALATELLGL 302
 OY 357 HCCCLPLLYAFYGVFREMMMLRLGCPNORGLOROPSSSRDSSMSETS 407
 DB 303 HSCCLPLLYAFIGOKFRYGLRLKILAIHGLISKDSLPKDSRPSFVASSGNT 353


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FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
FT TRAMSEM 85 105 2 (POTENTIAL).
FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
FT TRAMSEM 121 142 3 (POTENTIAL).
FT DOMAIN 123 163 CYTOPLASMIC (POTENTIAL).
FT TRAMSEM 143 163 4 (POTENTIAL).
FT DOMAIN 164 183 EXTRACELLULAR (POTENTIAL).
FT TRAMSEM 184 208 5 (POTENTIAL).
FT DOMAIN 209 231 6 (POTENTIAL).
FT TRAMSEM 232 251 6 (POTENTIAL).
FT DOMAIN 252 273 6 (POTENTIAL).
FT TRAMSEM 274 294 7 (POTENTIAL).
FT DOMAIN 295 315 7 (POTENTIAL).
FT TRAMSEM 316 360 CYTOPLASMIC (POTENTIAL).
FT DISULFID 119 196 BY SIMILARITY.
FT CAROHND 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHND 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 360 AA: 40625 MW: 94770C982A632D1 CRC64:

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Query Match 28.2% Score 606; DB 1; Length 360;
Best Local Similarity 38.4%; Pred. No. 5,1e-35;
Matches 141; Conservative 54; Mismatches 130; Indels 42; Gaps 6;

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QY 67 LEFSSSYIGENESDSCCTSPCCODESLN-----FDRAFLPALYSLLFLGLLGN 118
DB 8 LNSSILMEGFDEFGNYSCTPP-TEDYDYSPEISTETLNKAYAVVIALVALVELLSLGN 66
QY 119 GAVAAVLRSRTALSTDFELHLAVADTLVLTPLMAVDAVQVFGSLCKVAGALF 178
DB 67 SLVAVILSLRIGRSTVDYLLNLAMADLLFAFTPLTMASKAKGVFGSLCKVSLK 126
QY 179 NINFGALLLACISFDRLYNIVHATOLYRGRPARVTLT-----CLAWGICLLEF 229
DB 127 ENVEYSGILLACISMDRYLATVHATR-----TLQKHWKVFICIGIMALSVIL 176
QY 230 ALPDFELSAHND-----ERLANTHCQYNFPQYGRPALRYLDVAGFLPLVMAVC 281
DB 177 ALPTFLFRAYQPPYSDLVCYEDLGANTTKW-----RAIMRVLPTQFGLPLVLMELC 230
QY 282 VYHILAVLVSSRGQRRLRAMRLVVVVVAFALCWPTPYHLVLDILMDGALARNCGRES 341
DB 231 YGFTLRTLESADMGKHKRAMRYFAVAVLVFLCLMPLRYNLVLDITMRHVAVIAETQRNN 290
QY 342 RVDVAKSVTSGLVHMCNPLLYAVFVGVFRERMMLLRLLCQPNQRLQGRPOSSRRD 401
DB 291 DIGRALDAETELGFLHSCNPLIYVIGQKFRHGLKIMAHGLISKEFLAKGRPSFVG 350
QY 402 SSMSETS 408
DB 351 SSSGNTS 357

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RESULT 14
IL8A_HUMAN STANDARD; PRT; 350 AA.
ID IL8A_HUMAN
AC P25024;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE High affinity interleukin-8 receptor A (IL-8R A) (IL-8 receptor type
DE 1) (CXCR-1) (CDw128a).
GN IL8RA OR CXCR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RX MEDLINE-91368199; PubMed-1840701;
RA Holmes W.E., Lee J., Kuang W.-J., Rice G.C., Wood W.I.;
RT "Structure and functional expression of a human interleukin-8
RT receptor.";
RL Science 253:1278-1280(1991);

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RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE-93205012; PubMed-8384312;
RA Cerretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
RA Beckmann M.P.;
RT "Molecular characterization of receptors for human interleukin-8,
RT GRO/melanoma growth-stimulatory activity and neutrophil activating
RT peptide-2.";
RL Mol. Immunol. 30:359-367(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-93252387; PubMed-8486366;
RA Mollerleu C., Passage E., Mattei M.-G., Vassart G., Parmentier M.;
RT "The high-affinity interleukin 8 receptor gene (IL8RA) maps to the
RT 2q33-q36 region of the human genome: cloning of a pseudogene
RT (IL8RB) for the low-affinity receptor.";
RL Genomics 16:248-251(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE-Placenta;
RX MEDLINE-95014476; PubMed-7929358;
RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
RT "Comparison of the genomic organization and promoter function for
RT human interleukin-8 receptors A and B.";
RL J. Biol. Chem. 269:26381-26389(1994).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE-92355587; PubMed-1379593;
RA Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
RT "Characterization of two high affinity human interleukin-8
RT receptors.";
RL J. Biol. Chem. 267:16283-16287(1992).
RN [6]
RP STRUCTURE BY NMR OF 9-29 IN COMPLEX WITH IL-8.
RX MEDLINE-99148123; PubMed-10368283;
RA Skelton N.J., Quan C., Reilly D., Lowman H.;
RT "Structure of a CXCR chemokine-receptor fragment in complex with
RT interleukin-8.";
RL Structure 7:157-168(1999).
RN [7]
RP FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
RP NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
RP CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
RP G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIN SECOND
RP MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
RP AND TO MGSA (GRO) WITH A LOW AFFINITY.
RP SUBCELLULAR LOCATION: Integral membrane protein.
RP BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
RP DATABASE: NAME=PROW; NOTE=CD guide Cw128a entry;
RP WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cw128a.htm".
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CC -----
CC EMBL: L19591; AAB59436.1; -
CC EMBL: L19592; AAA59160.1; -
CC EMBL: M68932; AAA59159.1; -
CC EMBL: X65858; CAA46688.1; -
CC EMBL: U11870; AAA64378.1; -
CC PIR: A39445; A39445.
CC PDB: 1IIP; 23-DEC-98.
CC PDB: 1IIO; 23-DEC-98.
CC GCRDb; GCR_0175; -
CC GCRDb; GCR_0696; -
CC GCRDb; GCR_1832; -
CC GCRDb; GCR_1833; -
CC GCRDb; GCR_2052; -
CC MIM: 146929; -
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Chemotaxis; Polymorphism; 3d-structure.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT TRANSMEM 67 75
 FT TRANSMEM 76 96
 FT TRANSMEM 97 111
 FT TRANSMEM 112 133
 FT TRANSMEM 134 154
 FT TRANSMEM 155 174
 FT TRANSMEM 175 199
 FT TRANSMEM 200 220
 FT TRANSMEM 221 242
 FT TRANSMEM 243 264
 FT TRANSMEM 265 285
 FT TRANSMEM 286 308
 FT TRANSMEM 309 350
 FT CARBOHYD 3 16
 FT CARBOHYD 16 136
 FT DISULFID 110 187
 FT VARIANT 276 276
 FT T->S.
 FT FTID=VAR_003479.
 SQ SEQUENCE 350 AA; 39805 MW; 2463EEB51BEDD039 CRC64;
 Query Match 28.1%; Score 605.5; DB 1; Length 350;
 Best Local Similarity 39.7%; Pred No. 5.4e-35;
 Matches 135; Conservative 49; Mismatches 125; Indels 31; Gaps 5;

OY 88 PCPCODES-----LNDFRAFLPALYSLLFLGLNGAVALLSRRRLASTDTFLH 141
 DB 21 PRADEDYSPCMLETFETLTKYVIAVALVELLSLGLMVLTVSRGSRVTDVYLLN 80
 OY 142 LAVADLVLTPLPLAVDAVAVQVSSGLCKVAGALFNINFGALLLACISDRILNY 201
 DB 81 LAADLVLTPLPLAVDAVAVQVSSGLCKVAGALFNINFGALLLACISDRILNY 140
 OY 202 HATOLYRGRPPARVTLT-----CLAVWGICLFLPDLFELSAHDERLNATHCOY 252
 DB 141 HATR-----TITQRHLVKEFCVLCGCKGSLMNLSPFLFRQAYIHN--NSSPVCT 188
 OY 253 ----NPPQVGRALRVQLVAGFLPLVWACYAHILAVLVSRGRLRANRLVAVV 308
 DB 189 EYLGNDTAKRWVLRILPHFGFIVPLFWMLFCYGLTFLFAHNGKRRARVLEAVY 248
 OY 309 VAFALCWTPPHLVVLDILMDGALANRGRESRVVAKSVTSGLCYMHCCLPILYAVY 368
 DB 249 LIFLLCMLEPNVLLADDTLMRTQVIOETCERRNNIGRALDATEILGLFSLCLNPITYAFI 308
 OY 369 GYKFERMMVLLRLGCPNORGLOPSSSRSDSSETS 408
 DB 309 GQNFRRHGLKILAMHGLVSKFPLARHRTSYTSSVAVSS 348

RESULT 15
 IL8B_RAT STANDARD; PRT; 359 AA.
 AC P35407;
 DT 01-JUN-1994 (rel. 29, Created)
 DT 01-FEB-1996 (rel. 33, Last sequence update)
 DT 30-MAY-2000 (rel. 39, Last annotation update)
 DE High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (GRO/MGSA
 DE receptor).
 GN IL8RB OR CXCR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;

RX MEDLINE=97361587; PubMed=9218548;
 RA Gobi A.E., Huang M.R., Wang S., Zhou Y., Oeberg K.;
 RT "Molecular cloning and characterization of a cDNA encoding the rat
 RT interleukin-8 receptor";
 RL Biochim. Biophys. Acta 1326:171-177(1997).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RA Konishi K., Shibata F., Watanabe K., Tsurufuji S., Nakagawa H.,
 RA Fujioh M.;
 RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Spleen, and Lung;
 RX MEDLINE=97115810; PubMed=8955112;
 RA Dunstan C.-A.N., Salafra M.N., Adhikari S., Xia Y., Feng L.,
 RA Harrison J.K.;
 RT "Identification of two rat genes orthologous to the human
 RT interleukin-8 receptors.";
 RL J. Biol. Chem. 271:32770-32776(1996).
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC DR EMBL; X77797; CAA54824.1; -;
 CC DR EMBL; D63584; BAA09797.1; -;
 CC DR EMBL; U70988; AAC52961.1; -;
 CC DR PIR; S42096; S42096.
 CC DR GCRDB; GCR_0913; -;
 CC DR GCRDB; GCR_1405; -;
 CC DR GCRDB; GCR_1524; -;
 CC DR Interpro: IPR000276; GPCR_Rhodopsn.
 CC DR Interpro: IPR000832; GPCR_Secretin.
 CC DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Chemotaxis.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT TRANSMEM 75 83
 FT TRANSMEM 84 104
 FT TRANSMEM 105 119
 FT TRANSMEM 120 141
 FT TRANSMEM 142 162
 FT TRANSMEM 163 182
 FT TRANSMEM 183 207
 FT TRANSMEM 208 230
 FT TRANSMEM 231 250
 FT TRANSMEM 251 272
 FT TRANSMEM 273 296
 FT TRANSMEM 297 314
 FT TRANSMEM 315 359
 FT CARBOHYD 8 8
 FT CARBOHYD 201 203
 FT CARBOHYD 202 202
 FT DISULFID 118 195
 FT T->S.
 SQ SEQUENCE 359 AA; 40532 MW; EF547326A074ABDD CRC64;

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QY	111	FLGLGLGCAVAAVLLSRTALSTDTFLHLHAVADTLVLPLMAVDAVAQWFGSGL	170
Db	63	FLGLGLGCAVAAVLLSRTALSTDTFLHLHAVADTLVLPLMAVDAVAQWFGSGL	122
QY	171	CKVAGALFNINFYAGALLIACISPDRLYINVAHTOLYRRGPPARYTLCTLAWGLCLLRA	230
Db	123	CKVAGALFNINFYAGAFELIACISPDRLYSIVAHOTLYRRDPVWRVALTCTIYWGGLCVLRA	182
QY	231	LPDFTLSAHNDERLNATHCQYNFPDVGRTALRVLOLVAGFLPLVMAYCYAHILAVLL	290
Db	183	LPDFTLSASHDQRLNATHCQYNFPDVGRTALRVLOLVAGFLPLVMAYCYAHILAVLL	242
QY	291	VERGGRRLRAMRLVVVVVAFALCTPRYHLVYLVLDLMDLGLALARRCGESRYDAKSVT	350
Db	243	VERGGRRLRAMRLVVVVVAFVACMPYHLVYLVLDLMDVGLVARRCGESHVDVAKSVT	302
QY	351	SLGLGMHCCINFLLEAFVGVKFRERMMMLLRGCGNORGLROPSSSRDSSMSTSEA	410
Db	303	SGMGVTHCCINFLLEAFVGVKFRERMMMLLRGSGDONGPOROPSSSRRESSWSETTER	362
QY	411	SYSGL 415	
Db	363	SYGL 367	
RESULT 2			
QYQW6	09QW6	PRELIMINARY: PRT: 367 AA.	
AC	09QW6		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)		
DE	INTERFERON-INDUCIBLE PROTEIN 10 RECEPTOR.		
GN	CMKAR3 OR MCXCR3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Blood;		
RX	MEDLINE=99009219; PubMed=9790904;		
RA	Tanabe M., Tomimaga Y., Yatsunami K., Natumi S.;		
RT	"Cloning of the murine interferon-inducible protein 10 (IP-10)		
RL	Biochem. Biophys. Res. Commun. 251:41-48(1998).		
DR	EMBL; AB003174; BAA34045.1; -.		
DR	MED; MGI:1277207; Cmkar3.		
DR	Interpro: IPR004070; CXCchemok_receptor3.		
DR	Interpro: IPR000276; GPCR_Rhodopsn.		
DR	Pfam: PF00001; 7tm_1; 1.		
DR	PRINTS; PRO1532; CXCCHKINER3.		
DR	PRINTS; PRO0237; GPCRHHODOPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1; UNKNOWN_1.		
DR	PROSITE; PS50262; G_PROTEIN_RECPEP_F1_2; 1.		
KW	Receptor.		
SEQ	SEQUENCE 367 AA: 41017 MW: EF0348A8358AD951 CRC64:		
QY	Query Match	75.8%; Score 1629.5; DB 11; Length 367;	
	Best Local Similarity	86.3%; Pred. No. 8.9e-133;	
	Matches 315; Conservative 21; Mismatches 28; Indels 1; Gaps 1.		
Db	4	EYSEKQVLDASDFALFLKSTSTPYRGENESD-FSDSPCPDFTSNFRTFLPALYSLL	62
QY	111	FLGLGLGCAVAAVLLSRTALSTDTFLHLHAVADTLVLPLMAVDAVAQWFGSGL	170
Db	63	FLGLGLGCAVAAVLLSQGTALSTDTFLHLHAVADTLVLPLMAVDAVAQWFGSGL	122
QY	171	CKVAGALFNINFYAGALLIACISPDRLYINVAHTOLYRRGPPARYTLCTLAWGLCLLRA	230
Db	123	CKVAGALFNINFYAGAFELIACISPDRLYSIVAHOTLYRRDPVWRVALTCTIYWGGLCVLRA	182
QY	231	LPDFTLSAHNDERLNATHCQYNFPDVGRTALRVLOLVAGFLPLVMAYCYAHILAVLL	290
Db	183	LPDFTLSASHDQRLNATHCQYNFPDVGRTALRVLOLVAGFLPLVMAYCYAHILAVLL	242
QY	291	VERGGRRLRAMRLVVVVVAFALCTPRYHLVYLVLDLMDLGLALARRCGESRYDAKSVT	350
Db	243	VERGGRRLRAMRLVVVVVAFVACMPYHLVYLVLDLMDVGLVARRCGESHVDVAKSVT	302
QY	351	SLGLGMHCCINFLLEAFVGVKFRERMMMLLRGCGNORGLROPSSSRDSSMSTSEA	410
Db	303	SGMGVTHCCINFLLEAFVGVKFRERMMMLLRGSGDONGPOROPSSSRRESSWSETTER	362
QY	411	SYSGL 415	
Db	363	SYGL 367	

[illegible]

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DB 331 GFTHCCLPNIIVAFIGVFRNDFRILHCLGICISQETIQLLEVTYRKCCIESDNTTSS 390
RESULT 4
ID 09DGI1 PRELIMINARY: PRT: 358 AA.
AC 09DGI1:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4.
GN CXCR4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=21089206; PubMed=11272281;
RA Liang T.S., Hart J.K., Lu S., Martins-green M., Gao J.-L.,
RA Murphy P.M.;
RT "Cloning, mRNA distribution, and functional expression of an avian
RT counterpart of the chemokine receptor/HIV coreceptor CXCR4."
CC J. Leukoc. Biol. 69:297-305(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL, AF294794; AAC09054.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 358 AA; 40094 MW; 64E4977E29C86C9E CRC64;

Query Match 27.2%; Score 585; DB 13; Length 358;
Best Local Similarity 35.8%; Pred. No. 2.8e-44;
Matches 123; Conservative 65; Mismatches 134; Indels 22; Gaps 5;

OY 71 SSSY-DYGENESDSCCTSPCPQDFSLNFDRAFLPALYSLLFLGLGNGAVALLSRR 129
DB 24 SADYDYG-----PCFQHENADFNRIPLTIYSIIPLTGIINGLVIYWGQYK 73
OY 130 TALSTDFELLAVADTLVLTPLMAVDAAVQWFGSLCKVAGALENINFYAGALL 189
DB 74 KORSMTDKRLHLVADLLVLTLPFWSVDAISWYFGVNLCAVHYITVNLVSSVLL 133
OY 190 ACISFDYRLNIYHATQLYRRGPRARVTLTCLAVMGICLLEFALPDFFLSAHDERLNATH 249
DB 134 AFLSLDRFLAIVHATNSQRPRKLLAEKIYGVWMLPVALVTPDIIFASTSEV--GRTL 191
OY 250 COYNFPQVG-RTALVQLDLVAGFLLPLLVMAVCYAHILAVLLVSRGQRRRLRMRLVVVV 308
DB 192 CDRMYPRHNMWLSFRRQHIIVGLVLPGLIILTCYCIISKLSHGKQRKALKTTVILI 251
OY 309 VAFALCWTPIYHLVYVDLMDGALARNGRSRYDVAKSVTSGLCYHMCCLNPLLYAY 368
DB 252 LTFEACWLPYIYIGISIDFTFLGIVIRHRSUDTIYVHKWISITTEALAFHCCCLNPLIYAL 311
OY 369 GVKFRERMMMLL-----LRGCPNORGLQRPSSSRDSSM 404
DB 312 GAKFKTSAQNMLTSVSRGSSLKILSKRGHSSSVTSESSSF 355

RESULT 5
ID 09M2M7 PRELIMINARY: PRT: 347 AA.
AC 09M2M7:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).

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GN CXCR4.
OS Callimico goeldii (Goeldi's marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callimico.
OX NCBI_TaxID=9495;
RN [1]
RX SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF172236; AAF89356.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR003006; 7tm_1; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 347 AA; 39269 MW; A433F3D1BF7A4684 CRC64;

Query Match 26.8%; Score 577.5; DB 6; Length 347;
Best Local Similarity 35.3%; Pred. No. 1.3e-43;
Matches 122; Conservative 69; Mismatches 140; Indels 15; Gaps 4;

OY 68 ENFSSDYDGENESDSCCTSPCPQDFSLNFDRAFLPALYSLLFLGLGNGAVALLS 127
DB 5 DVTETMSGDGDS-----IKPCFRFNHFNRIPLTIYSIIPLTGIINGLVIYWGQY 60
OY 128 RTAALSTDTFELLAVADTLVLTPLMAVDAAVQWFGSLCKVAGALENINFYAGAL 187
DB 61 OKRLSMETDKYRLHLVADLLVLTLPFWADVAANWYGFELCAVHYITVNLVSSVL 120
OY 188 LLAQTSFDYRLNIYHATQLYRRGPRARVTLTCLAVMGICLLEFALPDFFLSAHDERLNA 247
DB 121 LLAFLSLDRFLAIVHATNSQRPRKLLAEKVYVGVWIPALLITPDTF--ANVSEADR 178
OY 248 THCOYNFP-QVGRFALRVQLVAGFLLPLLVMAVCYAHILAVLLVSRGQRRRLRMRLVV 306
DB 179 YICDRFYRNDLWVVFQPHIIVWGLIPGIVLSCYCIISKLSHGKQRKALKTTVI 238
OY 307 VVVALCWTPIYHLVYVDLMDGALARNGRSRYDVAKSVTSGLCYHMCCLNPLIYA 366
DB 239 LILAFACWLPYIYIGISIDFTFLIIRGCEFEVTVHWMISITTEALAFHCCCLNPLIYA 298
OY 367 FVGKFRERMMMLL-----LRGCPNORGLQRPSSSRDSSM 404
DB 299 FLGAKFKTSAQNMLTSVSRGSSLKILSKRGHSSSVTSESSSF 344

RESULT 6
ID 093237 PRELIMINARY: PRT: 372 AA.
AC 093237:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CXC CHEMOKINE RECEPTOR-1.
OS Cyprius carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=99367403; PubMed=10436187;
RA Fujiki K., Shin D., Nakao M., Yano T.;
RT "Molecular cloning of carp (Cyprinus carpio) CC chemokine, CXC
RT chemokine receptors, allograft inflammatory factor-1, and natural

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OY 68 ENFSSSYDGENESDSCCTSPPCPODFSLNPDRAFLPALYSLLFLGLGNCAVAAILLS 127
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 5 DNYTEMGSGDVS-----IKPCPFRENNANFNKIFLPTIYSIIFLGLYGNGLVILVMGY 60
OY 128 RTALSTDTFLLHLAVADTLVLVTLPLMAVDAVQWFGSLCKVAGALFNINFYAGAL 187
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 61 OKKLSMTDKYRLHLVSADLLFVITLPEFAVDAVANWYFGNFLCAVAVHYIVNLYSSVL 120
OY 188 ILACISFDRLYLVIAVATQLYRGRPARVTLTCLAWGCLLFLALDPDFTLSAHNDERLNA 247
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 121 ILAFISLDRLYLVIAVATNSQRPRLKLAEKVYVGVWIPALLTLTIDPFI--ANVSEADR 178
OY 248 THCOYNFP-QVGRALRVQLVAGFLPLLVMAACYAHILAVLVSRCGRRLRAMRLVVV 306
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 179 YICDRFYRNDLWVWVFOFOHIMVGLLPGLVILSCYCIISKLSKSHQKRAKLTIVY 238
OY 307 VVVAFALCMTPRHLVVLVDILMDGLALANCRGSRVDVAKSVTSGLGVMHCCLPDLVA 366
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 239 LILAFACWLPYYIGISIDSFILLEIKGCEFEVTVHKWISITELAFHCCLPDLVA 298
OY 367 FVGKFERERMMLL-----LRGCPNQRGLQROPSSSRDSSW 404
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 299 FLGAKFKTSAOHALTVSRSGLSKILSKGRGSHSVSTESSESSF 344
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RESULT 9

```
O9MZ2 PRELIMINARY; PRT; 347 AA.
ID O9MZ2
AC O9MZ2:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF172231; AAF89351.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER
SQ SEQUENCE 347 AA; 39209 MW; D853326462E15B22 CRC64;
```

```
Query Match 26.8%; Score 576.5; DB 6; Length 347;
Best Local Similarity 35.0%; Pred. No. 1.6e-43;
Matches 121; Conservative 70; Mismatches 140; Indels 15; Gaps 4;
```

```
OY 68 ENFSSSYDGENESDSCCTSPPCPODFSLNPDRAFLPALYSLLFLGLGNCAVAAILLS 127
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 5 DNYTEMGSGDVS-----IKPCPFRENNANFNKIFLPTIYSIIFLGLYGNGLVILVMGY 60
OY 128 RTALSTDTFLLHLAVADTLVLVTLPLMAVDAVQWFGSLCKVAGALFNINFYAGAL 187
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 61 OKKLSMTDKYRLHLVSADLLFVITLPEFAVDAVANWYFGNFLCAVAVHYIVNLYSSVL 120
OY 188 ILACISFDRLYLVIAVATQLYRGRPARVTLTCLAWGCLLFLALDPDFTLSAHNDERLNA 247
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
```

```
Db 121 ILAFISLDRLYLVIAVATNSQRPRLKLAEKVYVGVWIPALLTLTIDPFI--ANVSEADR 178
OY 248 THCOYNFP-QVGRALRVQLVAGFLPLLVMAACYAHILAVLVSRCGRRLRAMRLVVV 306
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 179 YICDRFYRNDLWVWVFOFOHIMVGLLPGLVILSCYCIISKLSKSHQKRAKLTIVY 238
OY 307 VVVAFALCMTPRHLVVLVDILMDGLALANCRGSRVDVAKSVTSGLGVMHCCLPDLVA 366
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 239 LILAFACWLPYYIGISIDSFILLEIKGCEFEVTVHKWISITELAFHCCLPDLVA 298
OY 367 FVGKFERERMMLL-----LRGCPNQRGLQROPSSSRDSSW 404
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 299 FLGAKFKTSAOHALTVSRSGLSKILSKGRGSHSVSTESSESSF 344
```

RESULT 10

```
O9MZ2 PRELIMINARY; PRT; 347 AA.
ID O9MZ2
AC O9MZ2:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF172232; AAF89352.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER
SQ SEQUENCE 347 AA; 39209 MW; D853326462E15B22 CRC64;
```

```
Query Match 26.8%; Score 576.5; DB 6; Length 347;
Best Local Similarity 35.0%; Pred. No. 1.6e-43;
Matches 121; Conservative 70; Mismatches 140; Indels 15; Gaps 4;
```

```
OY 68 ENFSSSYDGENESDSCCTSPPCPODFSLNPDRAFLPALYSLLFLGLGNCAVAAILLS 127
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 5 DNYTEMGSGDVS-----IKPCPFRENNANFNKIFLPTIYSIIFLGLYGNGLVILVMGY 60
OY 128 RTALSTDTFLLHLAVADTLVLVTLPLMAVDAVQWFGSLCKVAGALFNINFYAGAL 187
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 61 OKKLSMTDKYRLHLVSADLLFVITLPEFAVDAVANWYFGNFLCAVAVHYIVNLYSSVL 120
OY 188 ILACISFDRLYLVIAVATQLYRGRPARVTLTCLAWGCLLFLALDPDFTLSAHNDERLNA 247
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 121 ILAFISLDRLYLVIAVATNSQRPRLKLAEKVYVGVWIPALLTLTIDPFI--ANVSEADR 178
OY 248 THCOYNFP-QVGRALRVQLVAGFLPLLVMAACYAHILAVLVSRCGRRLRAMRLVVV 306
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 179 YICDRFYRNDLWVWVFOFOHIMVGLLPGLVILSCYCIISKLSKSHQKRAKLTIVY 238
OY 307 VVVAFALCMTPRHLVVLVDILMDGLALANCRGSRVDVAKSVTSGLGVMHCCLPDLVA 366
      :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 239 LILAFACWLPYYIGISIDSFILLEIKGCEFEVTVHKWISITELAFHCCLPDLVA 298
OY 367 FVGKFERERMMLL-----LRGCPNQRGLQROPSSSRDSSW 404
```

DB 299 FLGAKFKTSAQHALLTSVSRGSSIKLTKGKRGHSSVSTESSSSF 344

RESULT 11

Q9M2M8 PRELIMINARY: PRT; 347 AA.

AC Q9M2M8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrich.
OX NCBI_TaxId=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF172235; AAF89355.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_REC_P1_2; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 347 AA; 39152 MW; 925EC9FC1E8753 CRC64;

Query Match 26.8%; Score 576.5; DB 6; Length 347;
Best Local Similarity 35.3%; Pred. No. 1.6e-43;
Matches 123; Conservative 70; Mismatches 136; Indels 19; Gaps 6;

QY 68 ENSSSYDGENSDSCSPPCPDFSLNFDRAFLPALYSLLFLGLGNGAVALLS 127
DB 5 DNTTEELGSGDDVS---IKPCFRENHNFNFIPLTYISIFLGIYNGVILVMGY 60
QY 128 RTTALSTDTFLHLAVADTLVLTPLPAVDAVAVQWFGSGLCKVAGALFNINFYAGAL 187
DB 61 QKRLRMTDKYRLHLSTADLLFVITLPEFNAVDAVAVWVFGEFLCKAVHYIYVNLSSYL 120
QY 188 LLAACISFDRLYNVHATQLYRGRPARVT--LTCLAVWGICLLFLALPDFITLSAHHDERL 245
DB 121 ILAISILDRLAIVAHTSQSR--PKILAEKVYVGVWIPALLLTIPDFIF--ANVSEAD 176
QY 246 NATHCOYNP-QVGRPALVLOLVAGFLPLPLVMACYAHIIAVLVSRGQRRLRAMRLV 304
DB 177 DRYICDRFPNDLVVVFQFIHWGLLPGVILSCYCIISLSKSHSGHQRKALKTT 236
QY 305 VVVVDAALCWTPYHLVVDILMDGALARNGRESRVDAVSYSGLGYMCCINPLI 364
DB 237 VVILALFPACWLPYYIGISIDSIFLLEITRQGCFFENTYHKWISTIEALAFHCCINPLII 296
QY 365 YAFVGVKFRERMMML-----LRGCPNQGLOROPSSSRDSSW 404
DB 297 YAFLGAKFKTSAQHALLTSVSRGSSIKLTKGKRGHSSVSTESSSSF 344

RESULT 12

Q9M2M1 PRELIMINARY: PRT; 347 AA.

AC Q9M2M1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Eulemur macaco (Petterus macaco).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Eulemur.
OX NCBI_TaxId=30602;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF172242; AAF89362.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_REC_P1_2; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 347 AA; 39155 MW; 9BFA91A3824F7A7A CRC64;

Query Match 26.8%; Score 576.5; DB 6; Length 347;
Best Local Similarity 35.2%; Pred. No. 1.6e-43;
Matches 122; Conservative 68; Mismatches 140; Indels 17; Gaps 5;

QY 68 ENSSSYDGENSDSCSPPCPDFSLNFDRAFLPALYSLLFLGLGNGAVALLS 127
DB 5 DNTTEELGSGDDVS---IKPCFRENHNFNFIPLTYISIFLGIYNGVILVMGY 60
QY 128 RTTALSTDTFLHLAVADTLVLTPLPAVDAVAVQWFGSGLCKVAGALFNINFYAGAL 187
DB 61 QKRLRMTDKYRLHLSTADLLFVITLPEFNAVDAVAVWVFGEFLCKAVHYIYVNLSSYL 120
QY 188 LLAACISFDRLYNVHATQLYRGRPARVT--LTCLAVWGICLLFLALPDFITLSAHH--DERLN 246
DB 121 ILAISILDRLAIVAHTSQSRPKLSAEKVYVAGVLPALLLTIPDFITASVSEVDRY- 179
QY 247 ATHCOYNP-QVGRPALVLOLVAGFLPLPLVMACYAHIIAVLVSRGQRRLRAMRLV 305
DB 180 --TCDRLYPNDLVVVFQFIHWGLLPGVILSCYCIISLSKSHSGHQRKALKTTV 237
QY 306 VVVVDAALCWTPYHLVVDILMDGALARNGRESRVDAVSYSGLGYMCCINPLIY 365
DB 238 ILLAFACWLPYYIGISIDSIFLLEITRQGCFFENTYHKWISTIEALAFHCCINPLIY 297
QY 366 AEFVGVKFRERMMML-----LRGCPNQGLOROPSSSRDSSW 404
DB 298 AFLGAKFKTSAQHALLTSVSRGSSIKLTKGKRGHSSVSTESSSSF 344

RESULT 13

Q9M2P6 PRELIMINARY: PRT; 347 AA.

AC Q9M2P6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Presbytis johnii.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OX Presbytis.
OX NCBI_TaxId=98375;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in

Query	Subject	Score	Length	DB	Score	Length	DB	Score	Length	DB
68	ENFSSSYDYGENSEDSCTSPCCPODFSLNEDRAFLPALYSILFLGLLGNAGVAVALIS 127	26.8%	347	DB 6	26.8%	347	DB 6	26.8%	347	DB 6
5	DNYTEEMSGSDYDS---IKPCFPEENAHFRILPTIYSILFLGLYINGNLVILMYK 60	34.9%	347	DB 1	34.9%	347	DB 1	34.9%	347	DB 1
128	RTALISSTDTFLHLAAVADTLVTLPLAAVDAVAVQWFGSLCKAVAGLFINIFYAGAL 187	34.9%	347	DB 1	34.9%	347	DB 1	34.9%	347	DB 1
188	LLACISFPRYINIVATQLRGPPARVATLTCIAVWGLCLFALPDPFLS-AHDERLN 246	34.9%	347	DB 1	34.9%	347	DB 1	34.9%	347	DB 1
121	ILASTISLDRYLAIVATNSQKPRKLLAEKVYVGVWIPALLTLTIDPFIASVSEADRY- 179	34.9%	347	DB 1	34.9%	347	DB 1	34.9%	347	DB 1
247	ATHCOYNPP-OVGRATLAVLQIYAGFLPLVAVCAHIIILAVLSRGQRRLARLVV 305	34.9%	347	DB 1	34.9%	347	DB 1	34.9%	347	DB 1
180	-ICDRFYPNDLVAVVFEQHIMVGLLPGVILSCYCIISKLSKQKRAKATTV 237	34.9%	347	DB 1	34.9%	347	DB 1	34.9%	347	DB 1
306	VVVVAFALCWPYHLYLVLDIMDLGALARNCGRSRDVAKSVTSGLGVHCCPLPLY 365	34.9%	347	DB 1	34.9%	347	DB 1	34.9%	347	DB 1
238	ILILAFACWLPYIYIGISIDSFILIEIKOGCEPENTVAKWISITELAFHFCCLNPILY 297	34.9%	347	DB 1	34.9%	347	DB 1	34.9%	347	DB 1
366	AFVGVKFEREMMMLL-----LRLGCPNONGCLROPSSSRDSSW 404	34.9%	347	DB 1	34.9%	347	DB 1	34.9%	347	DB 1
298	AFLLAKFKRTSAOHALTYSRGSSLLKILSKGRGHSSVSTESSSE 344	34.9%	347	DB 1	34.9%	347	DB 1	34.9%	347	DB 1

DR	PROSITE: PS50262; G_PROTEIN_RECIP_FL2; 1.
KM	PROSITE: PS50290; IG_MHC; UNKNOWN.1.
DR	G-protein coupled receptor; glycoprotein; Receptor; Transmembrane.
FT	NON_TER 1
SO	SEQUENCE 347 AA; 39189 MW; 0AB960091D24874 CRC64;
Query Match	26.8%; Score 575.5; DB 6; Length 347;
Best Local Similarity	34.9%; Pred. No. 1.9e-43;
Matches 121: Conservative	71; Mismatches 138; Indels 17; Gaps 5
QY	68 EFNSSSYDYGEMNESDCCSPCCPODFSLNPPRAFLYSLFLGLLGNGAVALLS 127
DB	5 DNYTEBMGSGDDYS-----IKPCPFREAHFNPIFLPTLYSLIFLGLVGNGLVLMWG 60
QY	128 RRTALSTSTFELHLAVADTLVLTLPLAAVDAVAQVWGSGICKVAALFNIFYAGAL 187
DB	61 QKKLSMDKRYKHLISVADLLFVITLPEAVDAVANMYGNFLCKRVHYIYVNLKSYLV 120
QY	188 LIACISFDRLYNIVHATQLYRRGPPARYTLTCLAVWGLCLFALPDPIFLS-AHNDERLN 246
DB	121 ILAFISLDRLYLIVHATNSQKPRKLAEKVVYGVWVIMPALLTLPDIFPAVSEADRF- 179
QY	247 AHHQCYNFP-QVGRRLARVLQVAGFLPLVMAYCYAHILAVLVSRCQRRLARMLVY 305
DB	180 --TCREPYNDLWVVFQPHIMVGLDIGIYLSCYCIISLKSCHKOKRAKATTV 237
QY	306 VVVVAFALCWTFYHVLVLDLMDGALARNCGRESRVDAKSVTSGLYMCCNLPLLY 365
DB	238 IILIAFACWMLYYIGISIDISFLIEITIGQCEFEFTYHKWISITALEFFHCCLPILY 297
QY	366 AFVGVKFERMMMLL-----LRLGCPNORGLORPSSSRDSSW 404
DB	298 AFLGAKFTSQAHALTYSVRSGLSKILSKRGHSHSVTESSSF 344
RESULT 15	
Q9MZM6	PRELIMINARY; PRT; 347 AA.
ID	Q9MZM6
AC	Q9MZM6
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN	CXCR4.
OS	Calliebus moloch (Dusky titl).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Placentalia; Cebidae; Calliebinidae;
OC	Calliebus.
OX	NCBI_TaxID=9523;
OX	NCBI_TaxID=9523;
OX	NCBI_TaxID=9523;
RP	SEQUENCE FROM N. A.
RA	Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT	"Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in Primates."
RL	Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR	EMBL, AF172237; AAF89357.1.-
DR	InterPro: IPR00276; GPCR_Rhodopsn.
DR	InterPro: IPR003006; IG_MHC.
DR	Pfam: PF00001; 7tm.1; 1.
DR	PRINTS: PR00237; GPCR_RHODOPSN.
DR	PROSITE: PS00237; G_PROTEIN_RECIP_FL1; 1.
DR	PROSITE: PS00262; G_PROTEIN_RECIP_FL2; 1.
DR	PROSITE: PS00290; IG_MHC; UNKNOWN.1.
KW	G-protein coupled receptor; glycoprotein; Receptor; Transmembrane.
FT	NON_TER 1
SO	SEQUENCE 347 AA; 39352 MW; AAFECB08C61F0C5A6A CRC64;
Query Match	26.8%; Score 575.5; DB 6; Length 347;
Best Local Similarity	35.2%; Pred. No. 1.9e-43;
Matches 123: Conservative	69; Mismatches 138; Indels 19; Gaps 5

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 2, 2002, 12:08:10 : Search time 200 Seconds
(without alignments)
730.360 Million cell updates/sec

Title: US-09-101-518a-2
Perfect score: 2151
Sequence: 1 MELRKYPGRGLACTIVIGAA.....SSHRDSSWSEPSASYGL 415

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues
Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

- 1: /cgn2-6/ptodata/1/paa/PCYUS_COMB.pep.*
- 2: /cgn2-6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2-6/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgn2-6/ptodata/1/paa/US08_COMB.pep.*
- 5: /cgn2-6/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgn2-6/ptodata/1/paa/US082_COMB.pep.*
- 7: /cgn2-6/ptodata/1/paa/US083_COMB.pep.*
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- 15: /cgn2-6/ptodata/1/paa/US091_COMB.pep.*
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- 25: /cgn2-6/ptodata/1/paa/US101_COMB.pep.*
- 26: /cgn2-6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2142	99.6	415	1	PCT-US96-00499-2
2	2142	99.6	415	1	PCT-US96-00499A-2
3	2142	99.6	415	15	US-09-101-518a-2
4	2136	99.3	472	1	PCT-US00-26524B-6392
5	1891	87.9	368	15	US-09-170-496C-20
6	1891	87.9	368	15	US-09-170-496C-20
7	1891	87.9	368	15	US-09-170-496D-20

8	1891	87.9	368	20	US-09-624-594-2	Sequence 2, Appl
9	1891	87.9 <td>368</td> <td>20</td> <td>US-09-633-541-2</td> <td>Sequence 2, Appl</td>	368	20	US-09-633-541-2	Sequence 2, Appl
10	1891	87.9 <td>368</td> <td>20</td> <td>US-09-663-702-2</td> <td>Sequence 2, Appl</td>	368	20	US-09-663-702-2	Sequence 2, Appl
11	1891	87.9 <td>368</td> <td>20</td> <td>US-09-663-799-2</td> <td>Sequence 2, Appl</td>	368	20	US-09-663-799-2	Sequence 2, Appl
12	1885	87.6 <td>368</td> <td>15</td> <td>US-09-170-496C-174</td> <td>Sequence 174, App</td>	368	15	US-09-170-496C-174	Sequence 174, App
13	1885	87.6 <td>368</td> <td>15</td> <td>US-09-170-496D-174</td> <td>Sequence 174, App</td>	368	15	US-09-170-496D-174	Sequence 174, App
14	1626.5	75.6 <td>367</td> <td>14</td> <td>US-09-010-701C-22</td> <td>Sequence 22, Appl</td>	367	14	US-09-010-701C-22	Sequence 22, Appl
15	1519.5	70.6 <td>380</td> <td>26</td> <td>US-60-258-273-107</td> <td>Sequence 107, Appl</td>	380	26	US-60-258-273-107	Sequence 107, Appl
16	1281	59.6	271	26	US-60-213-169-424	Sequence 424, App
17	1281	59.6	271	26	US-60-213-170-424	Sequence 424, App
18	1197.5	55.7	970	26	US-60-212-635-534	Sequence 534, App
19	1172.5	54.5	944	26	US-60-229-515-947	Sequence 947, App
20	901	41.9	209	26	US-60-213-844-255	Sequence 255, App
21	661	30.7	357	1	PCT-US99-08395-20	Sequence 20, Appl
22	661	30.7	357	16	US-09-294-058-20	Sequence 20, Appl
23	637.5	29.6	399	1	PCT-US01-03800A-2394	Sequence 2394, App
24	637.5	29.6	399	1	PCT-US01-08631-43968	Sequence 43968, A
25	636.5	29.6	1490	26	US-60-207-317-223	Sequence 223, App
26	636	29.6	466	26	US-60-229-515-1218	Sequence 1218, App
27	636	29.6	466	26	US-60-229-515-1248	Sequence 1248, App
28	635.5	29.5	355	1	PCT-US01-16777-36	Sequence 36, Appl
29	635	29.5	372	12	US-08-802-627-6	Sequence 6, Appl
30	635	29.5	372	15	US-09-104-063-6	Sequence 6, Appl
31	635	29.5	372	15	US-09-170-496C-66	Sequence 66, Appl
32	635	29.5	372	15	US-09-170-496C-66	Sequence 66, Appl
33	635	29.5	372	15	US-09-170-496D-66	Sequence 66, Appl
34	635	29.5	372	18	US-09-420-784-5	Sequence 5, Appl
35	635	29.5	372	19	US-09-573-353-5	Sequence 5, Appl
36	635	29.5	378	1	PCT-US01-03800A-2243	Sequence 2243, App
37	635	29.5	390	26	US-60-229-515-741	Sequence 741, App
38	634.5	29.5	355	1	PCT-US01-16777-37	Sequence 37, Appl
39	633	29.4	353	1	PCT-US96-00499-9	Sequence 9, Appl
40	633	29.4	353	1	PCT-US96-00499A-9	Sequence 9, Appl
41	633	29.4	353	15	US-09-101-518-9	Sequence 9, Appl
42	633	29.4	355	1	PCT-US01-16777-27	Sequence 27, Appl
43	633	29.4	355	1	PCT-US01-16777-28	Sequence 28, Appl
44	633	29.4	355	1	PCT-US01-16777-30	Sequence 30, Appl
45	633	29.4	355	1	PCT-US93-10672-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

PCT-US96-00499-2

Sequence 2, Application PC/TUS9600499

GENERAL INFORMATION:

APPLICANT: LI, YI

TITLE OF INVENTION: Human G-Protein Chemokine Receptor

TITLE OF INVENTION: HSKTU68

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carella, Byrne, Baln, Gilfillan, Cecchi,

ADDRESS: Stewart & Olstein

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: NJ

COUNTRY: USA

ZIP: 07068-1739

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/00499

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-474

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-00499a-2

Query Match 99.6%; Score 2142; DB 1; Length 415;
Best Local Similarity 99.8%; Pred. No. 4.8e-193;
Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MELRRYGPRLAGTYIGGAAGSKSOTKSDSTIKKEFLPGLYTAPSSPPFPSSQVSDHQVIND 60
DB 1 MELRRYGPRLAGTYIGGAAGSKSOTKSDSTIKKEFLPGLYTAPSSPPFPSSQVSDHQVIND 60
OY 61 AEVAALLENFSSSYDYGENESDSCCTSPPCPODFSINFDRAFLPALYSILFLGLGNGA 120
DB 61 AEVAALLENFSSSYDYGENESDSCCTSPPCPODFSINFDRAFLPALNSILFLGLGNGA 120
OY 121 VAAVLSRRTALSTDTFLHLAVADTLVTLPLMAVDAAVQWFGSGLCVAGALFNI 180
DB 121 VAAVLSRRTALSTDTFLHLAVADTLVTLPLMAVDAAVQWFGSGLCVAGALFNI 180
OY 181 NFYAGALLIACISFDRYLNIYHATOLYRRGPPARYTLCIAWGLCLFLALPDFILSAH 240
DB 181 NFYAGALLIACISFDRYLNIYHATOLYRRGPPARYTLCIAWGLCLFLALPDFILSAH 240
OY 241 HDERLNATHCOYNFPQVGTALRVQLVAGFLPLLVMAACYAHILAVLSRGQRRLRA 300
DB 241 HDERLNATHCOYNFPQVGTALRVQLVAGFLPLLVMAACYAHILAVLSRGQRRLRA 300
OY 301 MLLVYVVAFAFALCMTPHLVLVLDLMDGLANCGRESVDVAKSVTSGLGVMHCL 360
DB 301 MLLVYVVAFAFALCMTPHLVLVLDLMDGLANCGRESVDVAKSVTSGLGVMHCL 360
OY 361 NPLLYAFVGVKREHMMMLLRLGCPNORGLOROPSSSRDSSMSETSEASYSGL 415
DB 361 NPLLYAFVGVKREHMMMLLRLGCPNORGLOROPSSSRDSSMSETSEASYSGL 415

RESULT 2
PCT-US96-00499a-2
Sequence 2, Application PC/TUS9600499A

GENERAL INFORMATION:
APPLICANT: LI, YI
TITLE OF INVENTION: Human G-Protein Chemokine Receptor
FILE REFERENCE: HSATU68
NUMBER OF SEQUENCES: 9
CURRENT FILING DATE: 1998-12-21
PRIORITY FILING DATE: 1996-01-11
ADDRESS: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESS: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00499A
FILING DATE: 11 JAN 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-474
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-00499a-2

Query Match 99.6%; Score 2142; DB 1; Length 415;
Best Local Similarity 99.8%; Pred. No. 4.8e-193;
Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MELRRYGPRLAGTYIGGAAGSKSOTKSDSTIKKEFLPGLYTAPSSPPFPSSQVSDHQVIND 60
DB 1 MELRRYGPRLAGTYIGGAAGSKSOTKSDSTIKKEFLPGLYTAPSSPPFPSSQVSDHQVIND 60
OY 61 AEVAALLENFSSSYDYGENESDSCCTSPPCPODFSINFDRAFLPALYSILFLGLGNGA 120
DB 61 AEVAALLENFSSSYDYGENESDSCCTSPPCPODFSINFDRAFLPALNSILFLGLGNGA 120
OY 121 VAAVLSRRTALSTDTFLHLAVADTLVTLPLMAVDAAVQWFGSGLCVAGALFNI 180
DB 121 VAAVLSRRTALSTDTFLHLAVADTLVTLPLMAVDAAVQWFGSGLCVAGALFNI 180
OY 181 NFYAGALLIACISFDRYLNIYHATOLYRRGPPARYTLCIAWGLCLFLALPDFILSAH 240
DB 181 NFYAGALLIACISFDRYLNIYHATOLYRRGPPARYTLCIAWGLCLFLALPDFILSAH 240
OY 241 HDERLNATHCOYNFPQVGTALRVQLVAGFLPLLVMAACYAHILAVLSRGQRRLRA 300
DB 241 HDERLNATHCOYNFPQVGTALRVQLVAGFLPLLVMAACYAHILAVLSRGQRRLRA 300
OY 301 MLLVYVVAFAFALCMTPHLVLVLDLMDGLANCGRESVDVAKSVTSGLGVMHCL 360
DB 301 MLLVYVVAFAFALCMTPHLVLVLDLMDGLANCGRESVDVAKSVTSGLGVMHCL 360
OY 361 NPLLYAFVGVKREHMMMLLRLGCPNORGLOROPSSSRDSSMSETSEASYSGL 415
DB 361 NPLLYAFVGVKREHMMMLLRLGCPNORGLOROPSSSRDSSMSETSEASYSGL 415

RESULT 3
US-09-101-518-2
Sequence 2, Application us/09101518

GENERAL INFORMATION:
APPLICANT: LI, YI
TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
FILE REFERENCE: P218PCT-US
CURRENT APPLICATION NUMBER: US/09/101,518
CURRENT FILING DATE: 1998-12-21
PRIORITY FILING DATE: 1996-01-11
ADDRESS: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESS: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00499A
FILING DATE: 11 JAN 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-474
TELECOMMUNICATION INFORMATION:

Query Match 99.6%; Score 2142; DB 1; Length 415;
Best Local Similarity 99.8%; Pred. No. 4.8e-193;
Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MELRRYGPRLAGTYIGGAAGSKSOTKSDSTIKKEFLPGLYTAPSSPPFPSSQVSDHQVIND 60
DB 1 MELRRYGPRLAGTYIGGAAGSKSOTKSDSTIKKEFLPGLYTAPSSPPFPSSQVSDHQVIND 60
OY 61 AEVAALLENFSSSYDYGENESDSCCTSPPCPODFSINFDRAFLPALYSILFLGLGNGA 120
DB 61 AEVAALLENFSSSYDYGENESDSCCTSPPCPODFSINFDRAFLPALNSILFLGLGNGA 120

QY	121	VAAVLSRRRLSTSTDPFLHLVAADTLVLTPLMVAADVOMVFGSGLCRKVGALEPNI	180
Db	121	VAAVLSRRRLSTSTDPFLHLVAADTLVLTPLMVAADVOMVFGSGLCRKVGALEPNI	180
QY	181	NFYAGALLLACISFDRLYNIVHATOLYRGRPARVTTTCLAVWGICLTFALPDFIFLSAH	240
Db	181	NFYAGALLLACISFDRLYNIVHATOLYRGRPARVTTTCLAVWGICLTFALPDFIFLSAH	240
QY	241	HDRLNATHCOYNEPQVGRTRALRYOLVAGFLPLLVAACTAHILAVLYSRQORLRA	300
Db	241	HDRLNATHCOYNEPQVGRTRALRYOLVAGFLPLLVAACTAHILAVLYSRQORLRA	300
QY	301	MLRVVVVVVAEALCWTPTRYHLVVDLMDLGAALRNCGRSRRVDYAKSVTSGLGYMHCL	360
Db	301	MLRVVVVVVAEALCWTPTRYHLVVDLMDLGAALRNCGRSRRVDYAKSVTSGLGYMHCL	360
QY	361	NPLLXAFGVGFRRERMMMLLRGLCCPNQRGLOQROPSSSRBDSNSENSEASYSGI	415
Db	361	NPLLXAFGVGFRRERMMMLLRGLCCPNQRGLOQROPSSSRBDSNSENSEASYSGI	415

```

RESULT 4
PCT-US00-26524B-6392
Sequence 6392, Application PC/TUS0026524B
GENERAL INFORMATION:
APPLICANT: Birse et. al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
FILE REFERENCE: PA005PCT
CURRENT APPLICATION NUMBER: PCT/US00/26524B
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6392
LENGTH: 472
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (139)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (164)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US00-26524B-6392

```

Query Match	99.3%	Score 2136;	DB 1;	Length 472;
Best Local Similarity	99.5%;	Pred. No. 2.1e-192;		
Matches 413; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	MELKRYPGRLAGVIGGAOSK	SQTSKDSITTFKEFLGGLYAPSP	PPSPVSHOYND	60
Db	58	MELKRYGRLAGVIGGAOSK	SQTSKDSITTFKEFLGGLYAPSP	PPSPVSHOYND	117
QY	61	AEVAALLLENSSYDYGENES	SDCCTSPCPQDSLENFDRALFALY	SLFLGILNGA	120
Db	118	AEVAALLLENSSYDYGENES	SDCCTSPCPQDSLENFDRALFALY	SLFLGILNGA	177
QY	121	VAAYLLSRRLASTDIFELH	LAVDLLVTLPLMAVDAQVWFSSGLCK	VAGALENI	180
Db	178	VAAYLLSRRLASTDIFELH	LAVDLLVTLPLMAVDAQVWFSSGLCK	VAGALENI	237
QY	181	NFYAGALLACISFDRLYN	IVHATQLYRGP	PARVTLTCLAWGILCLFLALPDEIFLSAH	240
Db	238	NFYAGALLACISFDRLYN	IVHATQLYRGP	PARVTLTCLAWGILCLFLALPDEIFLSAH	297
QY	241	HDEFLNATHCOYNPQYGR	RLARVLQVACFLPLFLVMAYCSAH	ITLAVLVSRGQRRRA	300
Db	298	HDEFLNATHCOYNPQYGR	RLARVLQVACFLPLFLVMAYCSAH	ITLAVLVSRGQRRRA	357

OY 301 MRIVVVVVAALICMTCPHYIVLVNLIIMDLALANCRRESVNDYAKSTSCIGYMHCL 360

Db 358 MRIVVVVVVAALICMTCPHYIVLVNLIIMDLGLANCRRESVNDYAKSTSCIGYMHCL 417

OY 361 NPLLYAAEVGVKFEREMMMLLLRLGCPNORGLOROPSSSRDSSWSETSASYSGL 415

Db 418 NPLLYAAEVGVKFEREMMMLLLRLGCPNORGLOROPSSSRDSSWSETSASYSGL 472

```

RESULT 5
US-09-170-496-20
: Sequence 20, Application US/09170496
:
: GENERAL INFORMATION:
:
: APPLICANT: Behan, Dominic P.
: APPLICANT: Chalmers, Derek T.
: APPLICANT: Liaw, Chen W.
: TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled Receptor
: TITLE OF INVENTION: Receptors
: FILE REFERENCE: AREN-0040
: CURRENT APPLICATION NUMBER: US/09/170.496
: CURRENT FILING DATE: 1998-10-13
: NUMBER OF SEQ ID NOS: 286
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 20
: LENGTH: 368
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
: US-09-170-496-20

```

Query Match	87.98;	Score 1891;	DB 15;	Length 368;
Best Local Similarity	99.78;	Pred. No. 2.1e-169;		
Matches 364;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0

QY	51	QVSDHQVINDAEVAALEENFSSYDYGENESQCTSPCPODESLNDRATPLATSL	110
Db	4	EVSDBQVINDAEVAALEENFSSSYDYGENESQCTSPCPODESLNDRATPLATSL	63
QY	111	FLGLGLNGAAVAVLLSRTALSSDTDFLLHLAVADTLVLTLPLMAADAQWFGSGL	170
Db	64	FLGLGLNGAAVAVLLSRTALSSDTDFLLHLAVADTLVLTLPLMAADAQWFGSGL	123
QY	171	CKVAGALENINPVAGALLLACISEDRYLNIYHAQOLYRRGPARYTLCLAVMGLCLLFA	230
Db	124	CKVAGALENINPVAGALLLACISFEDRYLNIYHAQOLYRRGPARYTLCLAVMGLCLLFA	183
QY	231	LPDFFFLSAHNDERLNATHCOYNFPQVGRATRLVQLVAGFLPLLVMAUYCAHTLAVLL	290
Db	184	LPDFFFLSAHNDERLNATHCOYNFPQVGRATRLVQLVAGFLPLLVMAUYCAHTLAVLL	243
QY	291	VSRQORLRLARLRLVVVVVAVAFALCWTPLYHLVLYVDILMDGLALBNCGRESVDVAKSVT	350
Db	244	VSRQORLRLARLRLVVVVVAVAFALCWTPLYHLVLYVDILMDGLALBNCGRESVDVAKSVT	303
QY	351	SGLGVMHCCMLPLLYAFVGVKFERERMMLLLRLGCPNQRGLOROPSSSRDSSWSETSEA	410
Db	304	SGLGVMHCCMLPLLYAFVGVKFERERMMLLLRLGCPNQRGLOROPSSSRDSSWSETSEA	363
QY	411	SYSGL 415	
Db	364	SYSGL 368	

```

RESULT 6
US-09-170-496C-20
; Sequence 20, Application US/09170496C
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled Receptors
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040

```

```
; CURRENT APPLICATION NUMBER: US/09/170,496C
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496C-20
```

```
Query Match          87.9%; Score 1891; DB 15; Length 368;
Best Local Similarity 99.7%; Pred. No. 2.1e-169;
Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 51 QVSDHQVINDAEVAALLENFSSSYDYGENESDSCCTSPCCPODFSLNFDRAFLPALYSLL 110
Db 4 EVSDHQVINDAEVAALLENFSSSYDYGENESDSCCTSPCCPODFSLNFDRAFLPALYSLL 63
Oy 111 FLGLLGNCAVAVALLSRRTALSTDTFLHLAVADTLVLTPLMAVDAVQWVFGSGL 170
Db 64 FLGLLGNCAVAVALLSRRTALSTDTFLHLAVADTLVLTPLMAVDAVQWVFGSGL 123
Oy 171 CKVAGALENINFYAGALLLACISFDRIYINIVATQLYRRGPARVTLTCLAWGICLLFA 230
Db 124 CKVAGALENINFYAGALLLACISFDRIYINIVATQLYRRGPARVTLTCLAWGICLLFA 183
Oy 231 LPDFIFLSAHDRLNATHCQYNFPQVGTALRVQLVAGFLLPPLVMAVCYAHILAVLL 290
Db 184 LPDFIFLSAHDRLNATHCQYNFPQVGTALRVQLVAGFLLPPLVMAVCYAHILAVLL 243
Oy 291 VSRGGRRLRAMRLVYVVVVAFAFCWTPYHLVYLVLDLMDGLALARNCGRESRVDAKSVT 350
Db 244 VSRGGRRLRAMRLVYVVVVAFAFCWTPYHLVYLVLDLMDGLALARNCGRESRVDAKSVT 303
Oy 351 SGLGYMHCCINLPLAFYGVKFRERMMMLLRLGCPNORGLOROPSSSRDSSMSETSEA 410
Db 304 SGLGYMHCCINLPLAFYGVKFRERMMMLLRLGCPNORGLOROPSSSRDSSMSETSEA 363
Oy 411 SYSGL 415
Db 364 SYSGL 368
```

```
RESULT 7
US-09-170-496D-20
; Sequence 20, Application US/09170496D
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-20
```

```
Query Match          87.9%; Score 1891; DB 15; Length 368;
Best Local Similarity 99.7%; Pred. No. 2.1e-169;
Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 51 QVSDHQVINDAEVAALLENFSSSYDYGENESDSCCTSPCCPODFSLNFDRAFLPALYSLL 110
Db 4 EVSDHQVINDAEVAALLENFSSSYDYGENESDSCCTSPCCPODFSLNFDRAFLPALYSLL 63
Oy 111 FLGLLGNCAVAVALLSRRTALSTDTFLHLAVADTLVLTPLMAVDAVQWVFGSGL 170
Db 64 FLGLLGNCAVAVALLSRRTALSTDTFLHLAVADTLVLTPLMAVDAVQWVFGSGL 123
```

```
Db 64 FLGLLGNCAVAVALLSRRTALSTDTFLHLAVADTLVLTPLMAVDAVQWVFGSGL 123
Oy 171 CKVAGALENINFYAGALLLACISFDRIYINIVATQLYRRGPARVTLTCLAWGICLLFA 230
Db 124 CKVAGALENINFYAGALLLACISFDRIYINIVATQLYRRGPARVTLTCLAWGICLLFA 183
Oy 231 LPDFIFLSAHDRLNATHCQYNFPQVGTALRVQLVAGFLLPPLVMAVCYAHILAVLL 290
Db 184 LPDFIFLSAHDRLNATHCQYNFPQVGTALRVQLVAGFLLPPLVMAVCYAHILAVLL 243
Oy 291 VSRGGRRLRAMRLVYVVVVAFAFCWTPYHLVYLVLDLMDGLALARNCGRESRVDAKSVT 350
Db 244 VSRGGRRLRAMRLVYVVVVAFAFCWTPYHLVYLVLDLMDGLALARNCGRESRVDAKSVT 303
Oy 351 SGLGYMHCCINLPLAFYGVKFRERMMMLLRLGCPNORGLOROPSSSRDSSMSETSEA 410
Db 304 SGLGYMHCCINLPLAFYGVKFRERMMMLLRLGCPNORGLOROPSSSRDSSMSETSEA 363
Oy 411 SYSGL 415
Db 364 SYSGL 368
```

```
RESULT 8
US-09-624-594-2
; Sequence 2, Application US/09624594
; GENERAL INFORMATION:
; APPLICANT: Moser, Bernhard
; APPLICANT: Moser, Bernhard
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/624,594
; FILING DATE: 25-JUL-2000
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,838
; FILING DATE: 10-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: TK196-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-624-594-2
```

```
Query Match          87.9%; Score 1891; DB 20; Length 368;
Best Local Similarity 99.7%; Pred. No. 2.1e-169;
Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 51 QVSDHQVINDAEVAALLENFSSSYDYGENESDSCCTSPCCPODFSLNFDRAFLPALYSLL 110
Db 4 EVSDHQVINDAEVAALLENFSSSYDYGENESDSCCTSPCCPODFSLNFDRAFLPALYSLL 63
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QY 111 FLGLGNGAVALLSRRALSTDTFLHLAVADTLVTLPLMAVDAVQWFGSGL 170
DB 64 FLGLGNGAVALLSRRALSTDTFLHLAVADTLVTLPLMAVDAVQWFGSGL 123
QY 171 CKVAGALENINFGALLLACTISFDRLNIVATOLYRRGPARVTLCLAWGICLLFA 230
DB 124 CKVAGALENINFGALLLACTISFDRLNIVATOLYRRGPARVTLCLAWGICLLFA 183
QY 231 LPDFTLSAHHDERLNATHCOYNFQVGTALRVQLVAAGFLPLLVMAVYCAHILAVLL 290
DB 184 LPDFTLSAHHDERLNATHCOYNFQVGTALRVQLVAAGFLPLLVMAVYCAHILAVLL 243
QY 291 VSRGQRRLRAMRLVVVVVAFALCWTPTHLVVLVDIIMDLGALARNCGRESHVDAKSVT 350
DB 244 VSRGQRRLRAMRLVVVVVAFALCWTPTHLVVLVDIIMDLGALARNCGRESHVDAKSVT 303
QY 351 SGLGYMHCCLNPLLYAFVGVKFRERMMMLLRGCPNORGLOROPSSSRDSSMSETSEA 410
DB 304 SGLGYMHCCLNPLLYAFVGVKFRERMMMLLRGCPNORGLOROPSSSRDSSMSETSEA 363
QY 411 SYSGL 415
DB 364 SYSGL 368

RESULT 9

US-09-633-541-2
: Sequence 2, Application US/09633541
: GENERAL INFORMATION:
: APPLICANT: Loetscher, Marcel
: APPLICANT: Moser, Bernhard
: TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3.
: TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Militia Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: USA
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/633,541
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/709,838
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Brook Esq., David E.
: REGISTRATION NUMBER: 22,592
: REFERENCE/DOCKET NUMBER: TK196-01
: TELEPHONE: (617) 861-6240
: TELEFAX: (617) 861-9540
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 368 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-633-541-2

Query Match 87.9%; Score 1891; DB 20; Length 368;
Best Local Similarity 99.7%; Pred. No. 2,1e-169;
Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 51 QVSDHQVLNDAEVAALLLENFSSSYDYGENSEDSCTSPCPQDPSLNDRAFLPALYSLL 110

DB 4 EYSDHQVLNDAEVAALLLENFSSSYDYGENSEDSCTSPCPQDPSLNDRAFLPALYSLL 63
QY 111 FLGLGNGAVALLSRRALSTDTFLHLAVADTLVTLPLMAVDAVQWFGSGL 170
DB 64 FLGLGNGAVALLSRRALSTDTFLHLAVADTLVTLPLMAVDAVQWFGSGL 123
QY 171 CKVAGALENINFGALLLACTISFDRLNIVATOLYRRGPARVTLCLAWGICLLFA 230
DB 124 CKVAGALENINFGALLLACTISFDRLNIVATOLYRRGPARVTLCLAWGICLLFA 183
QY 231 LPDFTLSAHHDERLNATHCOYNFQVGTALRVQLVAAGFLPLLVMAVYCAHILAVLL 290
DB 184 LPDFTLSAHHDERLNATHCOYNFQVGTALRVQLVAAGFLPLLVMAVYCAHILAVLL 243
QY 291 VSRGQRRLRAMRLVVVVVAFALCWTPTHLVVLVDIIMDLGALARNCGRESHVDAKSVT 350
DB 244 VSRGQRRLRAMRLVVVVVAFALCWTPTHLVVLVDIIMDLGALARNCGRESHVDAKSVT 303
QY 351 SGLGYMHCCLNPLLYAFVGVKFRERMMMLLRGCPNORGLOROPSSSRDSSMSETSEA 410
DB 304 SGLGYMHCCLNPLLYAFVGVKFRERMMMLLRGCPNORGLOROPSSSRDSSMSETSEA 363
QY 411 SYSGL 415
DB 364 SYSGL 368

RESULT 10

US-09-663-702-2
: Sequence 2, Application US/09663702
: GENERAL INFORMATION:
: APPLICANT: Loetscher, Marcel
: APPLICANT: Moser, Bernhard
: Qiu, Shixin
: Mackay, Charles R.
: TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3.
: TITLE OF INVENTION: ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Militia Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: USA
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/663,702
: FILING DATE: 15-SEP-2000
: CLASSIFICATION: <unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/829,839
: FILING DATE: <unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Brook Esq., David E.
: REGISTRATION NUMBER: 22,592
: REFERENCE/DOCKET NUMBER: TK196-01A
: TELEPHONE: (617) 861-6240
: TELEFAX: (617) 861-9540
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 368 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-663-702-2

Query Match 87.9%; Score 1891; DB 20; Length 368;
Best Local Similarity 99.7%; Pred. No. 2.1e-169;
Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 51 QVSDHQVINDAEVAALLLENFSSSYDYGENESDSCCTSPCCPODFSINPDRAPFLPALYSLL 110
:|||||
DB 4 EVSDHQVINDAEVAALLLENFSSSYDYGENESDSCCTSPCCPODFSINPDRAPFLPALYSLL 63
111 FLGLGNGAVAAYVLLSRTALSTDTFLHLAAVADTLVLTLPLMAVDAVQWVFGSGL 170
|||||
DB 64 FLGLGNGAVAAYVLLSRTALSTDTFLHLAAVADTLVLTLPLMAVDAVQWVFGSGL 123
171 KVGAGALFNINFYAGALLLACISFDRIYINIVHATQLYRRGPARVTLTCLAVWGICLLFA 230
|||||
DB 124 KVGAGALFNINFYAGALLLACISFDRIYINIVHATQLYRRGPARVTLTCLAVWGICLLFA 183
OY 231 LPDFTFLSAHDERLNATHCOYNPQVGTALRVQLVAGFLPLPLVMAVYCAHTLAVLL 290
|||||
DB 184 LPDFTFLSAHDERLNATHCOYNPQVGTALRVQLVAGFLPLPLVMAVYCAHTLAVLL 243
OY 291 VSRGQRRLRAMRLVYVVAFAFALCWTPIHLVYVLDIIMDLGALANCGRESRVDAKSVT 350
|||||
DB 244 VSRGQRRLRAMRLVYVVAFAFALCWTPIHLVYVLDIIMDLGALANCGRESRVDAKSVT 303
OY 351 SGLGYMHCCCLNPLLYAFVGVKFEREMMLLRLGCPNORGLOROPSSRRDSSWSETSEA 410
|||||
DB 304 SGLGYMHCCCLNPLLYAFVGVKFEREMMLLRLGCPNORGLOROPSSRRDSSWSETSEA 363
OY 411 SYSGL 415
|||||
DB 364 SYSGL 368

RESULT 11
US-09-663-799-2
; Sequence 2, Application US/09663799
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Marcel
; Moser, Bernhard
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
; NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/663,799
; FILING DATE: 15-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/709,838
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: TK196-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 amino acids
; TYPE: amino acid

TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-663-799-2

Query Match 87.9%; Score 1891; DB 20; Length 368;
Best Local Similarity 99.7%; Pred. No. 2.1e-169;
Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 51 QVSDHQVINDAEVAALLLENFSSSYDYGENESDSCCTSPCCPODFSINPDRAPFLPALYSLL 110
:|||||
DB 4 EVSDHQVINDAEVAALLLENFSSSYDYGENESDSCCTSPCCPODFSINPDRAPFLPALYSLL 63
111 FLGLGNGAVAAYVLLSRTALSTDTFLHLAAVADTLVLTLPLMAVDAVQWVFGSGL 170
|||||
DB 64 FLGLGNGAVAAYVLLSRTALSTDTFLHLAAVADTLVLTLPLMAVDAVQWVFGSGL 123
OY 171 KVGAGALFNINFYAGALLLACISFDRIYINIVHATQLYRRGPARVTLTCLAVWGICLLFA 230
|||||
DB 124 KVGAGALFNINFYAGALLLACISFDRIYINIVHATQLYRRGPARVTLTCLAVWGICLLFA 183
OY 231 LPDFTFLSAHDERLNATHCOYNPQVGTALRVQLVAGFLPLPLVMAVYCAHTLAVLL 290
|||||
DB 184 LPDFTFLSAHDERLNATHCOYNPQVGTALRVQLVAGFLPLPLVMAVYCAHTLAVLL 243
OY 291 VSRGQRRLRAMRLVYVVAFAFALCWTPIHLVYVLDIIMDLGALANCGRESRVDAKSVT 350
|||||
DB 244 VSRGQRRLRAMRLVYVVAFAFALCWTPIHLVYVLDIIMDLGALANCGRESRVDAKSVT 303
OY 351 SGLGYMHCCCLNPLLYAFVGVKFEREMMLLRLGCPNORGLOROPSSRRDSSWSETSEA 410
|||||
DB 304 SGLGYMHCCCLNPLLYAFVGVKFEREMMLLRLGCPNORGLOROPSSRRDSSWSETSEA 363
OY 411 SYSGL 415
|||||
DB 364 SYSGL 368

RESULT 12
US-09-170-496C-174
; Sequence 174, Application US/09170496C
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupl
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: ARBN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496C
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 174
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496C-174

Query Match 87.6%; Score 1885; DB 15; Length 368;
Best Local Similarity 99.5%; Pred. No. 7.7e-169;
Matches 363; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 51 QVSDHQVINDAEVAALLLENFSSSYDYGENESDSCCTSPCCPODFSINPDRAPFLPALYSLL 110
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DB 4 EVSDHQVINDAEVAALLLENFSSSYDYGENESDSCCTSPCCPODFSINPDRAPFLPALYSLL 63
111 FLGLGNGAVAAYVLLSRTALSTDTFLHLAAVADTLVLTLPLMAVDAVQWVFGSGL 170
|||||
DB 64 FLGLGNGAVAAYVLLSRTALSTDTFLHLAAVADTLVLTLPLMAVDAVQWVFGSGL 123
OY 171 KVGAGALFNINFYAGALLLACISFDRIYINIVHATQLYRRGPARVTLTCLAVWGICLLFA 230
|||||
DB 124 KVGAGALFNINFYAGALLLACISFDRIYINIVHATQLYRRGPARVTLTCLAVWGICLLFA 183

QY	231	LPDFFLESAHNDERLNATHCOYNFPQVGTALRYLQVLVAGFLPLLLVMAVYCAHILAVLL	290
Db	184	LPDFFLESAHNDERLNATHCOYNFPQVGTALRYLQVLVAGFLPLLLVMAVYCAHILAVLL	243
QY	291	VSRGQRRLRAKRLVVVVVAFALCWTPTYHLVVLVDLMDGLALRNCGRESRYDAKSVT	350
Db	244	VSRGQRRLRAKRLVVVVVAFALCWTPTYHLVVLVDLMDGLALRNCGRESRYDAKSVT	303
QY	351	SGLGVMHCCCLNPLLYAFVGVKFRERMMMLLLRLGCPNQRGLOROPSSSRDSSWSETSEA	410
Db	304	SGLGVMHCCCLNPLLYAFVGVKFRERMMMLLLRLGCPNQRGLOROPSSSRDSSWSETSEA	363
QY	411	SYSGL 415	
Db	364	SYSGL 368	

RESULT 13

US-09-170-496D-174

Sequence 174, Application US/09170496D

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Chalmers, Derek T.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled

TITLE OF INVENTION: Receptors

FILE REFERENCE: AREN-0040

CURRENT APPLICATION NUMBER: US/09/170,496D

CURRENT FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 294

SOFTWARE: PatentIn version 3.1

SEQ ID NO 174

LENGTH: 368

TYPE: PRT

ORGANISM: Homo sapiens

US-09-170-496D-174

Query Match

Best Local Similarity .99.5%; Pred. No 7.7e-169;

Matches 363; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 51 QVSDHQVLNDAEVAALLLENFSSSYDYGENESDSCCTSPCCPDGFSINFDRAFLPALYSLL 110

Db 4 EVSDHQVLNDAEVAALLLENFSSSYDYGENESDSCCTSPCCPDGFSINFDRAFLPALYSLL 63

QY 111 FLGLGLGGAVALVALLSRRTALSTDTFLHLAAVADTLVTLPLMAVDAAYQVWFGSGL 170

Db 64 FLGLGLGGAVALVALLSRRTALSTDTFLHLAAVADTLVTLPLMAVDAAYQVWFGSGL 123

QY 171 CKVAGALENINIFYAGALLLACISFDRYLNIYHATQLYRGRPARVTLTCLAWGCLPLA 230

Db 124 CKVAGALENINIFYAGALLLACISFDRYLNIYHATQLYRGRPARVTLTCLAWGCLPLA 183

QY 231 LPDFFLESAHNDERLNATHCOYNFPQVGTALRYLQVLVAGFLPLLLVMAVYCAHILAVLL 290

Db 184 LPDFFLESAHNDERLNATHCOYNFPQVGTALRYLQVLVAGFLPLLLVMAVYCAHILAVLL 243

QY 291 VSRGQRRLRAKRLVVVVVAFALCWTPTYHLVVLVDLMDGLALRNCGRESRYDAKSVT 350

Db 244 VSRGQRRLRAKRLVVVVVAFALCWTPTYHLVVLVDLMDGLALRNCGRESRYDAKSVT 303

QY 351 SG LGVMHCCCLNPLLYAFVGVKFRERMMMLLLRLGCPNQRGLOROPSSSRDSSWSETSEA 410

Db 304 SG LGVMHCCCLNPLLYAFVGVKFRERMMMLLLRLGCPNQRGLOROPSSSRDSSWSETSEA 363

QY 411 SYSGL 415

Db 364 SYSGL 368

RESULT 14

US-09-010-701C-22

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: Sequence 22 Application US/09010701C
: GENERAL INFORMATION:
: APPLICANT: Matson, Jeanine D.
: APPLICANT: Solo-Trejo, Hortensia
: APPLICANT: Hedrick, Joseph A.
: APPLICANT: Gorman, Daniel M.
: APPLICANT: Zlotnik, Albert
: TITLE OF INVENTION: Mammalian Chemokines; Receptors;
: TITLE OF INVENTION: Reagents; Uses
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DNAX Research Institute
: STREET: 901 California Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/010,701C
: FILING DATE: 22-JAN-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/036,715
: FILING DATE: 23-JAN-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Ching, Edwin P.
: REGISTRATION NUMBER: 34,090
: REFERENCE/DOCKET NUMBER: DX0689
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650)852-9196
: TELEFAX: (650)496-1200
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 367 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-010-701C-22

Query Match 75.6%; Score 1626.5; DB 14; Length 367;
Best Local Similarity 86.0%; Pred. No. 2e-144;
Matches 314; Conservative 22; Mismatches 28; Indels 1; Gaps 1

QY 51 QVSDHOVLNDAEVAALLNENSSSYDYGENESDSCCTSPCCPDFSINFDRAFLPALYSILL 110
DB 4 EVSEQVQVLDASDFALLENSTSPDYGENESD-FSDSPCCPDFSINFDRTFLPALYSILL 62

QY 111 FLGLGLGGAVAAVLLSRTALSSDTFLHLAAVADTLVTLPLMAVDAAVQWPGSGL 170
DB 63 FLGLGLGGAVAAVLLSRTALSSDTFLHLAAVADTLVTLPLMAVDAAVQWPGGL 122

QY 171 KVVAGALNININAYAGALLLACISFPRYLNIYHATOLYRGPRARYTITCLAVWGCLLFA 230
DB 123 KVVAGALNININAYAGALLLACISFPRYLNIYHATOLYRGPRARYTITCLAVWGCLLFA 182

QY 231 LPDFLELSAHHDERLNATHCOYNFPQVGRFALRVQLVAGFLPLPLMAVCYAHILAVLL 290
DB 183 LPDFLELSAANYDORLNATHCOYNFPQVGRFALRVQLVAGFLPLPLMAVCYAHILAVLL 242

QY 291 VSRGGRRLRARLIVVVVYVAPALCTPYHLVVLVDILMDGLALRNCRESRYDAKSVT 350
DB 243 VSRGGRRRRARLIVVVVYVAAFAVCTPYHLVVLVDILMDVGLARNCGRKSHVDKSVT 302

QY 351 SGLGVMHCCCLNPLFAFVGKFRERMMMLRLGQPNORGLROBSSSRDSSWSEPTSEA 410
DB 303 SGMGMHCCCLNPLFAFVGKFRERMMMLTRLRGSDQGRPOBSSSRDSSWSEPTSEA 362

QY 411 SYSGL 415

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Db 363 SYGL 367

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RESULT 15
US-60-258-273-107
; Sequence 107, Application US/60258273
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
; TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1001042-PROV
; CURRENT APPLICATION NUMBER: US/60/258,273
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Human
US-60-258-273-107
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Query Match 70.6%; Score 1519.5; DB 26; Length 380;
Best Local Similarity 92.1%; Pred. No. 2.6e-134;
Matches 302; Conservative 5; Mismatches 12; Indels 9; Gaps 2;

QY 41 TAPS---SPFPSSQVSDHQVLNDAEVAALLLENFSSSYDYGENESDSCCTSPPCPODFSL 96
Db 12 TPSSSQSTSPAMYLEVSDHQVLNDAEVAALLLENFSSSYDYGENESDSCCTSPPCPODFSL 71

QY 97 NEDRAFLPALYSLLFLGLGNGAVALLSRRTALSTDFTLLHLAVADTLVLTLPLW 156
Db 72 NEDRAFLPALYSLLFLGLGNGAVALLSRRTALSTDFTLLHLAVADTLVLTLPLW 131

QY 157 AVDAAVQWVFSGSLCKVAGALFNINFYAGALLACISFDRIYLNIVHATQLYRRGPPARVT 216
Db 132 AVDAAVQWVFSGSLCKVAGALFNINFYAGALLACISFDRIYLNIVHATQLYRRGPPARVT 191

QY 217 LTCLAVWGICLFLALPDFTFLSAHDERLNATHCOYNFPQVGRFALRVLQLVAGFLPL 276
Db 192 LTCLAVWGICLFLALPDFTFLSAHDERLNATHCOYNFPQVGRFALRVLQLVAGFLPL 251

QY 277 VMAYCYAHLAVLLVSRGQRLRAMRLVVVVVAFALCWTPLYHLVVLVDILMDGALARN 336
Db 252 VMAYCYAHLAVLLVSRGQRLRAMRLVVVVVAFALCWTPLYHLVVLVDILMDGALARN 311

QY 337 CGRESRVDAKSVTSGLGYMHCCLNPL 364
Db 312 CGRESRV---VRQGVGHLRPGIHAL 334
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Search completed: November 2, 2002, 12:14:54
Job time : 203 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 2, 2002, 12:07:05 : Search time 123 Seconds
(without alignments)
1014,235 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYPGRLAGTIVIGCAA.....SSRRDSSWSEPSASYGL 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1112697 seqs, 300604653 residues

Total number of hits satisfying chosen parameters: 1112697

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending-Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCr_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/PCr_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
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8: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2151	100.0	415	9	US-09-101-518A-2
2	2136	99.3	472	11	US-10-106-698-6402
3	1891	87.9	368	11	US-10-251-686-2
4	1891	87.9	368	11	US-10-251-385-20
5	1885	87.6	368	11	US-10-251-385-174
6	661	30.7	357	9	US-09-694-401A-20
7	661	30.7	357	11	US-10-224-855-66
8	635	29.5	372	11	US-10-251-385-66
9	633	29.4	353	9	US-09-101-518A-9
10	633	29.4	355	9	US-09-625-573-8
11	633	29.4	360	2	PCT-US02-07946A-16
12	633	29.4	360	11	US-10-099-007A-16
13	633	29.4	372	11	US-10-251-385-200
14	610	28.4	377	11	US-10-143-982-194
15	606.5	28.2	350	2	PCT-US02-15638-3
16	606.5	28.2	350	2	PCT-US02-07946A-15
17	606.5	28.2	350	11	US-10-099-007A-15
18	605.5	28.1	350	9	US-09-625-573-7
19	602	28.0	378	11	US-10-143-982-290
20	602	28.0	378	11	US-10-211-364-780

21	602	28.0	378	11	US-10-212-054-862	Sequence 862, App
22	602	28.0	378	11	US-10-073-073-338	Sequence 338, App
23	602	28.0	378	11	US-10-216-428-142	Sequence 142, App
24	602	28.0	378	11	US-10-216-436-526	Sequence 526, App
25	602	28.0	378	11	US-10-216-693-220	Sequence 220, App
26	602	28.0	378	11	US-10-219-917-240	Sequence 240, App
27	588	27.3	399	11	US-10-143-982-244	Sequence 244, App
28	586	27.2	378	9	US-09-694-401A-13	Sequence 13, App
29	586	27.2	378	11	US-10-224-855-13	Sequence 13, App
30	586	27.2	378	11	US-10-251-385-74	Sequence 74, App
31	584	27.2	359	9	US-09-646-785A-3	Sequence 3, App
32	584	27.2	378	11	US-10-251-385-204	Sequence 204, App
33	577.5	26.8	352	9	US-09-625-573-6	Sequence 6, App
34	576.5	26.8	352	2	PCT-US01-51165-126	Sequence 126, App
35	576.5	26.8	352	9	US-09-813-651B-85	Sequence 85, App
36	576.5	26.8	352	9	US-09-646-785A-1	Sequence 1, App
37	576.5	26.8	352	9	US-09-647-501-2	Sequence 1, App
38	576.5	26.8	352	11	US-10-151-274-4	Sequence 4, App
39	576.5	26.8	352	11	US-10-160-401-3	Sequence 3, App
40	576.5	26.8	352	11	US-10-014-322A-126	Sequence 126, App
41	570.5	26.5	353	11	US-10-143-982-200	Sequence 200, App
42	567.5	26.4	378	9	US-09-694-401A-16	Sequence 16, App
43	567.5	26.4	378	11	US-10-224-855-16	Sequence 16, App
44	566.5	26.3	378	11	US-10-164-649-5	Sequence 5, App
45	566	26.3	378	9	US-09-686-020A-7	Sequence 7, App

ALIGNMENTS

RESULT 1
US-09-101-518A-2
Sequence 2, Application US/09101518A
GENERAL INFORMATION:
APPLICANT: LI, YI
TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
FILE REFERENCE: PF218US
CURRENT APPLICATION NUMBER: US/09/101,518A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: PCT/US96/00499
PRIOR FILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
US-09-101-518A-2

Query Match 100.0%: Score 2151; DB 9; Length 415;
Best Local Similarity 100.0%: Pred. No. 6.1e-174;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MELRKYPGRLAGTIVIGCAAQSKSQTIRKEFLPGLYTAPSSPPPSQVSDHQVLD	60
DB	1	MELRKYPGRLAGTIVIGCAAQSKSQTIRKEFLPGLYTAPSSPPPSQVSDHQVLD	60
QY	61	AEVAALLNFSSSYDYGENSEDSCTSPPCPDQFSINEDRAFLPALYSLLFLGLGNGA	120
DB	61	AEVAALLNFSSSYDYGENSEDSCTSPPCPDQFSINEDRAFLPALYSLLFLGLGNGA	120
QY	121	VAAVLLSRRTALSSDPTFLHLAVADTLVTLPLMAVDAAVQWFGSLCKVAAALFNI	180
DB	121	VAAVLLSRRTALSSDPTFLHLAVADTLVTLPLMAVDAAVQWFGSLCKVAAALFNI	180
QY	181	NEVAGALLACISFPRYLNIIVATOLYRRGPARATLNCIAVWGCLLFAIPDFLSAH	240
DB	181	NEVAGALLACISFPRYLNIIVATOLYRRGPARATLNCIAVWGCLLFAIPDFLSAH	240
QY	241	HDERLNATHCQYNPOVGFRTALRLVLAAGFLPLLVNAYCYCAHILAVLVSRGQRRLRA	300
DB	241	HDERLNATHCQYNPOVGFRTALRLVLAAGFLPLLVNAYCYCAHILAVLVSRGQRRLRA	300


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Db 304 SGLGYMHCCINPLLYAFYGVKFRERMMMLLLRLGCPNORGLOROPSSSRDSSWSETSEA 363
Qy 411 SYSGL 415
| | | | |
Db 364 SYSGL 368

RESULT 4
US-10-251-385-20
; Sequence 20, Application US/10251385
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-20

Query Match 87.9%; Score 1891; DB 11: Length 368;
Best Local Similarity 99.7%; Pred. No. 5.8e-152;
Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 51 QVSDHQVLNDAEVAALLLENFSSSYDYGENESDSCCTSPCPQDFSLNFDRAFLPALYSLL 110
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Db 4 EYSDHQVLNDAEVAALLLENFSSSYDYGENESDSCCTSPCPQDFSLNFDRAFLPALYSLL 63

Qy 111 FLGLGNGAVALLSRRTALSSDTFLHLAVADTLVLPLMAVDAVAQWVFGSGL 170
| | | | |
Db 64 FLGLGNGAVALLSRRTALSSDTFLHLAVADTLVLPLMAVDAVAQWVFGSGL 123

Qy 171 CKVAGALFNINFYAGALLACISFDRIYINVAHQLYRRGPARVTLTCLAWGICLLEFA 230
| | | | |
Db 124 CKVAGALFNINFYAGALLACISFDRIYINVAHQLYRRGPARVTLTCLAWGICLLEFA 183

Qy 231 LPDFIFLSAHHDERLNATHCOYNFPOVGRFALRVQLVAGFLPLPLVMAVYCAHILAVLL 290
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Db 184 LPDFIFLSAHHDERLNATHCOYNFPOVGRFALRVQLVAGFLPLPLVMAVYCAHILAVLL 243

Qy 291 VSRGQRRLRAMRLVYVVAFAALCWTPLYLVVLDIIMDLGALARCGRESRVDAKSVT 350
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Db 244 VSRGQRRLRAMRLVYVVAFAALCWTPLYLVVLDIIMDLGALARCGRESRVDAKSVT 303

Qy 351 SGLGYMHCCINPLLYAFYGVKFRERMMMLLLRLGCPNORGLOROPSSSRDSSWSETSEA 410
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Db 304 SGLGYMHCCINPLLYAFYGVKFRERMMMLLLRLGCPNORGLOROPSSSRDSSWSETSEA 363

Qy 411 SYSGL 415
| | | | |
Db 364 SYSGL 368

RESULT 5
US-10-251-385-174
; Sequence 174, Application US/10251385
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
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; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 174
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-174

Query Match 87.6%; Score 1885; DB 11: Length 368;
Best Local Similarity 99.5%; Pred. No. 1.9e-151;
Matches 363; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 51 QVSDHQVLNDAEVAALLLENFSSSYDYGENESDSCCTSPCPQDFSLNFDRAFLPALYSLL 110
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Db 4 EYSDHQVLNDAEVAALLLENFSSSYDYGENESDSCCTSPCPQDFSLNFDRAFLPALYSLL 63

Qy 111 FLGLGNGAVALLSRRTALSSDTFLHLAVADTLVLPLMAVDAVAQWVFGSGL 170
| | | | |
Db 64 FLGLGNGAVALLSRRTALSSDTFLHLAVADTLVLPLMAVDAVAQWVFGSGL 123

Qy 171 CKVAGALFNINFYAGALLACISFDRIYINVAHQLYRRGPARVTLTCLAWGICLLEFA 230
| | | | |
Db 124 CKVAGALFNINFYAGALLACISFDRIYINVAHQLYRRGPARVTLTCLAWGICLLEFA 183

Qy 231 LPDFIFLSAHHDERLNATHCOYNFPOVGRFALRVQLVAGFLPLPLVMAVYCAHILAVLL 290
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Db 184 LPDFIFLSAHHDERLNATHCOYNFPOVGRFALRVQLVAGFLPLPLVMAVYCAHILAVLL 243

Qy 291 VSRGQRRLRAMRLVYVVAFAALCWTPLYLVVLDIIMDLGALARCGRESRVDAKSVT 350
| | | | |
Db 244 VSRGQRRLRAMRLVYVVAFAALCWTPLYLVVLDIIMDLGALARCGRESRVDAKSVT 303

Qy 351 SGLGYMHCCINPLLYAFYGVKFRERMMMLLLRLGCPNORGLOROPSSSRDSSWSETSEA 410
| | | | |
Db 304 SGLGYMHCCINPLLYAFYGVKFRERMMMLLLRLGCPNORGLOROPSSSRDSSWSETSEA 363

Qy 411 SYSGL 415
| | | | |
Db 364 SYSGL 368

RESULT 6
US-09-694-401A-20
; Sequence 20, Application US/09694401A
; GENERAL INFORMATION:
; APPLICANT: Gutierrez-Ramos, Jose Carlos
; APPLICANT: Gonzalez, Jose Angel
; TITLE OF INVENTION: NOVEL MOLECULES OF THE BGCR-RELATED PROTEIN FAMILY AND USES T
; FILE REFERENCE: 07334-317001
; CURRENT APPLICATION NUMBER: US/09/694,401A
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 09/294,058
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: US 09/061,753
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US-09-694-401A-20

Query Match 30.7%; Score 661; DB 9: Length 357;
Best Local Similarity 40.1%; Pred. No. 1e-47;
Matches 141; Conservative 65; Mismatches 122; Indels 24; Gaps 6;
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Db 12 ENT$SYD$Y$O$Y$E$L-----L$CK$E$D$R$N$F$A$K$Y$E$P$IM$SL$IF$V$G$LL$N$S$V$L$Y$T$A$ 64

OY 128 R$T$A$L$S$T$D$F$E$L$L$H$A$V$A$D$T$V$L$T$P$E$L$M$A$D$A$V$O$N$E$F$G$G$L$C$K$Y$A$G$A$L$E$N$F$Y$A$G$A$L 187
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 Y$K$R$T$M$D$V$L$M$A$V$A$D$D$L$F$E$L$L$T$P$E$F$M$A$V$A$N$H$G$E$V$A$M$C$K$D$L$S$G$Y$T$P$N$F$V$G$M$L 124

OY 188 L$A$C$I$S$P$R$Y$N$I$Y$H$A$V$O$L$Y$R$G$P$A$V$U$L-----T$C$A$V$G$D$L$E$L$F$L$P$O$F$I$S$H$A$N$D$E 24.3
    ||||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 L$A$C$I$S$D$R$Y$A$I$Y$O$A$I$S$A$N$H$H-----R$S$R$V$L$L$S$K$Y$I$C$Y$G$W$A$V$L$A$I$S$I$P$E$L$Y$S$T$V--N$E 180
    ||||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 244 R$L$A$N$H$C$O$Y$N$F$P$O$Y$G$R$A$L$R$Y---I$Q$V$A$G$E$L$P$L$L$M$A$Y$C$Y$A$N$H$I$A$V$L$Y$N$S$G$O$R$R$L$R 299
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 L$G$D$V$R$C$S$P$I$Y$S$E$G$T$A$L$K$A$L$I$O$G$L$E$M$V$O$F$E$V$P$L$M$A$F$C$Y$V$L$I$K$T$L$O$A$Q$N$S$K$R$K 240

OY 300 A$M$L$R$U$N$V$V$A$F$A$L$C$M$P$Y$H$L$V$V$D$D$I$M$D$G$A$L$A$R$N$C$R$E$S$R$D$V$A$K$S$T$G$L$Y$G$H$N$C 359
    || : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 A$L$K$Y$I$A$N$V$V$E$I$Y$O$L$P$Y$N$V$V$L$Y$O$I$A$N$G$I$L$S$C$E$T$S$K$Q$D$I$A$I$O$Y$T$E$S$A$F$H$C 3000

OY 360 L$N$P$L$L$Y$A$F$Y$G$K$F$E$R$R$M$M$L$L$R$G$C$P$N$O$G$L$O$R$O$P$S$S$R$D$S$W$E$T$S$A$S 411
    ||||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 301 L$N$P$L$Y$A$F$I$G$K$F$R$N$Y$L$M$K$A$K$D$G$----L$R$E$O$W$S$A$R$H$E$S$T$S$R$E$F$S 347

```

```

RESULT 7
US-10-224-855-20
? Sequence 20, Application US/10224855
? GENERAL INFORMATION:
? APPLICANT: Gonzalo, Jose Angel
? APPLICANT: Gutierrez-Ramos, Jose Carlos
? TITLE OF INVENTION: NOVEL MOLECULES OF THE BGCR-RELATED PROTEIN FAMILY
? TITLE OF INVENTION: AND US$ THEREOF
? FILE REFERENCE: 07334-317001
? CURRENT APPLICATION NUMBER: US/10/224,855
? CURRENT FILING DATE: 2002-08-21
? PRIOR APPLICATION NUMBER: US/09/694,401
? PRIOR FILING DATE: 2000-10-23
? PRIOR APPLICATION NUMBER: US 09/294,058
? PRIOR FILING DATE: 1999-04-16
? PRIOR APPLICATION NUMBER: US 09/061,753
? PRIOR FILING DATE: 1998-04-16
? NUMBER OF SEQ ID NOS: 32
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 20
? LENGTH: 357
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Consensus sequence
US-10-224-855-20

```

Query Match	30.7%;	Score 661;	DB 11;	Length 357;
Best Local Similarity	40.1%;	Pred. No. 1e-47;		
Matches 141;	Conservative 65;	Mismatches 122;	Indels 24;	Gaps 6;

[illegible][illegible]

```

, RESULT 8
, US-10-251-385-66
, Sequence 66, Application US/10251385
, GENERAL INFORMATION:
, APPLICANT: Behan, Dominic P.
, APPLICANT: Chalmers, Derek T.
, APPLICANT: Liaw, Chen W.
, TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
, TITLE OF INVENTION: Protein-Coupled
, TITLE OF INVENTION: Receptors
, FILE REFERENCE: AREN-0040
, CURRENT APPLICATION NUMBER: US/10/251,385
, CURRENT FILING DATE: 2002-09-20
, PRIOR APPLICATION NUMBER: US/09/170,496
, PRIOR FILING DATE: 1998-10-13
, NUMBER OF SEQ ID NOS: 294
, SOFTWARE: PatentIn version 3.1

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; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-66

```

Query Match	29.5%;	Score 635;	DB 11;	Length 372;
Best Local Similarity	40.8%;	Pred. No. 1.7e-45;		
Matches 147;	Conservative 50;	Mismatches 145;	Indels 18;	Gaps 8;

Qy	67	LENNSSSV- ---DGENED-SCGSPCPQ- ---DFSLNPDRAFLPALYSILFLGILG	119
Db	11	LENLEDEFWELDRIDNDISLYENHILCPATEGFLMASTKAVFPVAYSLFLFLGVLGNV	70
Qy	120	AAVAALLSRRATLSSTDTEFLHLHADVTLVLTPLIYAAVAAQVWVSGIGCKVAGALFN	179
Db	71	LVLVLEHNRHSTSTETFLFLHADVLLFLFLPFAVAEGSVGWLTGTEKVLIALHK	130
Qy	180	INFAVAGALLACISGDRPLTNVHATOLYRGRPARVLTTLCAWGCILFLALDPFL--	237
Db	131	VNFYCSLTLACILAVDRILAYHVAHVRHRLLSITHTGCTLVGFLLAPELPELFAKY	190
Qy	238	SAHDERLNTAHCOYNEPOYGT- ---ALFVLOLVAGFLPLLLVMAVCYAHILAVL-LV	291
Db	191	SGCHNNNSL--PCTFSQENOAETHAMFTSRFLYHVAAGFLPMLVMGCVGVGNHRLROA	248
Qy	292	SRGOSRLIEMRLVVVVVYAFRLICTPRHIVLVNLTIDGLGILANCSRERVDVAKSVTS	351
Db	249	QRPROROKAVAVALLVYSIFFLCSPHIVIEFDTLARKLAVDNCTKLSNLSPLAITMCE	308
Qy	352	GLGYWHCCLNPLLYAEVGVKFEREMMILLRLGCPNORGLOROPSSRRDSSMSVSEAS	411
Db	309	FLGAGHCCNMLNLTGVGVKRSRDLSTRITLTGCTGPAASICOLEPWSMR--SLSISESNAT	367

RESULT 9
US-09-101-518A-9
; Sequence 9, Application US/09101518A

1 TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSA1U68
2
3 FILE REFERENCE: PR21805
4
5 CURRENT APPLICATION NUMBER: US/09/101,518A
6
7 CURRENT FILING DATE: 2002-03-18
8
9 PRIOR APPLICATION NUMBER: PCT/US96/00499
10
11 PRIOR FILING DATE: 1996-01-11
12
13 NUMBER OF SEQ ID NOS: 9


```

OY      243 ERLNATHQVNPVG-----FTALRYVLQLVAGFLDELPLMAVCYAIIILAVLVSRCQR   296
        : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB     190 SNWSGA-C---YEDMGNNTANMRMLRLLRPDSFGFIVPLLIMFCYTGLTTLRFKAHMGQ   245

OY      297 RLRAARLVVVVAAPALCWPTEPHLVLDIIMDLGALARNGRESRVDAKSVTSGLGYM       356
        : ||||| : || : || : || : || : || : || : || : || : || : || : || : || :
DB     246 KHRARVRIFAVALIFELLCWLPYNLYNLADLTLMRRQVIDETGERNRHHIDRALDITEIGILT   305

OY      357 HCCLNPLEIAFYGVAFERERMAMLLLRCLCPNQGLIQROPSSSRDDSSMSSETS          408
        -||||-||||| : || : : | : : | : : | : : | : : | : : | : : | : : | :
DB     306 HSCLNPIIFYAFIGOKFRHGKLKIILAIGHLSKDLSLPKDRSPSFVGGSSSGHTS         357


RESULT 12
US-10-099-007A-16
; Sequence 16, Application US/10099007A
; GENERAL INFORMATION:
; APPLICANT: Theodore Torphy
; TITLE OF INVENTION: CHRONIC OBSTRUCTIVE PULMONARY DISEASE-RELATED IMMUNOGLOBULIN
; TITLE OF INVENTION: DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN-0286
; CURRENT APPLICATION NUMBER: US/10/099_007A
; CURRENT FILING DATE: 2002-03-14
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver 2.0
; SEQ ID NO 16
; LENGTH: 360
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-099-007A-16


Query Match              29.4% Score 633; DB 11; Length 360;
Best Local Similarity    40.1%; Pred.No. 2.4e-45;
Matches 141; Conservative 51; Mismatches 130; Indels 30; Gaps 6;


OY      72 SSYDVGENESDSCCSPPCDSESLNPRATPLPALYSLLFIILLIGNAVAAILRSRTA    131
        -|-|--|:-||:-||::||::-||:|||||----||--|
DB     21 SNYSTISSTLPPLDLADACEPE-SLEIKKYVTVIITAYLVLFLLSLGNSLVMVLTVLSRGV   79

OY     132 LSTDTPHLHLAVADTTLLVTLLPMADAQAOWYGSGICKVAGALENFINYACALLDAC      191
        -|-|-|:|:|:|:| | |||||:|:| | | | | | | | | | | | | | | | | | |
DB     80 RSYTDVYLNLIALMDLFPALTFLPTMASKVGMIFGTFLCKVDSLKEKNYVTSGLILLAC    139

OY     192 ISDFRIYLIVARQTOLIRGRPARVTLT-----CLAWGCILFLPADPFILSAHHD      242
        -|-|-|-|-|-|HATR-----TLTGKRXYLKVFICLSINGILLSLLLPAVLERFRYYVS   189
DB     140 IVDHYLIAIHATR-----TLTGKRXYLKVFICLSINGILLSLLLPAVLERFRYYVS   189

OY     243 ERLNATHQVNPVG-----FTALRYVLQLVAGFLDEPLMAVCYAIIILAVLVSRCQR    296
        ::||:|:~| | | | | | ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB     190 SNWSGA-C---YEDMGNNTANMRMLRLLRPDSFGFIVPLLIMFCYTGLTTLRFKAHMGQ   245

OY     297 RLRAARELVVVVAAPALCWPTEPHLVLDIIMDLGALARNGRESRVDAKSVTSGLGYM       356
        : ||||| : || : || : || : || : || : || : || : || : || : || : || : || :
DB     246 KHRARVRIFAVALIFELLCWLPYNLYNLADLTLMRRQVIDETGERNRHHIDRALDITEIGILT   305

OY     357 HCCLNPLEIAFYGVAFERERMAMLLLRCLCPNQGLIQROPSSSRDDSSMSSETS          408
        -||||-||||| : || : ~| : : | : : | : : | : : | : : | : : | : : | :
DB     306 HSCLNPIIFYAFIGOKFRHGKLKIILAIGHLSKDLSLPKDRSPSFVGGSSSGHTS         357


RESULT 13
US-10-251-385-200
; Sequence 200, Application US/10251385
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251.385
; CURRENT FILING DATE: 2002-09-20
```

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; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 200
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-200

Query Match
Best Local Similarity 29.4%; Score 633; DB 11; Length 372;
Matches 147; Conservative 49; Mismatches 146; Indels 18; Gaps 8

67 LENFSSSY---DYGENESD-SCCTSPCCQ---DPSLNDRAFLPALYSLEFLGLGNG 119
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 LENEDLEWELDRLDNYNDTSLVENHLCGPATGCPLMASKAFVAYSLIFELGIVGNV 70

QY 120 AYAANVLSRRFLSSTDFFLLHLAAVDLLVLTPLMAVDAAVQVWFGSGCLKVAGALEN 179
- - - - - : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 LVLVTLIERHQRRSSTETFFLHLAAVDLLVLELFPAAVAGSGVWLGTEFLCKTYIAHK 130

QY 180 INFVAGALLLACTISDRYNTIYHAQVLRGRRPARTECLAWGCLLFPALPDFEL-- 237
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 VNFVGSLLLACTIADRYLAIVHAHVAHAKRRLLSIHTCGTITWLGFLPAETILFAKY 190

QY 238 -SAHDERLNATHCQYNFPOVGRT---ALRYLQLVAGFLPLPLWACYAHILAVL-LV 291
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 SGCHHNNSL--PRCFESQENQAEITAMFTSRFLYHAGFLPLMLVWGMCYGVVHRLRA 248

QY 232 SRGQRRLRAMLRVVVVVAFAFCWTPYHLVLDVILMDIGALARNCGRESRDVAKSVTS 351
- - - - - : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 249 QRRPORAKARVAIIIVTSTIFFLCWSPYHIVIFELDTLARKAVDNCKLNGSLPVITMCE 308

QY 332 GIGVWHCCINPLVAFVGVKFERERMMMLLRIGCPNRGRLQRPSSRRDSSMSETSEAS 411
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 FLGLAHCCINPLVTFPAGVKFRSDLSRLTLKGTGCPASLCOLFPSWR--SSLSESEAT 367

RESULT 14
US-10-143-982-194
; Sequence 194, Application US/10143982
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P738C1N
; CURRENT APPLICATION NUMBER: US/10/143,982
; CURRENT FILING DATE: 2002-05-14
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 396
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 194
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-143-982-194

Query Match
Best Local Similarity 28.4%; Score 610; DB 11; Length 377;
Matches 142; Conservative 48; Mismatches 129; Indels 46; Gaps 7

QY 78 ENESDSCCTSPCCPDF--SLNF-----DRAFLPAL-----YSLFLEGLL 116
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 23 EEEEDMSNTIDPQMDPDDINTGMPRADEDEXSPCKLEFETINKYVVIAYAVLPLSL 82

QY 117 GNGAVALVLSRRFLSSTDFFLLHLAAVDLLVLTPLMAVDAAVQVWFGSGCLKVAGA 176
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 GNSIYMLVLTYSRVSRYTDVYLLNLALADLLFALTPLPMAASKVNGWIFGFLCKVYSL 142

QY 177 LFNINIFYGALLLACTISDRYNTIYHAQVLRGRRPARTELT-----CLAWGCLL 227
- - - - - : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 143 LKEVNFYSGILLLACTISVDRYLAIVHAATR-----TLQKRHLVYKFCVLCGCGLSM 192

```


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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: November 2, 2002, 12:20:26 ; Search time 1898 seconds
(without alignments)
4575.613 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELKRYGPRGLACTVIGCAA.....SSSRDSSWSETSYSYSGL 415

Scoring table: BLOSUM62
Xgapop 10.0, Ygapext 0.5
Xgapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USFO/US09101518/runat_29102002.091101_24/app-query.fasta.1.563
-DB=genembl -QWRT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTWMT=ptc -HEAPS-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09101518.cgn.1.1182 @runat.29102002.091101_24 -NCP=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMECUT=120
-WARR_TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*
15: gb_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	2151	100.0	271144	9	HSXDPB	AL590763 Homo sapi
2	2146	99.8	1563	9	HSCRL2	Z79783 H.sapiens G
3	2073	96.4	1293	9	HSU32674	U32674 Human Orpha
4	1897	88.2	1670	6	AR117009	AR117009 Sequence
5	1897	88.2	1670	9	HSGCRIN8	X95876 H.sapiens m
6	1644.5	76.5	1678	10	AF223642	AF223642 Rattus no
7	1632.5	75.9	1608	10	AB003174	AB003174 Mus muscu
8	1626.5	75.6	1525	10	AF045146	AF045146 Mus muscu
9	643	29.9	262652	2	AC105645	AC105645 Rattus no
10	641	29.8	1236	10	NRGPCNLR	X71463 R.norvegicu
11	640	29.8	2517	6	AR107998	AR107998 Sequence
12	640	29.8	2517	10	MMBLR1	X71788 M.musculus
13	637.5	29.6	2836	9	HOMILRB	L19593 Homo sapien
14	637.5	29.6	2856	11	G28560	G28560 human STS S
15	636	29.6	2847	9	HS18RB4	U11869 Human inter
16	636	29.6	13089	9	HOMILRB	M73969 Human inter
17	635	29.5	1510	9	HUMINTLEU8	AR015971 Sequence
18	635	29.5	1679	6	AR015971	AR060749 Sequence
19	635	29.5	1679	6	AR070434	AR070434 Sequence
20	635	29.5	1679	6	AR103431	AR103431 Sequence
21	635	29.5	1679	6	AR103431	AR103431 Sequence
22	635	29.5	1679	6	AR103431	AR103431 Sequence
23	635	29.5	1679	6	AR103431	AR103431 Sequence
24	635	29.5	1679	6	AR103431	AR103431 Sequence
25	635	29.5	1679	6	AR103431	AR103431 Sequence
26	635	29.5	1679	6	AR103431	AR103431 Sequence
27	635	29.5	1679	6	AR103431	AR103431 Sequence
28	635	29.5	1679	6	AR103431	AR103431 Sequence
29	635	29.5	1679	6	AR103431	AR103431 Sequence
30	633.5	29.5	158634	2	AP000909	AP000909 Homo sapi
31	633	29.4	1068	23	EL1245	EL1245 Human CDNA
32	632.5	29.4	163594	2	AP000877	AP000877 Homo sapi
33	632.5	29.4	244847	2	AP002357	AP002357 Homo sapi
C 34	629.5	29.3	1060	9	MMWCILRB	X91116 M.mulatta M
35	628	29.2	3011	6	AX281745	AX281745 Sequence
36	622	28.9	1060	9	PILRB	X91113 P.trogodyt
37	618.5	28.8	1122	9	MMILBR	X91112 M.mulatta M
38	615.5	28.6	1068	4	RABILBRC	M74240 Oryctolagus
39	615.5	28.6	1232	4	RABILBRC	M82873 Oryctolagus
40	615	28.6	1206	4	RABILBRC	L24445 Oryctolagus
41	614.5	28.6	2245	9	HSAILRBG	X65858 H.sapiens g
42	614.5	28.6	4452	9	HSU11870	U11870 Human inter
43	614.5	28.6	9265	9	HOMILRBAB	L19592 Homo sapien
C 44	614.5	28.6	98433	9	AC097483	AC097483 Homo sapi
45	614	28.5	1060	9	CGILBRB	X91114 G.gorilla G

ALIGNMENTS

RESULT 1
HSXDPB/c
LOCUS
DEFINITION HSXDPB 271144 bp DNA linear PRI 17-JUN-2001
region GUB1-DXS559 map Xq13.1, complete sequence.
ACCESSION AL590763 AJ239319
VERSION AL590763.1 GI:13751778
KEYWORDS
SOURCE human.

ORGANISM	Homo sapiens
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 271144) Ramser,J., Heltmann,K., Subdriak,R., Koslira,A., Klages,S., Steffens,C., Borzym,K., Kube,M., Lehnach,S., Marguardt,I., Schneelichen,S., Starke,A., Thompson,C., Hennig,S., Francis,F., Nemeth,A., Monaco,A., Lehnach,H. and Reinhardt,R.
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 271144)
AUTHORS	MPIMG.
TITLE	Direct Submission
JOURNAL	Submitted (15-FEB-1999) MPIMG, Abt. Lehnach, Max Planck Institut Fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany Bases 1..5000 overlap with AL590762 (HSXDPA).
COMMENT	Location/Qualifiers
FEATURES	1..271144
source	/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="X" /map="Xq13.1" /clone="PAC RPCI-3 485K11" /clone="PAC RPCI-1 177K5" /clone="PAC RPCI-1 2113" /clone="PAC RPCI-3 423F18" /clone="PAC RPCI-1 104C1" /clone="cosmid cosE3" /clone="BAC OX1" /clone="PAC RPCI-1 56F19" /clone.lib="RPC11.3-5 Human PAC library, originating institute: Roswell Park Cancer Institute, Creator: Pieter de Jong, P. Ioannou" /note="region between markers GJB1-DXS559"
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Score:	2151.00 Matches: 415
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Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	9 Gaps: 0
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QY 21	GInSerLysSerGlnThrLysSerAspSerIleThrLysGlnPheLeuProGlyLeuTyr 40
Db 159128	CAGAGTAAATTCACAGCTAATTCAGACTCAATACCAAAAGAGTTCCGCCAGGCCCTTAC 159069
QY 41	ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
Db 159068	ACAGCCCTTCCTCCCGCGTTCGCCGCTCACAGGTGAGTACCAACCAAGTCTAAATGAC 159009
QY 61	AlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerLysTyrAspTyrGlyGluAsnGlu 80
Db 159008	GCGGAGTTTGGCGCCCTCTCGTGAGAACTTCAGCTTCTTCATAGCTATGAGGAAGAACGAG 158949
QY 81	SerAspSerCysCysThrSerProCysProGlnAspPheSerLeuAsnPheAspArg 100
Db 158948	ATGAGACTCGTGCTGACTTCGCCGCCCTGCCCACAGGACTTCAGCTCGAATCTGCACCGG 158889
QY 101	AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla 120
Db 158888	GCGTTCCTGCACGCCCTCTACAGACTCTCTCTCTGCTGGGGGCGTGGGGCAAGGCGCG 158829
QY 121	ValAlaAlaValLeuLeuSerArgTgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
Db 158828	GTGGCAGCGCTGTGCTGTGAGCCCGCGAGACGCCCTGAGCAGCACCGACACTTCCTGCTC 158769

QY	141	HisDeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAla	160
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QY	161	AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle	180
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QY	181	AsnPheTYrAlaGlyAlaLeuLeuDeuAlaCysIleSerPheAspArgTYrLeuAsnIle	200
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QY	201	ValHisAlaThrGlnLeuTYrArgArgGlyProProAlaArgValThiLeuThrcysLeu	220
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QY	221	AlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis	240
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QY	241	HisAspGlyAlaArgLeuAsnAlaThrHisCysGlnTYrAsnPheProGlnValGlyArgThr	260
Db	158468	CACGACGACGCGCTCACGCCACCCACCTGCCAATGCAACTTCCACAGATGGGGCCGACG	158409
QY	261	AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTYr	280
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QY	301	MetArgLeuValValValValValAlaAlaPheAlaLeuCysTYrTrpProTYrHisLeu	320
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QY	321	ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyTYrGlu	340
Db	158228	GGTGGCTGGTGTGACATCTCTCAATGGACCTGGGGCGCTTTGGCCCCGCACTGTGGCAGAA	158169
QY	341	SerArgValAspValAlaAlaLysSerValThiSerGlyLeuGlyTYrMetHisCysCysLeu	360
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QY	361	AsnProLeuLeuTYrAlaPheValGlyValLysPheArgGlyArgMetTrpMetLeuLeu	380
Db	158108	AACCGCGTCTATACCCCTTTGTAGGGGTCAAGTTCCGGGACGGATGGATGCTGCTGC	158049
QY	381	LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg	400
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RESULT 2			
HSCRR2			
LOCUS		HSCRR2	1563 bp DNA linear PRI 26-JUL-1997
DEFINITION			H.sapiens G protein-coupled receptor CKR-L2.
ACCESSION			279783
VERSION			279783.1 GI:2281709
KEYWORDS			G protein-coupled Receptor CKR-L2.
SOURCE			human.
ORGANISM			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS			Gutierrez, J., Varona, R., Zaballos, A., Lind, P. and Marquez, G.
TITLE			unpublished
JOURNAL			2 (bases 1 to 1563)

AUTHORS Zaballios, A.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1996) Angel Zaballios, Research, Pharmacia &
Upjohn, Antonio Lopez 109, Madrid, 28026, Spain
FEATURES
source location/Qualifiers
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BASE COUNT 272 a 497 c 479 g 315 t
ORIGIN
Alignment Scores:
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Score: 2146.00 Matches: 414
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QY 21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
DB 315 CAGAGTAATTCACAGACTAATTCAGACTCAATCACAAGAGAGTCTCGCAGGCCCTTTTAC 374
QY 41 ThrAlaProSerSerProPheProSerGlnValSerAspHisGlnValLeuAsnAsp 60
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QY 61 AlaGluValAlaAlaLeuLeuGluAsnPheSerSerTyrAspTyrGlyGluAsnGlu 80
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QY 81 SerAspSerCysCysThrSerProPheProGlnAspPheSerLeuAsnPheAspArg 100
DB 495 AGTGAAGTCTGCTGTAACCTCCCGCCCTCCACAGACTTCAGCTTGAATTCGACCG 554
QY 101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGlyLeuLeuGlnValAla 120
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QY 121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
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QY 141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuThrAlaValAla 160
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QY 161 AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyValAlaLeuPheAsnIle 180
DB 735 GCGGCTCAAGTGGGCTCTTGCTGCTGCGCTTCGCAAAAGTGGCAGGTGCCCTTTCACACATC 794
QY 181 AsnPheTyrAlaGlyValAlaLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
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DB 795 AACCTCTACGACGAGCCCTCTGCTGCTGCATCAGCTTTGACCGCTACGACATA 854
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DB 855 GTTCATGCCACAGCTCAACCGCGGGGCGCCGCGCGCTGACCCCTACCTGCTG 914
QY 221 AlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
DB 915 GCTGCTGGGGGCTCTGCTGCTTTTCGCTTCACAGCTTCACTTCTCTGCTGGCCAC 974
QY 241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr 260
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QY 361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 380
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DB 1395 TTGCGCTGGGGCGCCCAACAGAGAGGCTCCACAGGACGATCTGCTCCCGCGG 1454
QY 401 AspSerSerTrpSerGlnThrSerGluAlaSerTyrSerGlyLeu 415
DB 1455 GATTCACTGCTGCTGACACTCAGAGGCTCTACTCGGCGTTG 1499
RESULT 3
HSU32674 1293 bp DNA linear PRI 05-JUN-1996
LOCUS
DEFINITION
ACCESSION U32674 Human orphan receptor GPR9 (GPR9) gene, partial cds.
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1293)
Marchese, A., Helber, M., Nguyen, T., Heng, H.H.Q., Saidi, V.A.,
Cheng, R., Murphy, P.M., Tsui, L.-C., Shi, X., George, S.R., O'Dowd, B.F.
and Docherty, J.M.
Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
and GPR14, encoding receptors related to Interleukin 8,
neuropeptide Y, and somatostatin receptors
Genomics 29 (2), 335-344 (1995)
96115583
2 (bases 1 to 1293)
Marchese, A., Helber, M., Nguyen, T., Heng, H.H.Q., Saidi, V.A.,
Cheng, R., Murphy, P.M., Tsui, L.-C., Shi, X., George, S.R., O'Dowd, B.F.
and Docherty, J.M.
Direct Submission
Submitted (31-JUN-1995) B.F. O'Dowd, Department of Pharmacology,
University of Toronto, 8 Taddle Creek Rd., Toronto, Ontario M5S

FEATURES 1A8, Canada
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ORIGIN
Alignment Scores:
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DB 121 CAAGTCTAAATGACGCCGAGGTGGCGCCCTCGAGAACTTCAGCTTCCTATGAC 180
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QY 96 LeuAsnPhesAspArgIaIaPheLeuProAlaLeuTyrrSerLeuAsnPhesLeuGIIn 115
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QY 236 PheLeuSerAlaHisHisAspGIuArgLeuAsnAlaThrHisCysGIInTyrrAsnPhesPro 255
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RESULT 4
AR117009 1670 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 1 from patent US 6140064.
ACCESSION AR117009
VERSION AR117009.1 GI:14097915
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1670)
AUTHORS Loetscher M, and Moser B.
TITLE Method of detecting or identifying ligands, inhibitors or promoters
of CXc chemokine receptor 3
JOURNAL Patent: US 6140064-A 1 31-OCT-2000;
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Score: 1897.00 Matches: 369
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Best Local Similarity: 97.36% Mismatches: 5

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Db	96	GTGTAAATACCCCGAGGTTGGCCCTTCCTGGAACTTGACGCTTCTCTATACAT	155	
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Db	996	CACGTGTGCTCAACCGGTGTGTATGCTTTGTAGAGGGTCAACATTCCTCGGAGGAGATG	1055	

Oy 377 TrrpeltleutleuLaagLeuglycysProasrGlnarglyLeuGlnargtInproser 396
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Oy 397 SerSerAargarGaSpSerSerTTPSerGluThrSerGluAlaSerTyrSerGlyLeu 415
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RESULT 5	
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LOCUS	
DEFINITION	H.sapiens mRNA for G-protein coupled receptor.
ACCESSION	X95876
VERSION	X95876.1 GI:1552845
KEYWORDS	G protein-coupled receptor; interleukin-8 receptor.
SOURCE	human.

polyA_signal 1602. 1607

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ORIGIN				

Alignment Scores:

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Score:	1897.00
Percent Similarity:	97.63%
Best Local Similarity:	97.36%
Query Match:	88.13%
RB:	9
Gaps:	1

US-09-101-518A-2 (1-415) x HSGPCRIN8 (1-1670)

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OY	57	ValLeuAsnAspAlaGluValAlaAlaLeuGluAsnPhseSerSerTyrAspTyr	76
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OY	77	GlyGluAsnGluSerAspSerCysThrSerProCysProGluAspHseSerLeu	96
Db	156	GGAGAAAACGAGAGTACCTGTGTCTACTCCCGCCCTGCCACAGSACTTCAGCTG	215
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OY	157	AlaValAspAlaAlaValAlaGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla	176
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OY	177	LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg	196
Db	456	CTCTTCAACATCAACATCTTACGCGAGGAGGCGCTCTGCTGGCTGCATACGCTTACGCG	515
OY	197	TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr	216
Db	516	TACTGTGAACATAGTTCATGCGACCGCTTACCGCGGGGGGCCCCCGGCGCGCTGAC	575
OY	217	LeuThrCysLeuAlaValIleTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheLeu	236
Db	576	CTCACCTGCCGCTGTCTGGGGGCTCTGCTCTTTCCTTCCCTCCAGACTTCATCTTC	635
OY	237	LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln	256
Db	636	CTGTGCGGCCACCGACGAGCGCCCTCAAGCGCACCCATGCCAATCACTTCCACAG	695
OY	257	ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu	276
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OY	317	ProTyrHisLeuValIleLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn	336
Db	876	CCCATACACGTGGGTGGGTGGGTGACATCCTATGAGCACTGGGCGCTTGGCCGCGAC	935
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DEFINITION	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds.				
ACCESSION	AF223642				
VERSION	AF223642.1 GI:8572056				
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ORGANISM	Rattus norvegicus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
AUTHORS	1 (bases 1 to 1678) Wang, X., Li, X., Schmidt, D. B., Foley, J. J., Barone, F. C., Ames, R. S. and Sarau, H. M.				
TITLE	Identification and molecular characterization of rat CXCR3: receptor expression and interferon-inducible protein-10 binding are increased in focal stroke				
JOURNAL	Mol. Pharmacol. 57 (6), 1190-1198 (2000)				
MEDLINE	20286573				
PUBMED	10825390				
REFERENCE	2 (bases 1 to 1678) Wang, X., Li, X., Schmidt, D. B., Foley, J. J., Barone, F. C., Ames, R. S. and Sarau, H. M.				
JOURNAL	Direct Submission Submitted (11-JAN-2000) Cardiovascular Sciences, Dupont Pharmaceuticals, Experimental Station E400/3420B, Wilmington, DE 19880/0400, USA				
FEATURES	Location/Qualifiers				
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Alignment Scores:					
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Percent Similarity:	86.24%	Conservative:	27		
Best local Similarity:	79.61%	Mismatch:	37		
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DB:	10	Gaps:	3		
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QY 269 AlaGlyPheLeuLeuProLeuLeuValMetAlaIaTyrCysTyrAlaHisIleLeuAlaVal 288
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QY 369 GlyValLysPheArgGluArgMetThrMetLeuLeuArgLeuGlyCysProAsnGln 388
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RESULT 7
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LOCUS AB003174 1608 bp mRNA linear ROD 28-OCT-1998

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DEFINITION Mus musculus mRNA for Interferon-inducible protein 10 receptor,
complete cds.
ACCESSION AB003174
VERSION AB003174.1 GI:3798731
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ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1608)
AUTHORS Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
TITLE Tamaru, M.
JOURNAL Direct Submission
MEDLINE Submitted (17-Apr-1997) Masahiro Tamaru, Japan Tobacco Inc. Central
FEATURES Laboratory; 13-2, Fukura 1-chome, Kanazawa-ku, Yokohama,
2 (sites) Kanagawa 236, Japan (E-mail: tamaru@lkr1.ftl.co.jp,
tel:81-45-786-7694, fax:81-45-786-7692)
REFERENCE Tamaru, M., Tomioka, Y., Yatsunami, K. and Narumi, S.
AUTHORS Cloning of the murine interferon-inducible protein 10 (IP-10)
TITLE receptor and its specific expression in lymphoid organs
JOURNAL Blochem. Biophys. Res. Commun. 251 (1), 41-48 (1998)
FEATURES 99009219
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LVAGFLPLVWAVCYAHILVAVLIVSRQRRARLVVVVVAFAVCMTPHVLVIVL
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Pred. No.: 6,22e-137 Length: 1608
Score: 1632.50 Matches: 323
Percent Similarity: 85.75% Conservative: 26
Best Local Similarity: 79.36% Mismatches: 39
Query Match: 75.89% Indels: 19
DB: 10 Gaps: 3
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Db 54 GAC-----CCACAGCCACAGCCGAGAGCAGCAGCAAGCCAG 92
QY 49 ProSerGlnValSerAspHisGlnValLeuAsnAspAlaGlyValAlaAlaLeuLeuGlu 68
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QY 69 AsnPheSerSerSerTyrAspTyrGlyGluAaNGluSerAspSerCysCysThrSerPro 88

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QY 171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuAla 190
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 AC105645
 AC105645.1 GI:18092868
 VERSION
 KEYWORDS HTG; PHASE1; HTGS_DRAFT.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 262652)
 Muzny D.M., Adams C., Adio-Oduola B., Ali-Osman F.R., Allen C.,
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TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT

Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
 Coyle, M.D., Dathore, S.R., David, R., Davila, M., Davis, C.,
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 Weinstein, G. and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 262652)
 Worley, K.C.
 Direct Submission
 Submitted (09-JAN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GNMV
 Center clone name: CH230-205K13
 ----- Summary Statistics
 Assembly program: Phrap, version 0.990329First call to
 findPhrapList
 Consensus quality: 230579 bases at least Q40
 Consensus quality: 238922 bases at least Q30
 Consensus quality: 245707 bases at least Q20
 Estimated insert size: 234543; sum-of-contigs estimation
 Quality coverage: 0x in Q20 bases; average-tp estimation
 Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length.
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 75 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 * 15333 15332: gap of unknown length
 * 15333 27159: contig of 11827 bp in length
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* 36909 37008: gap of unknown length
* 37009 46032: contig of 9024 bp in length
* 46033 46132: gap of unknown length
* 46133 55881: contig of 9749 bp in length
* 55882 55981: gap of unknown length
* 55982 63023: contig of 7042 bp in length
* 63024 63123: gap of unknown length
* 63124 71683: contig of 8560 bp in length
* 71684 71783: gap of unknown length
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* 161921 162020: gap of unknown length
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* 165494 165593: gap of unknown length
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* 168208 168307: gap of unknown length
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* 171753 171852: gap of unknown length
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* 173964 174063: gap of unknown length
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* 177546 177645: gap of unknown length
* 177646 181056: contig of 3411 bp in length
* 181057 181156: gap of unknown length
* 181157 184088: contig of 2932 bp in length
* 184089 184188: gap of unknown length
* 184189 186675: contig of 2467 bp in length
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* 204217 205763: contig of 1347 bp in length
* 205763 205863: gap of unknown length
* 205864 207940: contig of 2077 bp in length
* 207941 208040: gap of unknown length
* 208041 208935: contig of 1795 bp in length
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* 211575 211674: gap of unknown length
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* 229055 229154: gap of unknown length
* 229155 230540: contig of 1386 bp in length
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* 230641 233011: contig of 2371 bp in length
* 233012 233111: gap of unknown length
* 233112 234171: contig of 1060 bp in length
* 234172 234271: gap of unknown length
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Alignment Scores:

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Score: 643.00 Matches: 150
Percent Similarity: 55.00% Conservative: 48
Best Local Similarity: 41.67% Mismatches: 142
Query Match: 29.89% Indels: 20
DB: Gaps: 7
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US-09-101-518a-2 (1-415) x AC105645 (1-262652)

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QY 89 Pro-----CysProGlnAsp-----PheSerLeuAsnPhSeasp 99
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QY 100 ArgAlaPheLeuProAlaLeuTyrrSerLeuPheLeuGlyLeuLeuGlyAsnGly 119
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QY 120 AlaValAlaValAlaLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
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DB 38612 CTCGTACTGTGTAATCTCTGAGAGGACACCGGACACTCGAGGCTCAACGAGACCTTCCG 38671
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Oy 257 ValGlyArgThr-----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
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Oy 312 AlaLeuCysTyrThrProTyrH1sLeuValValLeuValAlaPheLeuMetAspLeuGly 331
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Oy 332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspAlaAlaCysSerValThrSer 351
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Oy 352 GlyLeuGlyTyrMetH1sCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValys 371
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ACCESSION X71463 S59748
VERSION X71463.1 GI:599926
KEYWORDS G-protein coupled receptor; NLR gene.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1236)
AUTHORS Kouba,M., Vanetti,M., Wang,X., Schafer,M. and Hollt,V.
TITLE Cloning of a novel putative G-protein-coupled receptor (NLR) which
is expressed in neuronal and lymphatic tissue
JOURNAL FEBS Lett. 321 (2-3), 173-178 (1993)
MEDLINE 93338948
REFERENCE 2 (bases 1 to 1236)
AUTHORS Kouba,M.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1993) M. Kouba, Dept. of Physiology, Univ. of
Munich, Pettenhoferstrasse 12, D-8000 Muenchen 2, FRG
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Query Match: 29.80% Indels: 14
DB: 10 Gaps: 6

US-09-101-518A-2 (1-415) x NRGPCMLR (1-1236)
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Oy 90 CysProGlnAspPheSerSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeu 109
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Oy 110 LeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArg 129
Db 187 ATCTTCTCTCTGGGTATGATGAGGAGAACATCTCTGTAATCTCTGGAGAGGACCGG 246
Oy 130 ThrAlaLeuSerSerThrAspThrPheLeuLeuH1sLeuAlaValAlaAspThrLeuLeu 149
Db 247 CACACTCGGAGCTCAACGAGGACCTTCTGTTCCACTGGCAGTACCGACCTTCTCTTG 306
Oy 150 ValLeuThrLeuProLeuTyrPalaValAspAlaAlaValGlnTyrValPheGlySerGly 169
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Oy 210 GlyProProAlaArgValThrLeuThrCysLeuAlaValTyrPoliLeuCysLeuLeuPhe 229
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Accession	Source	Organism	Length	Score	Percent Similarity	Best Local Similarity	Query Match	DB
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547	GCCCTTCGCAAGAACTCTCTTTGCGAAGGTTGTCACCACTCATACAGACGATCTTAA	GCCCTTCGCAAGAACTCTCTTTGCGAAGGTTGTCACCACTCATACAGACGATCTTAA	603	640.00	56.29%	40.86%	29.75%	6
247	AlaThrHisCysGlyTyrGlnPheProGlnValGlyArgThr-----AlaLeu	AlaThrHisCysGlyTyrGlnPheProGlnValGlyArgThr-----AlaLeu	262	640.00	56.29%	40.86%	29.75%	6
604	---CCACAGGTGATCTCTCCCAAGAAATGAAGCCGAACACTAGAACCTGGTTCGCTCC	---CCACAGGTGATCTCTCCCAAGAAATGAAGCCGAACACTAGAACCTGGTTCGCTCC	660	640.00	56.29%	40.86%	29.75%	6
263	ArgValIleuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetaIleTyrCysTyr	ArgValIleuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetaIleTyrCysTyr	282	640.00	56.29%	40.86%	29.75%	6
661	CGGTTCTCTTACCAACACTGGGGCTTCCTGCTACACGATCTGTGATGAGCTGGTGTAT	CGGTTCTCTTACCAACACTGGGGCTTCCTGCTACACGATCTGTGATGAGCTGGTGTAT	720	640.00	56.29%	40.86%	29.75%	6
283	AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgArgLeuArgAlaMet	AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgArgLeuArgAlaMet	301	640.00	56.29%	40.86%	29.75%	6
721	GTCGAGTGGTGTACACAGCTATTGTGACGGCCGCGCCCTCAGAGGGAGAGAGATGC	GTCGAGTGGTGTACACAGCTATTGTGACGGCCGCGCCCTCAGAGGGAGAGAGATGC	780	640.00	56.29%	40.86%	29.75%	6
302	ArgLeuValValValValValAlaPheAlaLeuCysTyrThrProTyrHisLeuVal	ArgLeuValValValValValAlaPheAlaLeuCysTyrThrProTyrHisLeuVal	321	640.00	56.29%	40.86%	29.75%	6
781	AGGGTGGCCATTTGGTGTGACAGCATCTTCTCTCTGCTGTGTCACCACTATTC	AGGGTGGCCATTTGGTGTGACAGCATCTTCTCTCTGCTGTGTCACCACTATTC	840	640.00	56.29%	40.86%	29.75%	6
322	ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlnSer	ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlnSer	341	640.00	56.29%	40.86%	29.75%	6
841	ATCTTCCTCGATACACTGGAAAGGCTGGAAGGCTGTGACACAGCATGGCAATTGAGTGCC	ATCTTCCTCGATACACTGGAAAGGCTGGAAGGCTGTGACACAGCATGGCAATTGAGTGCC	900	640.00	56.29%	40.86%	29.75%	6
342	ArgValAspPvalAlaLysSerValThrSerGlyLeuGlnIleTyrMetHisCysGlyLeuAn	ArgValAspPvalAlaLysSerValThrSerGlyLeuGlnIleTyrMetHisCysGlyLeuAn	361	640.00	56.29%	40.86%	29.75%	6
901	TCCTCTCAGTGGCTATGACACTTATGTGCAATTCTCGGGCTGGCTACGCTGTTCAT	TCCTCTCAGTGGCTATGACACTTATGTGCAATTCTCGGGCTGGCTACGCTGTTCAT	960	640.00	56.29%	40.86%	29.75%	6
362	ProLeuLeuTyrAlaPheValGlyValLysPheArgGlyIuArgMetTyrMetLeuLeu	ProLeuLeuTyrAlaPheValGlyValLysPheArgGlyIuArgMetTyrMetLeuLeu	381	640.00	56.29%	40.86%	29.75%	6
961	CCCATGCTCTACACTTCGCTGGCGGTAAGTTCCGAGATGACTTGTCTGCTGAC	CCCATGCTCTACACTTCGCTGGCGGTAAGTTCCGAGATGACTTGTCTGCTGAC	1020	640.00	56.29%	40.86%	29.75%	6
382	ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerArgArgasp	ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerArgArgasp	401	640.00	56.29%	40.86%	29.75%	6
1021	AGGCTGGGCTGTGCTGGCCGCTCCCT---TGTACACTCTTTCCGGGCTGGGCGCAAG	AGGCTGGGCTGTGCTGGCCGCTCCCT---TGTACACTCTTTCCGGGCTGGGCGCAAG	1077	640.00	56.29%	40.86%	29.75%	6
402	ServerTyrPserIuThrSerGlnLaser	ServerTyrPserIuThrSerGlnLaser	411	640.00	56.29%	40.86%	29.75%	6
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DEFINITION	Sequence 5 from patent US 6110695.							
ACCESSION	ARI07998							
VERSION	ARI07998.1	GI:12823485						
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unknown.							
REFERENCE	1 (bases 1 to 2517)							
AUTHORS	Gunn, M. Dee, Williams, L. T. and Cyster, J. G.							
TITLE	Modulating the interaction of the chemokine, B Lymphocyte							
JOURNAL	Hematopoietic, and its Receptor, BML							
FEATURES	Patent: US 6110695-A 5 29-AUG-2000;							
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Oy	110	LeuPheLeuGlyLeuLeuGlyVaSngLyAlaValAlaValLeuLeuSerArgArg	129
Db	187	ATCTTCCTCCGGGTATGATGGGAATCATCTGCTGTCTGTATTCCTGGAGGACCGCG	246
Oy	130	ThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeu	149
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Db	367	CTTCGCAAAAGCTGATGCTGCTGTCCACAGATAAATTTCTACTGCGACAGCTGCTGTG	426
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Oy	302	ArgLeuValValValAlaValAlaPheAlaLeuCysTrpThrProGlyHisLeuVal	321
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Oy	382	ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerArgArgAsp	401
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DEFINITION	M.musculus blr-1 gene for Burkitt lymphoma receptor 1 homologue.				
ACCESSION	X71788				
VERSION	X71788.1	GI:2598563			
KEYWORDS	blr1 gene; G-protein coupled receptor; glycoprotein; transmembrane;				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2517)				
AUTHORS	Kaiser,E., Forster,R., Wolf,I., Ebensperger,C., Kuehl,W.M. and Lipp,M.				
TITLE	The G protein-coupled receptor BLR1 is involved in murine B cell differentiation and is also expressed in neuronal tissues				
JOURNAL	Eur. J. Immunol. 23 (10), 2533-2539 (1993)				
MEDLINE	94009211				
REFERENCE	2 (bases 1 to 2517)				
AUTHORS	Lipp,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (03-MAY-1993) M. Lipp, Inst. f. Biochemie der Univ. Muenchen, Am Klopferspitz 18a, D-82152 Martinsried, FRG				
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QY	90	CysProGlnAspPheSerLeuasnPhesapRglaAlaPheLeuProAlaTyrSerLeu	109
DB	127	GTGAGAGGACCTTACTGACGCTCTTTAAGCGGATTCATGCTTGAGGCTTACAGCTTC	186
QY	110	LeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArg	129
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DB	247	CACACTCGGAGCTCAACGAGACCTTCTGTTCACCCCGCAGTAGCGGACCTTCTTA	306
QY	150	ValLeuThrLeuProLeuThrAlaValAlaAlaValAlaGlnTrpValPheGlySerGly	169
DB	307	GTCTTCATCTCTGCTTTTGCACTGGCTAGGGGCTCTGTGGTTGGGCTTAGGACCTTC	366
QY	170	LeuCyLysValAlaGlyAlaLeuPheAsnIleAsnPheryAlaGlyAlaLeuLeuLeu	189
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QY	210	GlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCyLeuLeuPhe	229
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QY	247	AlaThrHisCysGlnTyrAsnPhedProGlnValGlyArgThr-----AlaLeu	267
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QY	302	ArgLeuValValValValValAlaPheAlaLeuCyStrpThrProTyrHisLeuVal	321
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QY	37 ProGlyLeuTyThrAlaProSerSerProPhePro--ProSerGlnValSerAspHis	55	
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DB	526 GAACACGAA---TCCCTGGAAATCAACAAGATTTTGGTGTCATTATCTATGCCCTGTA	56/22	
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DB	583 TTTCCTGCTGACGCTGCTGGAAATCTCCTGCTGATGCTGGTCACTTATATACAGAGGTC	64/2	
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ACCESSION	U11869		
VERSION	U11869.1	GI:511801	
KEYWORDS	.		

SEGMENT	4 of 4
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AUTHORS	1 (bases 1 to 2847)
TITLE	Ahuja,S.K., Shetty,A., Tiffany,H.L. and Murphy,P.M.
JOURNAL	Comparison of the genomic organization and promoter function for
MEDLINE	human interleukin-8 receptors A and B
REFERENCE	J. Biol. Chem. 269 (42), 26581-26589 (1994)
AUTHORS	Submitted (06-JUL-1994) Sunil K. Ahuja, Laboratory of Host
TITLE	Defenses, National Institutes of Health, National Institute of
JOURNAL	Allergy and Infectious Diseases, NIH, Bldg 10, Rm 11N109, Bethesda,
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Query Match: 29.57% Indels: 46  
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QY 57 ValLeuAsnAspAlaGlnValAlaAlaLeuGluAsnPh-----Ser 71  
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DB 1238 AGTAATTACAGTACAGCTCCTACCCCTCTTCTACTAGATGCCGCCCATGTGAA 1297  
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DB 1637 -----ACACTGACCCAGAAAGCGCTACTGTGTCAAATTCATATATGCTCAGCATC 1684  
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Job time : 2183 secs

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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: November 2, 2002, 12:08:55 : Search time 209 Seconds

(without alignments)
3409.184 Million cell updates/sec

Title: US-09-101-518A-2

Perfect score: 2151

Sequence: 1 MELRKYPGRLAGTGTGGA.....SSRRDSMSSESEASYSGL 415

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Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2136	99.3	1877	22	AAH735033	Human colon cancer
3	1909	88.7	1159	20	AAZ32713	Human chemokine re
4	1897	88.2	1670	19	AAV26557	Human IP-10/Mlg re
5	1891	87.9	1107	21	AAA30593	Human G protein-co
6	1885	87.6	1107	21	AAA30714	DNA encoding human
7	1627.5	75.7	1620	19	AAV43793	Rodent chemokine r
8	640.5	29.8	1068	24	ABK16598	DNA encoding verve
9	640	29.8	2517	20	AAH87709	Mouse Burkitt's ly
10	639.5	29.7	1068	24	ABK16599	DNA encoding baboo
11	637.5	29.6	1886	22	ABA09268	Human IL-8R B homo
12	637.5	29.6	2785	23	AA577796	DNA encoding novel
13	636	29.6	12789	24	AA516876	Human interleukin
14	635.5	29.5	1068	24	ABK16596	DNA encoding rhesu
15	635	29.5	1106	13	AAQ30012	Sequence encoding
16	635	29.5	1119	21	AAA30626	Human G protein-co
17	635	29.5	1510	14	AAQ38747	Human IL-8 recepto
18	635	29.5	1510	21	AAE20993	Human low adenosin
19	635	29.5	1510	21	AAA34871	Human adenosine re
20	635	29.5	1679	13	AAQ37107	New platelet facto
21	635	29.5	1679	16	AAQ99009	Chemokine superfam
22	635	29.5	1679	16	AAQ80522	Human lymphocyte p
23	635	29.5	1748	16	AAQ99008	Interleukin 8 rece
24	635	29.5	1750	21	AAE20991	Human low adenosin
25	635	29.5	1750	21	AAA34869	Human adenosine re
26	635	29.5	2818	20	AAH87710	Human Burkitt's ly
27	635	29.5	3620	22	ABH09117	Human Burkitt lymph
28	635	29.5	9319	21	AAE20995	Human low adenosin
29	635	29.5	9319	21	AAA34873	Human adenosine re
30	633	29.4	1068	17	AAA40128	Human IL-8 recepto
31	633	29.4	1068	24	ABK16589	DNA encoding human
32	633	29.4	1068	24	ABK16590	DNA encoding chim
33	633	29.4	1068	24	ABK16592	DNA encoding goril
34	633	29.4	1119	21	AAA30727	DNA encoding human
35	632.5	29.4	1068	24	ABK16594	DNA encoding orang
36	631.5	29.4	1068	24	ABK16597	DNA encoding rhesu
37	628	29.2	3011	24	AA594899	Human DNA sequence
38	623	29.0	1068	24	ABK16595	DNA encoding orang
39	622.5	28.9	4017	23	AA583768	DNA encoding novel
40	622	28.9	1053	24	ABK16591	DNA encoding chim
41	621.5	28.9	1200	13	AAQ30011	Sequence encoding
42	621.5	28.9	1200	16	AAQ99949	Recombinant high a
43	621	28.9	1068	24	ABK16593	DNA encoding goril
44	620	28.8	1106	16	AAQ99952	Recombinant high a
45	615	28.6	1373	16	AAQ99951	Recombinant high a

ALIGNMENTS

RESULT 1
AAAT72800
ID AAT72800 standard; cDNA; 1876 BP.

AAAT72800;
XX
28-SEP-1997 (first entry)

DE Human G-protein chemokine receptor HSATU68 cDNA.

XX HSATU68; G-protein chemokine receptor; 7-transmembrane receptor;

KW signal transduction; gene therapy; diagnosis; ss.

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT 173..1420

FT /*tag= a

FT primer_bind complement (173..190)
FT primer_bind /*tag= b
FT primer_bind 1402..1420
FT /*tag= c
XX
XX MO9725340-1.
XX
XX 17-JUL-1997.
XX
XX 11-JAN-1996; 96WO-US00499.
XX
XX 11-JAN-1996; 96WO-US00499.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX LI Y;
XX
XX WPI: 1997-372810/34.
XX
XX P-PSDB; AAM19780.
XX
XX DNA encoding new isolated human G-protein chemokine receptor - used
XX to develop products for treating, e.g. autoimmune diseases, chronic
XX infections, allergy, malignancy, inflammation or shock
XX
XX Claim 1: Fig 1a-d; 54pp; English.
XX
XX A cDNA clone (AA72800) codes for a newly identified human G-protein
XX chemokine receptor (AAM19780) designated HSATU68. It was identified
XX in a human genomic library derived from activated T cells. HSATU68
XX nucleic acids be used to produce HSATU68 in prokaryotic or
XX eukaryotic host cells, as probes for the detection, screening and
XX diagnosis of diseases caused by mutations in the HSATU68 gene, and
XX in the gene therapy of conditions related to underexpression of the
XX receptor its ligand.
XX
XX Sequence 1876 BP; 343 A; 625 C; 520 G; 388 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 9,98e-230 Length: 1876
XX Score: 2142.00 Matches: 414
XX Percent Similarity: 99.76% Conservative: 0
XX Best Local Similarity: 99.76% Mismatches: 1
XX Query Match: 99.58% Indels: 0
XX DB: 18 Gaps: 0
XX
XX US-09-101-518a-2 (1-415) x AAT72800 (1-1876)
XX
XX
XX 1 MetGluLeuArgTyrGlyProGlyArgLeuAlaGlyThrValIleGlyAlaAla 20
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 173 ATGGAGTTTGAAGGAAAGCGCCCTGGAGAGCTGGCGGACAGTTATAGAGAGCTGCT 232
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGlnPheLeuProGlyLeuTyr 40
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 233 CAGAGTAATTCACAGACTAATATGACTCAATACAAAAGAGTTCTGCCAGGCTTTAC 232
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 41 ThrAlaProSerSerProPheProSerGlnValSerAspHisGlnValLeuAsnAsp 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 293 ACAGCGCTTCCCTCCCGTCCCGCTCAGAGGTGAGTACCAAGGCTGTAATATGAC 352
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 61 AlaGluValAlaAlaLeuLeuGlnAsnPheSerSerSerTyrAspIlyGlnGln 80
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 353 GCCGAGGTGGCCGCTCCCTGGAGAACTTCAGCTTCCTATGACTATGAGAAACGAG 412
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 81 SerAspSerCysThrSerProPheProGlyAsnAspPheSerLeuAsnAspArg 100
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 413 AGTGACTCGGCTGTACTCTCCGCCCTGCCACAGAGACTTTCAGACTTCGACCGG 472
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuGlnGlyAla 120
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 473 GCCTTCCTGCGACCGCTCAACAGACTCTCTCTTCTGCTGGGCTGCTGGCAACGGCGG 532
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 140
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 533 GTGGCAGCCGCTGCTGTAGCCGCGGACAGCCCTGAGCAGACGACCTTCGCTC 592
XX
XX 141 HisLeuAlaValAlaAspThrLeuValLeuThrLeuProLeuThrPalAlaAspAla 160
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 593 CACCTAGCTGTACAGACAGAGCTGTGTGTCTACACTGCGGCTCTGGGAGTGAGCGCT 652
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 161 AlaValGlnTrpValPheGlySerGlyLeuCysValAlaGlyAlaLeuPheAsnIle 180
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 653 GCCGTCCAGTGGGCTTTGGCTCTGGCTCTGCCTGCAAGTGGACAGTCCCTTCAACATC 712
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 181 AsnPheTyrAlaGlyAlaLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 713 AACTCTAGCAGAGACCCCTCTGTGGCTGTGATAGCTTTTACCGCTACCTGAACATA 772
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 201 ValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeu 220
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 773 GTTCATGCCACCCAGCTTACCCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 832
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 221 AlaValTrpGlyLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 833 GCTGTGGGGGGCTGTGCTGCTTTGCGCCCTCCAGACTTCATCTTCCGTGCGGCCAC 892
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr 260
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 893 CACGAGAGCGCCTCAACGCCACCCACCTGCCAATACACTTCCACAGGTGGGCCCCACG 952
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuValMetAlaTyr 280
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 953 GCTCTGGGGGTGTGACGCTGGGTGGCTTTCTGTGCTGCTGCTGCTGCTGCTGCTGCT 1012
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 281 CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgAla 300
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1013 TGCATAGCCACATCTCGGGCGGTGCTGCTTCCAGAGGGGCCAGCGGCGCTGCGGGCC 1072
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 301 MetArgLeuValValValValValAlaPheAlaLeuLeuCysTrpThrProTyrHisLeu 320
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1073 ATCGGCTGT 1132
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 321 ValValLeuValAlaPheLeuMetAspLeuGlyAlaAlaLeuAlaArgAsnCysGlyArgGlu 340
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1133 GTGTGCTGTGTGACATCTCCATGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1192
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysLeu 360
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1193 AGCAGGTAGACGTGGCCCAAGTGGTCACTCAGGCTGGGCTAATGCACTGCTGCTC 1252
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetThrMetLeuLeu 380
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1253 AACCCGCTGTCTATGCTTTGTAGGGGTCAAGTCCGGAGCGGATGTGATGTGTCTC 1312
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg 400
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1313 TTGCGCTGTGGCTGCCCAACAGAGAGGCTCCAGAGGACGCAATCGTCTTCCCGCGG 1372
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 401 AspSerSerTrpSerGlnThrSerGlnAlaSerTyrSerGlyLeu 415
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1373 GATTCACTCGTGTGAGAGCTCAGAGGCTCCTACTCGGGCTTG 1417
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX
XX RESULT 2
XX AAH35033
XX ID AAH35033 standard; cDNA: 1877 BP.
XX
XX AAH35033;
XX
XX 03-SEP-2001 (first entry)
XX
XX Human colon cancer antigen encoding cDNA SEQ ID NO:2115.
XX
XX Human: colon cancer; colon cancer antigen; diagnosis; detection;
XX
XX colorectal carcinoma; chromosome 8; ss.
XX
XX Homo sapiens.
XX
XX

PN	WM0200122920-A2.
PD	XX
PF	05-APR-2001.
PR	XX
PS	28-SEP-2000; 2000MO-US26524.
PT	XX
PX	29-SEP-1999; 99US-0157137.
RA	03-NOV-1999; 99US-0163280.
RB	XX
RC	(HUMA-) HUMAN GENOME SCI INC.
RD	Ruben SM, Barash SC, Birse CE, Rosen CA;
RE	WPI: 2001-235357/24.
RF	P-PSDB; AAG75628.
RG	Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
RH	useful for preventing, diagnosing and/or treating colorectal cancers -
RI	Claim 1; Page 3596-3597; 9803pp: English.
RJ	XX
RK	AHH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
RL	cancer-associated nucleic acid molecules (N) and proteins (P), where
RM	the proteins are collectively known as colon cancer antigens. The colon
RN	cancer antigens have cytostatic activity and can be used in gene
RO	therapy and vaccine production. N and P may be used in the prevention,
RP	diagnosis and treatment of diseases associated with inappropriate P
RQ	expression. For example, N and P may be used to treat disorders
RR	associated with decreased expression by rectifying mutations or deletions
RS	in a patient's genome that affect the activity of P by expressing
RT	inactive proteins or to supplement the patient's own production of P.
RU	Additionally, N may be used to produce the colon cancer-associated Ps,
RV	by inserting the nucleic acids into a host cell and culturing the cell
RW	to express the proteins. N and P can be used in the prevention, diagnosis
RX	and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
RY	present invention.
RZ	CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
S0	missing at time of publication, meaning no sequences are present for
SA	SEQ ID NO:1027 to 1052, 7921 and 7922.
SB	XX
SC	S0 Sequence 1877 BP; 343 A; 625 C; 518 G; 388 T; 3 other;
SD	Alignment Scores:
SE	Pred. No.: 4,7e+229 Length: 1877
SF	Score: 2136.00 Matches: 413
SG	Percent Similarity: 99.52% Conservative: 0
SH	Best Local Similarity: 99.52% Mismatches: 2
SI	Query Match: 99.30% Indels: 0
SJ	Gaps: 0
SK	US-09-101-518A-2 (1-415) x AAH35033 (1-1877)
SL	OY 1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyAlaAla 20
SM	Db 173 ATGGAGTTGAGGAAGAATCAGCGCCCTGGAAACTGGCGGGACATTATAGAGAGAGTGCT 232
SN	OY 21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
SO	Db 233 CAGAGTAATAATCAAGACTTAATTCAGACTCAATCACAAAAGATTCTCCGACGAGGCCTTTAC 292
SP	OY 41 ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
SQ	Db 293 ACAGGCCCTTCTCCCTCCGTTCGCCCTTCACAGGTGAGTAGTACCACCAAGTGTCTAAATGAC 352
SR	OY 61 AlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyraSptYrGlyGluAsnGlu 80
SS	Db 353 GCCGAGGTTCGCCCTCTCTGGAGAACTTCAGCTTCTCATGACATATGAGAAAAACGAG 412
ST	OY 81 SerAspSerCyCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
SV	Db 413 ACTGAMTGGTGTATGACCTCCCGCCCTCCCAACAGAACTTCAGCGCTTCGACCGG 472

[illegible]

Dh 1097 TCGTCTCCCGCGGAGATTCACTGCTGTGAGACCTCAGAGGCTCTACTCGGGCTTG 1156
RESULT 4
AAV26557
ID AAV26557 standard; DNA; 1670 BP.
XX AAV26557:
AC
XX
XX 14-AUG-1998 (first entry)
DT
XX
DE Human IP-10/Mlg receptor CXCR3 gene.
XX
XX ds; chemokine receptor; cellular signal; treatment; T cell;
KM inflammatory disease; antitumour; antiviral.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 69..1175
FT /*tag- a
FT /product= "IP-10/Mlg receptor CXCR3"
FT 1534..1539
FT /*tag- b
FT 1624..1670
FT polyA_site /*tag- c
XX
XX MO811218-A1.
XX
XX 19-MAR-1998.
PD
XX
XX 10-SEP-1997; 97MO-US15915.
PF
XX
XX 31-MAR-1997; 97US-0829839.
PR 10-SEP-1996; 96US-0709838.
PR
XX
XX (KOCH-) KOCHER INST THEODOR.
PA (LEUK-) LEUKOSITE INC.
XX
XX Loetscher M, Mackay CR, Moser B, Qin S;
PI WPI; 1998-207381/18.
DR P-PSDB; AAW54371.
XX
XX DNA encoding CXCR3 chemokine receptor 3 - inhibitors and promoters of
PT which are useful for treatment of inflammation or in anti-tumour or
PT anti-viral therapy
XX
XX Claim 6; Fig 1; 137pp; English.
XX
XX The mammalian CXCR3 chemokine receptor 3 (CXCR3) gene encodes a protein
CC which can selectively bind one or more chemokines and can mediate
CC cellular signalling and/or a cellular response in response. Inhibitors
CC and promoters of mammalian CXCR3 can be detected and identified using
CC host cells expressing CXCR3. CXCR3 inhibitors can be used for treatment
CC of inflammatory diseases which are T cell mediated. CXCR3 promoters are
CC useful for antitumour or antiviral therapy.
XX
XX Sequence 1670 BP; 272 A; 574 C; 436 G; 388 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 2,47e-202 Length: 1670
Score: 1897.00 Matches: 369
Percent Similarity: 97.63% Conservative: 1
Best Local Similarity: 97.36% Mismatches: 5
Query Match: 88.19% Indels: 4
Gaps: 1
US-09-101-518a-2 (1-415) x AAV26557 (1-1670)
Oy 41 ThrAlaProSer-----SerProPheProProSerGlnValSerAspHisGln 56
Dh 36 ACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 95

Oy 57 ValLeuAsnAspAlaGluValAlaLeuLeuGluAsnPheSerSerTyrAspTyr 76
Dh 96 GTGCTAAATGACGCCGAGGTTCCGCCCTCTGGAGAACTTACGCTTCTCATACAT 155
Oy 77 GlyGluAsnGluSerAspSerCysThrSerProProCysProGlnAspPheSerLeu 96
Dh 156 GGAGAAAG 215
Oy 97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGluLeu 116
Dh 216 AACTTCGACCGGGCTTCCTGACAGCCCTTACACCTTCCTTCTCTGCGGCTG 275
Oy 117 GlyAsnGlyAlaValAlaValAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
Dh 276 GGCAACGGCGCGGTGGCAACCGCTGCTGACCCGGGAGACCGCTGAGCACCGAC 335
Oy 137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTyr 156
Dh 336 AACTTCGCTGCTCAGCTGAGCTGACAGACAGCTGCTGCTGACACTGCCGCTG 395
Oy 157 AlaValAspAlaAlaValAlaGlnTyrValPheGlySerGlyLeuCysLysValAlaGlyAla 176
Dh 396 GCAGTGGACCGCTGCCGTCAGTGGGCTTGTGCTTGGCTTGCMAAGTGGCAGGTGCC 455
Oy 177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuAlaCysIleSerPheAspArg 196
Dh 456 CTCTTCAACATCACTTCTTACGACAGAGCCCTCTGCTGCGCTGATCAGCTTTCACGCG 515
Oy 197 TyrLeuAsnIleValAlaHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
Dh 516 TACCTGAACATAGTTCATGACCCAGCTCAGCCGCGGGGGGCCCGCGCGCTGAC 575
Oy 217 LeuThrCysLeuAlaValTyrGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
Dh 576 CTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 635
Oy 237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
Dh 636 CTGTGCGCCACACAGAGAGAGGCTCAACGCGCACCTGCAATACACTTCCACAG 695
Oy 257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
Dh 696 GTGGCGCCGACGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 755
Oy 277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
Dh 756 GTCATGGCTACTGCTATGCCACATCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 815
Oy 297 ArgLeuArgAlaMetArgLeuValValAlaValAlaPheAlaLeuCysThrThr 316
Dh 816 CGCTGCGCGCCATCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 875
Oy 317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
Dh 876 CCGTATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 935
Oy 337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
Dh 936 TGTGGCCAGAAAGCAGGCTAGACCTGGCCAAAGTCGTACCTCAGGCGCTGGCTGACATG 995
Oy 357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
Dh 996 CACTGCTGCTCAACCCGCTGCTCATCTTGTAGGGGCTCAAGTCCGGAGGCGGATG 1055
Oy 377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
Dh 1056 TGGATGCTGCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1115
Oy 397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
Dh 1116 TCTTCCCGCGGAGTTCATCTGCTGTGAGACCTCAGAGGCTCTCTACTCGGGCTTG 1172
RESULT 5

AAA30593
ID AAA30593 standard; cDNA; 1107 BP.
XX
AC AAA30593;
XX
DT 21-Aug-2000 (first entry)
XX
DE Human G protein-coupled receptor GPR9 cDNA.
XX
KW G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist; ss.
XX
OS Homo sapiens.
PN M020022129-A1.
PD 20-Apr-2000.
XX
PF 12-Oct-1999; 99MO-US23938.
XX
PR 13-Oct-1998; 98US-0170496.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Behan DP, Chalmers DT, Liaw CW;
XX
DR WPI; 2000-329165/28.
P-PSDB; AAY90614.
XX
XX Non-endogenous constitutively activated human G protein-coupled
PT receptors; useful for identifying agonists for use as pharmaceutical
PT agents -
XX
PS Example 1; Page 115; 341pp; English.
XX
CC The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC AAY90677 and AAY90683-990687), and to DNA encoding them (AAA30709-A30743
CC and AAA30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC or Ala, and is preferably Lys. When the endogenous residue at this
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC The 15 amino acid stretch between the substituted amino acid and the Pro
CC may be endogenous, non-endogenous, or a mixture of endogenous and
CC non-endogenous residues. The constitutively active GPCRs are useful for
CC identifying antagonists, agonists and partial agonists for use as
CC pharmaceutical agents. The mutant proteins are also useful in research
CC settings for elucidating the roles of the receptors in normal and
CC diseased conditions. Antagonists for a particular GPCR are useful for
CC treating diseases and disorders associated with that receptor. Because
CC the novel mutant GPCRs are constitutively active, they can be used
CC directly for screening of compounds without the need for endogenous
CC ligands. The present sequence represents cDNA encoding a human wild-type
CC GPCR used in an exemplification of the invention. This was cloned and
CC subjected to site-directed mutagenesis (SDM) to generate DNA encoding
CC the corresponding mutant of the invention.
XX
SQ Sequence 1107 BP; 163 A; 380 C; 324 G; 240 T; 0 other;

Alignment Scores:
Pred. No.: 6.15e-202 Length: 1107
Score: 1891.00 Matches: 364
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.73% Mismatches: 0
Query Match: 87.91% Indels: 0
DB: 21 Gaps: 0

US-09-101-518a-2 (1-415) x AAA30593 (1-1107)

QY 51 GlnValSerAspHisGlnValIleuAsnAspAlaGluValAlaAlaIleuLeuGluAsnGpc 70
DB 10 GAGGTGAGTACACACCAAGTGTAAATGACGCCGAGGTTGCCCTCCTGGAGAACTTC 69
QY 71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProCys 90
DB 70 AGCTTCTCTATGACTATGAGAAAAACGAGACTGCTGCTTACCTCCCGCCCTGTC 129
QY 91 ProGlnAspPheSerIleuAsnPheAspArgAlaPheIleuProAlaIleuTyrSerIleu 110
DB 130 CCACAGAGACTTACGCTGAACTTCGACCGGCGGCTTCTGCGCCCTCTACAGCTCTCC 189
QY 111 PheIleuLeuGlyIleuLeuGlyAsnGlyAlaValAlaAlaValIleuLeuSerArgArgThr 130
DB 190 TTTCTGCTGGGGCTCTGGGCAAGCGGGGCTGCGGCAAGCGCTCTGAGCGGGGACA 249
QY 131 AlaIleuSerSerThrAspThrPheIleuLeuHisIleuAlaValAlaAspThrIleuVal 150
DB 250 GCCCTGAGCAGCAGCAGCAGCCTTCCCTGCTCCACTAGCTGTAGCAGACAGCCTGCTGGTG 309
QY 151 LeuThrIleuProLeuThrAlaValAlaAspAlaValAlaGlnThrValPheGlySerGlyIleu 170
DB 310 CTGACACTGCGCTCTGGGCACTGAGCGCTGCGCTGCAAGGAGGTCTTGGCTTGAGCTTC 369
QY 171 CysLysValAlaGlyAlaIleuPheAsnIleAsnPheTyrAlaGlyAlaIleuLeuLeuAla 190
DB 370 TGCAAAAGTGGCAGGTGCCCTTCAACATCACTCTACGAGGAGCCCTCTGCTGGCC 429
QY 191 CysIleSerPheAspArgTyrIleuAsnIleValHisAlaThrGlnIleuTyrArgArgly 210
DB 430 TGCAATCAGCTTGGACCGGTACCTGAACATAGTTCATGCGCACCCACTTACCGCGGGGG 489
QY 211 ProProAlaArgValThrLeuThrCysLeuAlaValAlaTyrGlyIleuCysLeuPheAla 230
DB 490 CCCCCGGCCCGGTACCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
QY 231 LeuProAspPheIlePheIleuSerAlaHisHisAspGluArgIleuAsnAlaThrHisCys 250
DB 550 CTCACAGACTTATCTTCTGCTGCGGCCACACGAGAGCGGCTCAAGCCACCCAGTCG 609
QY 251 GlnTyrAsnPheProGlnValGlyArgThrAlaIleuArgValIleuGlnIleuValAlaGly 270
DB 610 CAATCAACACTTCCACAGATGGCGCCAGCGGCTCTGCGGGTCTCCTGCTGCTGCTGCTG 669
QY 271 PheIleuLeuProLeuLeuValIleuAlaTyrCysTyrAlaHisIleuAlaValIleuLeu 290
DB 670 TTTCTGCTGCCCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 729
QY 291 ValSerArgGlyGlnArgArgIleuArgAlaMetArgIleuValAlaValAlaValAla 310
DB 730 GTTCCAGAGGGCCACAGCGCGCTGCGGGCCATGCGGCTGTGTGTGTGTGTGTG 789
QY 311 PheAlaIleuCysTyrThrProTyrHisIleuValAlaIleuValAspIleuMetAspIleu 330
DB 790 TTTGGCCCTCTGTGGACCCCTTATCCTGTGGTGTGTGTGTGTGTGTGTGTGTGTG 849
QY 331 GlyAlaIleuAlaArgAsnCysGlyArgGluSerArgValAlaValAlaLysSerValThr 350
DB 830 GCGGCTTTGGCCCGCACTG 909
QY 351 SerGlyIleuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyVal 370
DB 910 TCAGGCTGTGGGTATACATGACATGCTGCTCAACCCGCTGTCTATGCTTTGTATAGGGTTC 969
QY 371 LysPheArgGluArgMetTrpMetIleuLeuLeuArgGlyCysProAsnGlnArgGly 390
DB 970 AAGTTCGCGGAGCGGATGTGATGCTCTTGTGCTCTGCGGCTGCGCCACAGAGAGAGG 1029
QY 391 LeuGlnArgGlnProSerSerArgArgAspSerSerTrpSerGluThrSerGluAla 410
DB 1030 CTCAGAGAGCAGCCATTCGTTTCCCGCGGCGGATTCATCTGCTGTGAGACCTCAAGAGCC 1089

OY 411 SerTyrSerGlyLeu 415
|||||
Db 1090 TCCTACTGCGGCTTG 1104

RESULT 6

AAA30714
ID AAA30714 standard; DNA; 1107 BP.

AC AAA30714;

DT 21-AUG-2000 (first entry)

DE DNA encoding human mutant G protein-coupled receptor GPR9 (M254K).

XX G protein-coupled receptor; GPCR; constitutively active;

KM Intracellular loop 3; transmembrane domain 6; drug screening;

XX agonist; antagonist; mutant; ss.

OS Homo sapiens.

XX Synthetic.

PN WO200022129-A1.

XX 20-APR-2000.

PF 12-OCT-1999; 99WO-US23938.

PR 13-OCT-1998; 98US-0170496.

PA (AREN-) ARENA PHARM INC.

PI Behan DP, Chalmers DT, Llaw CM;

DR WPI: 2000-329165/28.

XX P-PSDB: AA190648.

PT Non-endogenous constitutively activated human G protein-coupled

PT receptors, useful for identifying agonists for use as pharmaceutical

PS agents -

XX Example 2; Page 223; 341bp; English.

XX The invention relates to constitutively active, non-endogenous versions

CC of endogenous human orphan G protein-coupled receptors (GPCRs, AA190643-

CC AA190677 and AA190683-Y0687), and to DNA encoding them (AAA30709-A30743

CC and AAA30775-A30779). The mutant proteins of the invention contain a

CC mutation in a portion of the protein comprising intracellular loop 3

CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,

CC is substituted for an endogenous residue in IC3 at a position 16 amino

CC acids N-terminal of an endogenous proline in TM6 to form a sequence

CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg

CC or Ala, and is preferably Lys. When the endogenous residue at this

CC position is Lys, this residue is replaced by His, Arg or preferably Ala.

CC The 15 amino acid stretch between the substituted amino acid and the Pro

CC may be endogenous, non-endogenous, or a mixture of endogenous and

CC non-endogenous residues. The constitutively active GPCRs are useful for

CC identifying antagonists, agonists and partial agonists for use as

CC pharmaceutical agents. The mutant proteins are also useful in research

CC settings for elucidating the roles of the receptors in normal and

CC diseased conditions. Antagonists for a particular GPCR are useful for

CC treating diseases and disorders associated with that receptor. Because

CC the novel mutant GPCRs are constitutively active, they can be used

CC directly for screening of compounds without the need for endogenous

CC ligands. Sequences AAA30709-AAA30743 and AAA30775-A30779 represent DNAs

CC encoding the mutant human GPCRs of the invention.

CC

XX

XX

XX

Query Match: 87.63% Indels: 0
DB: 21 Gaps: 0
US-09-101-518a-2 (1-415) x AAA30714 (1-1107)

OY 51 GlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaLeuLeuGluAsnPhe 70

Db 10 GAGGTAGTGACCAACAGTGTAAATGACCGGAGGTCCCGCCCTCGAGAACTTC 69

OY 71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProPocys 90

Db 70 AGCTCTTCCTATGACTATGAGAAACGAGAGTACTCGTGTACTCCCGCCCTGC 129

OY 91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeu 110

Db 130 CCACGAGACTTCAGCCGAACTTCGACCGGCTCTCTGCGACGCTCTACAGCTTC 189

OY 111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130

Db 190 TTTCTGCTGGGGCTGCTGGGCAACGGCGGCTGGACCGCTGCTGACCGCGGACA 249

OY 131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuVal 150

Db 250 GCCCTGAGCAGCACACGACCTTCCTGCTCCACTAGCTAGACAGACAGCTGCTG 309

OY 151 LeuThrLeuProLeuTyrAlaValAlaAspAlaValAlaGlnThrValPheGlySerGlyLeu 170

Db 310 CTACACTGCGGCTGCTGGGAGTGAGCGTGGCTCCAGTGGCTTTGGCTTGGGCTC 369

OY 171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuAla 190

Db 370 TGCAGAGTGGCAGAGTGGCCCTTCACATCACTTACACGAGAGGCCCTGCTGGCC 429

OY 191 CysLysSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210

Db 430 TGCATCAGCTTTACCCCTCACTGAACATGATTCATCCACACGACTCTACCGCGGG 489

OY 211 ProProAlaArgValThrLeuThrCysLeuAlaValThrPheGlyLeuLeuPheAla 230

Db 490 CCGCGGCGCGGCGGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549

OY 231 LeuProAspPheIlePheLeuSerAlaHisAspIleArgLeuAsnAlaThrHisCys 250

Db 550 CTCACAGACTTCACTTCCTCGTGGCGCCACACGAGAGCGCCACACGCCACTGTC 609

OY 251 GlnTyrAsnPheProGlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGly 270

Db 610 CAATACAACTTCCACAGGTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 669

OY 271 PheLeuLeuProLeuLeuValMetAlaIleTyrCysTyrAlaHisIleLeuAlaValLeu 290

Db 670 TTTCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 729

OY 291 ValSerArgGlyGlnArgAlaGlyLeuArgAlaMetArgLeuValValAlaValAla 310

Db 730 GTTTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 789

OY 311 PheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeu 330

Db 790 TTTGCGCTTGTGGAACCCCTGATCACTGCTGCTGCTGCTGCTGCTGCTGCTG 849

OY 331 GlyAlaLeuAlaArgAsnGlyArgGluSerArgValAspValAlaLysSerValThr 350

Db 850 GGGGCTTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 909

OY 351 SerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyVal 370

Db 910 TCAGGCGCTGGGCTACATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 969

OY 371 LysPheArgGlyIleArgMetTyrPheMetLeuLeuArgLeuGlyCysProAsnGlnArgGly 390

Db 970 AAGTTCGCGGAGCGATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1029

Alignment Scores:

Pred. No.: 2,89e-201 Length: 1107
Score: 1885.00 Matches: 363
Percent Similarity: 99.73% Conservative: 1
Best Local Similarity: 99.45% Mismatches: 1

```
OY 391 LeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAla 410
      |||
Db 1030 CTCACAGGACGACGACATGCTTCCCGCGGATTTCATCTGTGTGAGACCTCAGAGGCC 1089
OY 411 SerTrpSerGlyLeu 415
      |||
Db 1090 TCCTACTCGGGCTTG 1104

RESULT 7
AAV43793
ID AAV43793 standard; cDNA: 1620 BP.
XX
AC AAV43793;
DT 20-OCT-1998 (first entry)
XX
XX Rodent chemokine receptor HST01.1 nucleotide sequence.
DE
XX Chemokine; primate; human; rodent; chemokine receptor; asthma;
KW inflammatory response; immune response; leukocyte migration; GPCR;
KW leukocyte adhesion; chemottractant; modulation; antiviral response;
KW cellular morphology modification response; G-protein coupled receptor;
KW phosphoinositide lipid turnover; abnormal proliferation; regeneration;
KW atrophy; HST01.1, ss.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
FH 66..1169
FT CDS /tag= a
FT /product= "chemokine receptor HST01.1"
XX
XX W09832858-A2.
XX
XX 30-JUL-1998.
XX
XX 22-JAN-1998; 98WO-US00902.
XX
XX 23-JAN-1997; 97US-0036715.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Gorman DM, Hedrick JA, Mattson JD, Soto-trejo H;
XX Zlotnik A;
XX
XX WPI: 1998-427954/36.
XX P-PSDB: AAM69999.
XX
XX Rodent and primate chemokines and chemokine receptors - useful
XX diagnostically and therapeutically to treat conditions associated
XX with abnormal physiology or development e.g. inflammatory conditions
XX
XX Example 3; Pages 89-92; 105pp; English.
XX
XX This represents a rodent chemokine receptor HST01.1 nucleotide sequence.
XX The invention provides novel primate and rodent chemokines and chemokine
XX receptors. The chemokines, receptors and binding compounds (optionally
XX antibodies/fragments specifically binding the chemokines) are useful
XX therapeutically to treat conditions associated with abnormal physiology
XX or development e.g. inflammatory conditions such as asthma. Chemokines
XX are important in immune and inflammatory responses in that they induce
XX leukocyte migration and adhesion. They are also chemottractants for
XX several cells involved in inflammation and can induce other biological
XX responses e.g. modulation of second messenger levels (e.g. Ca++),
XX cellular morphology modification responses, phosphoinositide lipid
XX turnover, possible antiviral responses etc. The chemokine receptors of
XX the invention exhibit structural properties of G-protein coupled
XX receptors (GPCR), although their ligands have not yet been identified.
XX The chemokine and chemokine receptor polypeptides are useful to produce
XX ligand:receptor complexes in vivo or in assay techniques. Assays may
XX also involve chemical antagonists which block complex production or
XX utilize competitive binding. Binding compounds identified (agonists or
XX antagonists) can be used to modulate the physiological responses in cells
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CC (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal
CC proliferation, regeneration, generation and atrophy. The polypeptides
CC are also used to produce antibodies useful diagnostically, for drug
CC screening or for polypeptide purification. The polynucleotides are useful
CC to produce probes for detecting the polypeptides, and to isolate the
CC polypeptides or related sequences, especially from other species. They
CC also allow transformation of cells for polypeptide production.
XX
SQ Sequence 1620 BP; 366 A; 457 C; 405 G; 392 T; 0 other;
XX
Alignment Scores:
Pred. No.: 3,89e-172 Length: 1620
Score: 1627.50 Matches: 316
Percent Similarity: 89.97% Conservative: 25
Best Local Similarity: 83.38% Mismatches: 37
Query Match: 75.66% Indels: 1
DB: 19 gaps: 1
XX
US-09-101-518a-2 (1-415) x AAV43793 (1-1620)
OY 37 ProGlyLeuThrThrAlaProSerSerProPheProPheProSerGlnValSerAspHisGln 56
      |||
Db 33 CCACAGCAGCCACAGCCGCGAGCACCAGCAGCAGCATGACTTGAAGTTAGACGTCA 92
OY 57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheserSerTrpAspTrp 76
      |||
Db 93 GTGCTAGATGCTTCGGACCTTTCCTTGGAAGAACAGACACCTCCCTCAGATTAT 152
OY 77 GlyGluAsnGluSerAspSerCysTrpSerProProCysProGlnAspPheSerLeu 96
      |||
Db 153 GGGGAAACACAGAGCGAC--TTCTGTGACTCCCGCCGCGCCACAGGATTTACACCTG 209
OY 97 AsnPhesAspArgAlaPheLeuProAlaLeuTrpSerLeuPheLeuGlyLeuLeu 116
      |||
Db 210 AACTTTGACAGAACCTTCTCCGACGCTTACAGCTCCTCTTCTTGCGGGGCTGCTA 269
OY 117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
      |||
Db 270 GGCATATGGGGCGGTGGCTGCTGTACTGATGACGACGACCTCCGACAGCAGGAC 329
OY 137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
      |||
Db 330 ACCTTCCTGCTCCACCTGGCTGAGCCGAGTTCGTGCTGTTACTCTTCATTGTGG 389
OY 157 AlaValAspAlaAlaValGlnTrpValAlaPheGlySerGlyLeuCysLysValAlaGlyAla 176
      |||
Db 390 GCAGTGATGCTCTGTCGACGAGGTTTGGCCCTGCGCTTCGCAAGTGGACGGCC 449
OY 177 LeuPheAsnLeuAsnPhetyrAlaGlyAlaLeuLeuAlaCysIleSerPheAspArg 196
      |||
Db 450 TTGTTCACATCAACTTTCATGACAGGGGCTTCCTGCTGCTGTAAAGCTTCGACAGA 509
OY 197 TyrLeuAsnLeuValHisAlaThrGlnLeuTrpArgArgGlyProProAlaArgValThr 216
      |||
Db 510 TATCTGAGCATTAATGACAGCCAGCATCTACCGAGGAGCCCGGGTACCTGAGCC 569
OY 217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
      |||
Db 570 CTCACCTGATTAATGTATAGGGGTCTGTGCTCTTTCCTCCACAGATTTCATCTAC 629
OY 237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTrpAsnPhesProGln 256
      |||
Db 630 CTATCGACCAATCAATGATGACGCCCTCAATGACCCACCATTCGACATTCGCCACAG 689
OY 257 ValGlyArgThrAlaLeuArgValAlaGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
      |||
Db 690 GTGGGTGACACGCTGTGCTGATGACAGCTAGTGGCTGGTTCCGTGCGCCCTTCTG 749
OY 277 ValMetAlaTrpCysTrpAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
      |||
Db 750 GTATATGCGCTACGCTATGCGCCATATCTTAAGCTTCTGTGTTCTCCAGAGCCAGAGG 809
OY 297 ArgLeuArgAlaMetArgLeuValValValValAlaValAlaPheAlaLeuCysTrpTrp 316
```

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DB 810 CGTTTCGAGCATAGAGGTAGTGTAGTGTGGCAGCCTTGTGCTCTCTGCGAGACC 869
QY 317 ProtyrhisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
DB 870 CCTTTCACCTGGTGGTGTAGTATATCCATGAGATGGAGATTGGCCGCCAAC 929
QY 337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTrpMet 356
DB 930 TGTGTCGAAAAAGCCACCTGGATGTGGCAAGTCACCTCGGGCATGGGGTACATG 989
QY 357 HlscscYsLeuAsnProLeuLeuTyralaPheValGlyValLysPheArgGluArgMet 376
DB 990 CACTGCTGCTCAATCCGCTGCTATGCTTGTGGAGTGAAGTTCAGAGAAAAATG 1049
QY 377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgInProSer 396
DB 1050 TGGATGTGTTCACCGCTGGGCGCTCTGTGACACAGAGAGGCCCCAGCGCAGCGCTCA 1109
QY 397 SerSerArgAspSerSerTrpSerGluThrSerGluAlaSerTySerGlyLeu 415
DB 1110 TCTTCACGAGAGAAATCATCTGTGTGAGACACTGAGGCTCTACCTGGGCTTG 1166
RESULT 8
ABK16598
ID ABK16598 standard; DNA: 1068 BP.
XX
AC ABK16598;
XX
DT 14-MAR-2002 (first entry)
XX
DE DNA encoding vervet monkey CXCR2 receptor.
XX
KW Human; baboon; chimpanzee; vervet monkey; rhesus macaque;
KM orangutan; gorilla; tree shrew; dog; analgesic; antiinflammatoxy;
KW bradykinin 1 receptor; CXCR2 receptor; pain; inflammation; ds.
XX
OS Cercopithecus pygerythrus.
XX
PN WO200190134-A1.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US16777.
XX
PR 22-MAY-2000; 2000US-0576160.
XX
PA (PHAR-) PHARMACOPEDIA INC.
PI
PI Hollick R, Zhao J, Swanson R, Webb M, Strohl B, Baldwin JJ;
PI Auld DS;
XX
DR WPI: 2002-106172/14.
XX
P-PSDB: AAU80491.
XX
PT Identifying modulators of receptor activity using orthologues of human
PT receptors by contacting a compound with receptors from two species, and
PT measuring the effect of the compound on the receptors -
XX
PS Claim 49; Page 100; 108bp; English.
XX
CC The invention relates to identifying modulators of receptor activity
CC using orthologues of human receptors by contacting a compound with
CC receptors from two species, and measuring the effect of the compound on
CC the receptors. Included is an isolated nucleic acid (I) comprising a
CC nucleotide sequence encoding bradykinin B1 receptor (II); or encoding a
CC CXCR2 receptor (III). The method is useful for identifying a compound
CC having dual specificity to modulate the activity of a desired polypeptide
CC in two different species. The method is useful for identifying a non-
CC human animal model for testing compounds with potential efficacy as human
CC receptor modulators. The method comprises contacting a test compound with
CC receptors from at least two species; measuring an effect of the compound
CC on the receptors; and selecting an animal model representing a species
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CC having a receptor that exhibits the desired effect when contacted with
CC the test compound. Also described is a method for identifying a compound
CC that modulates (II) or (III) activity, where a compound is an agonist,
CC antagonist, suppressor, inhibitor and inducer, useful in treatment of
CC pain and inflammation and other receptor related pathologies. ABK16599-
CC ABK16574 and ABK16589-ABK16599 represent bradykinin 1 and CXCR2 receptor
CC coding sequences of the invention.
SQ Sequence 1068 BP; 219 A; 325 C; 244 G; 280 T; 0 other:
Alignment Scores:
Pred. No.: 9, 54e-62 Length: 1068
Score: 640.50 Matches: 145
Percent Similarity: 55.05% Conservative: 51
Best Local Similarity: 40.73% Mismatches: 129
Query Match: 29.78% Indels: 31
DB: 24 Gaps: 7
US-09-101-518a-2 (1-415) x ABK16598 (1-1068)
QY 68 GluAsnPheSerSerSerTyraSprTyrglyGluAsnGluSerAspSerCysThrSer 87
DB 37 GAAGATTTT---AGTAATTACAGATTACAGCTGACCTGCCCTCTACACAGATGTC 93
QY 88 PROPROCysPRGGLAsnRheSerLeuAsnRheAspArgAlaRheLeuProAlaLeuTy 107
DB 94 ACCCCATGTGCAGACACAGA--TCCCTGGAAATTCACAAAGTATTGTGTGCTATATCTAT 150
QY 108 SerLeuLeuPheLeuLeuGlyLeuGlyLeuGlyAsnGlyAlaValAlaValLeuLeuSer 127
DB 151 GCCCTGGTATTCTGCTGAGCTGCTGAGCAAACTCCCTGTATGCTGCTCATCTTACAC 210
QY 128 ArgArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThr 147
DB 211 ASCAGAGTGGCGGCGGCTCCCTACATGATGTCTACATGATGACCTGGGCGGACSTA 270
QY 148 LeuLeuValLeuThrLeuProLeuThrAlaValAlaAspAlaValAlaGlnTrpAlaPheGly 167
DB 271 CTGTTTGGCCCTGACCTGGCAATCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 330
QY 168 SerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyraGlyAlaLeu 187
DB 331 ACATTCCTGTGCAAGGTGCTGCATCCTCGAAGGAAGTAACTGTGCACGTGCGACATCTG 390
QY 188 LeuLeuAlaCysIleSerPheAspArgTyLeuAsnIleValHisAlaThrGlnLeuTy 207
DB 391 CTACTGGCCCTGCATGATGATGAGCCGTTACCTGACATGTGCATGTCACACAGC----- 444
QY 208 ArgArgGlyProProAlaArgValThrLeuThr----- 218
DB 445 -----ACACTGACCCAGAACGCGCTACTGTGTCAGTTTCGTA 480
QY 219 CysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheLeuLeuSer 238
DB 481 TGTCTCAGCATGTGGGGTGTGCTTACTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
QY 239 AlaHisHisAspGlyArgLeuAsnAlaThrHisCysGlnIleTyraAsnPheProGlnValGly 258
DB 541 ACTGTCTACCCGACCTATGTAGCCAGTCC--TGC-----TATGAGAGACATGGGC 588
QY 259 -----ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyRheLeu 272
DB 589 AACAAATACAGCAAAATGGGAGTGTGGTGGGATCTGCCAGACCTTGTCTTCAAC 648
QY 273 LeuProLeuValAlaMetAlaTyrcysTyraHisIleLeuAlaValLeuValSer 292
DB 649 TTGCGACATGTGATGATGATGTCTTGTGATGATGATGATGATGATGATGATGATGATG 708
QY 293 ArgGlyGlnArgArgLeuArgAlaMetArgLeuValAlaValAlaValAlaPheAla 312
DB 709 CACATGGGCGCAAGAACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 768
QY 313 LeuCysTrpThrProTyHisLeuValValLeuValAlaPheIleLeuMetAspLeuGlyAla 332
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Db      ||||||| ||||||| ||||||| ||||||| ||| |||||
769 CTTCTCTGGCTGCTCCCTACACCTGCTGCTGACAGACATCTCATGAGACCCCGTTG 828
Oy      333 LeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrsGly 352
      ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      829 ATCAAGAGACCTGTCTACACGCCGCAATGACATGCAGCCGGCCCTGATGCCACGAGATT 888
Oy      353 LeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPhe 372
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      889 CTGGGCAATCTTACAGAGCTGCTCAACCCCATCATCTACGCTTCATGTGGCAGAAAGTTC 948
Oy      373 ArgGluArgMetTyrMetLeuLeuLeuArgGlyCysProAsnGlnArgGlyLeuGln 392
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      949 CCGCATGAGCTCTCAGATTCATGACACATGCATGCTTGATGATGAGGAGACTCCCTGCC 1008
Oy      393 ArgGlnProSerSerArgArgAspSerSerTyrPserGluThrSer 408
      ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1009 AAGAGACAGAGCCTTCTTTGCTTTGCTTTCTTCAAGGACACATTC 1056

RESULT 9
AAx87709
ID      AAX87709 standard; cDNA; 2517 BP.
XX
AC      AAX87709;
XX
DT      26-OCT-1999 (first entry)
XX
DE      Mouse Burkitt's lymphoma receptor 1 (BLR1) cDNA.
XX
KM      Burkitt's lymphoma receptor 1; BLR1; mouse;
KM      B lymphocyte chemotactant; BLC; chemokine; ligand;
KM      drug screening; leukaemia; autoimmune disease; therapy; ds.
XX
OS      Mus musculus.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..1125
FT      /*tag= a
XX
PN      W09928468-A1.
XX
PD      10-JUN-1999.
XX
PF      02-DEC-1998; 98WO-US25561.
XX
PR      02-DEC-1997; 97US-0982493.
XX
PA      (REGC ) UNIV CALIFORNIA.
XX
PI      Cyster JG, Gunn MD, Williams LT;
XX
DR      WPI; 1999-493764/41.
DR      P-PSDB; AAY06643.
XX
PT      Modulating interaction of a Burkitt's Lymphoma Receptor 1
XX      polypeptide and ligand, useful in drug screens
XX
PS      Example: Page 33-34; 42pp; English.
XX
CC      This is the nucleotide sequence of murine cDNA coding for a
CC      Burkitt's lymphoma receptor 1 (BLR1, see AAY06643). The invention
CC      relates to methods for modulating the interaction of BLR1 with
CC      its ligand, B lymphocyte chemotactant (BLC, see AAY06641). The
CC      methods comprise combining BLR1 and BLC polypeptides with a
CC      candidate modulator agent under conditions whereby, but for the
CC      presence of the agent, the polypeptides engage in a first
CC      interaction, and determining a second interaction of the
CC      polypeptides in the presence of the agent, wherein a difference
CC      between the first and second interactions indicates that the agent
CC      modulates the interaction of the polypeptides. The modulator is
CC      preferably an antagonist, especially dominant negative, form of
CC      BLC. BLC and BLC agonists and antagonists may be useful for
CC      treating viral (e.g. HIV) infections, lymphoma, B lineage

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CC      leukaemia, and autoimmune diseases such as rheumatoid arthritis,
CC      thyroiditis and diabetes.
XX
SQ      Sequence 2517 BP: 620 A; 727 C; 601 G; 569 T; 0 other;

Alignment Scores:
Pred. No.:      4.09e-61      Length:      2517
Score:      640.00      Matches:      143
Percent Similarity:      56.29%      Conservative:      54
Best Local Similarity:      40.86%      Mismatches:      139
Query Match:      29.75%      Indels:      14
DB:      Gaps:      6

US-09-101-518a-2 (1-415) x AAX87709 (1-2517)
Oy      70 PheSerSerSerTyrArgpyrGlyGluAsnGlySerAspSerCysGlyThrSerProPro 89
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      76 TACAGTACAGACGACGAGATTCCTCCCTACAGACAGTACATTCCTGCTTACA----- 126
Oy      90 CysProGlnAspPheSerSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeu 109
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      127 GTGAGAGACCTTACTAGAGTCCTTTAAGCGGCTTTCATGCTGTGCGCTACAGACCTC 186
Oy      110 LeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArg 129
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      187 ACTTCTCTCTGGGTATGATGGAAACATCTGTGCTGTGTAATCTCGGAGAGACCGG 246
Oy      130 ThrAlaLeuSerSerThrSprThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeu 149
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      247 CACACTGGAGCTCAACGACGATTCCTGTTCCACTGCACTGACATCCACTTCTCTTA 306
Oy      150 ValLeuThrLeuProLeuTyrAlaValAlaAspAlaAlaValGlnTyrAlaPheGlySerGly 169
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      307 GTCTTATCTCTGCTTTTCCAGAGCGTGAAGGCTGTGTGGTGGTGGTCTTAGGACCTTC 366
Oy      170 LeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeu 189
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      367 CTCTGCAAAACTGTATCTCTGCAAGATCAATTTCTACTGCGAGACCTGCTCGTG 426
Oy      190 AlaCysIleSerPheAspArgTyrIleuAsnIleValHisAlaThrGlnLeuTyrArg 209
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      427 GCCTGTATAGCTGATGACGCGTACGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
Oy      210 GlyProProAlaArgValThrLeuThrCysLeuAlaValAlaTyrGlyLeuCysLeuLeuPhe 229
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      487 CGTCGACCTCTCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 546
Oy      230 AlaLeuProAspPheIlePheLeuSerAla-----HisHisAspIleuArgLeuAsn 246
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      547 GCCTTACCGGAACCTCTCTTGGCAAGTTGGCCAACTCATACAAACGACATCTCTTA--- 603
Oy      247 AlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr-----AlaLeu 262
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      604 ---CCACAGTGCACCTTCTCCAGGAAACGAAAGCGGAACCTGCTTACCTCC 660
Oy      263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyr 282
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      661 CGTTTCTTACACATCGGGGGCTTCTTACATCGATCGATCTGTATGGAGTGTATAC 720
Oy      283 AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgArgLeuAlaMet 301
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      721 GTGGGCGGTGTCACAGCTACTGAGGCCAGCGCGCCCTACAGCGGAGAGAGCGGCTC 780
Oy      302 ArgLeuValValValValValValAlaPheAlaLeuCysTyrThrProGlyHisLeuVal 321
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      781 AGGGTGGCCATTTTATGTGCAAGCATTTTCTCTGTGTGGTGGCTTACCATCATGTGTC 840
Oy      322 ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaAlaArgAsnCysGlyArgGluSer 341
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      841 ACTTCTCTGATACACTGAGAGCGTGAAGGCTGTGAATAGACAGCTGCAGCTGAGTGGC 900
Oy      342 ArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsn 361
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 901 TATCTCTCTGTCGCCATCACCTTGTGTGAATTCTTGCGCCCTGGCAGACACTCTGTCTCAAT 960

Oy 362 ProLeuLeuTyfAlaPheValGlYalValysPheArgIuAryMetTrpMeLeuLeu 381
||||| ||| ||||| ||||| :||| |||||
Db 961 CCCAGTCCTTTACACCCTTCGCCTGAAGATTCCGAGAGTACCTCTCGGCTTTCAC 1020

Oy 382 ArgLeuGlyCySProAsnGlnArgGlyLeuGlnArgGlnProSerSerArgAlaASP 401
:::||| ||| ||| ||| ::||| |||
Db 1021 AAGCTGGGCTGTGCTGGCCCCGGCTCCCTT--TGGCAACTTTTCCCACTGGCGCAAG 1077

Oy 402 SerSerTrpSerGluThrSerGluAlaSer 411
||||| ||||| :||| |||||
Db 1078 AGTAGTCTCTGTAGTCAGAGAATGCTACT 1107

RESULT 10
ID ABK16599
XX ABK16599 standard; DNA; 1068 BP.
XX
XX ABK16599;
AC
XX
XX
Dt 14-MAR-2002 (first entry)
XX
De DNA encoding baboon CXCR2 receptor.

Kw Human; baboon; chimpanzee; vervet monkey; rhesus macaque;
Xm orangutan; gollia; tree shrew; dog; analgesic; antiinflammatory;
Rv bradykinin I receptor; CXCR2 receptor; pain; inflammation; ds.
XX
XX Papio hamdryus.
OS
XX
XX WO200190134-A1.
PN
XX
XX 29-NOV-2001.
Pd
XX
Pf 22-MAY-2001; 2001WO-US16777.
Pr
XX
Pr 22-MAY-2000; 2000US-0576160.
Pa (PHAR-) PHARMACOPEIA INC.
Pi Horlick R, Zhao J, Swanson R, Webb M, Strohl B, Baldwin JJ;
PI Auld DS;
Dr WPI: 2002-106172/14.
DR P-PSDB; AAU80492.

Pt Identifying modulators of receptor activity using orthologues of human
Pt receptors by contacting a compound with receptors from two species, and
Pt measuring the effect of the compound on the receptors -
XX
XX Claim 49; Page 100-101; 108pp; English.

XX The invention relates to identifying modulators of receptor activity
Cc using orthologues of human receptors by contacting a compound with
Cc receptors from two species, and measuring the effect of the compound on
Cc the receptors. Included is an isolated nucleic acid (I) comprising a
Cc nucleotide sequence encoding bradykinin B1 receptor (II); or encoding a
Cc CXCR2 receptor (III). The method is useful for identifying a compound
Cc having dual specificity to modulate the activity of a desired polypeptide
Cc in two different species. The method is useful for identifying a non-
Cc human animal model for testing compounds with potential efficacy as human
Cc receptor modulators. The method comprises contacting a test compound with
Cc receptors from at least two species; measuring an effect of the compound
Cc on the receptors; and selecting an animal model representing a species
Cc having a receptor that exhibits the desired effect when contacted with
Cc the test compound. Also described is a method for identifying a compound
Cc that modulates (II) or (III) activity, where a compound is an agonist,
Cc antagonist, suppressor, inhibitor and inducer, useful in treatment of
Cc pain and inflammation and other receptor related pathologies. ABK16599-
Cc ABK16574 and ABK16589-ABK16599 represent bradykinin I and CXCR2 receptor
Cc coding sequences of the invention.
XX
XX Sequence 1068 BP; 214 A; 327 C; 244 G; 282 T; 1 other;

Alignment Scores:		1.24e-61	Length:	1068
Pred. No.:		639..50	Matches:	145
Score:		56.45%	Conservative:	52
Best Local Similarity:		41.55%	Mismatches:	135
Query Match:		29.73%	Indels:	17
DB:		24	Gaps:	7
US-09-101-518A-2 (1-415) x ABK16599 (1-1068)				
QY	68	GIUASNPHESESERSETSERIYASPIRGLYGLUANGSIUSERASPSERCYSCTHRSER	87	
DB	37	GAAGATTTT---AGTAATTACAGTTACAGCGCTGACCTGCCCTTCTCTACACGATGC	93	
QY	88	PROFCYSPROGLINASPHESESERLEUANSNPHEASPARGALAPHELEUPROIALLEUTYR	107	
DB	94	GCCCATGTCGACACGAA---TCCCTAGAAATCAACAGATATTGTGTCATATCAT	150	
QY	108	SERLEULEUPHELEULENGLYLEULENGLYSNGLYALVALALALVALLEULEUSER	127	
DB	151	GCCCGTGATTCCTCTAGCTGCTGGGAAACCTCCCTCGATGCTGCTCATCTTCAC	210	
QY	128	ACGATGTHALALEUSERSETTHRSAPHRPHELEUHSIENSLAVALALVALASPTH	144	
DB	211	ACGAGGTCGCCGCTCATCATCATATGCTACCTACCTACGAACTGGCGATGGCGACTA	270	
QY	148	LEULEUVALLEUTHLEUPROLEUTPRALVALASPALALVALALGINTPRVALPHEGLY	167	
DB	271	CGTTTGGCCCTACCTGTCCTGCCATCGGCTGCCCAAGTGAATGGCTGATTTTGGC	330	
QY	168	SERGLYLEUCYSLYSVALALAGLYALALEUHEANSIENAPHEIYRALAGLYALEU	187	
DB	331	ACATTCCTGTGAAAGTGTCTCACTCCTGAAGACGACCACTTCATAGTGCATCTG	390	
QY	188	LEULEUALACYSILSESERPHEASPARGTGYLEUANSIENALHISALATHRGLN-----	205	
DB	391	CTACGCGCCTGCATGAGTGTGACCGCTTACCTGGCGCATTTGCATGCCACAGCACATG	450	
QY	206	LEUTYRATGATGAGLYPROPROIALARGVALTHIRLEUTHIRCYSLLEUALVALTPRGLYLEU	225	
DB	451	ATCCGAAAGCGC-----TACTTGGTCAAGTTTCATATTCCTCAGCATCTGGGGCTTG	501	
QY	226	CYSLEULEUPHEALALEUPROASPHLELPHLEUSERALAHISIASPGLIARGLEU	245	
DB	502	TCCCTGTCTGTGGCCCTGCGCTCTTACTTTTCCGAAAGGCTGTCTACCCRCCTATATT	561	
QY	246	ASNALATHRHISACYSGLINTYRASNAPHEPROGLINAGLY-----ARG	258	
DB	562	ACCCACATC---TGC-----TATAGGACATGGGCAACATACAGCAAAATGGCGG	608	
QY	260	THRALALEUARGVALLEUGLLEUVALALAGLYPHELEULEUPROLEULEUVALMETALA	279	
DB	610	ATGAGTGTGCGGATCTGCCCCACGACCTTGGCTTCATCTGCGCGCTGATCATCTGTG	666	
QY	280	TYRYSYTPRALAHISILLEUALALVALLEULEUVALSERATGGLYGLINATGATGLEUARG	299	
DB	670	TTCTCTATGATTCACCTCTGGCAGCTGTGTTAAGGCCACATGGGAGCAAAACACCGG	728	
QY	300	ALAMEATGYLEUVALVALVALVALVALVALALAPHEALALEUCYSTPRTHPROTYRHIS	319	
DB	730	GCGATGGCGGTCATCTTGTGCTGTCTCTCATCTTCCACTTTCTGTGGTCCCTACAC	789	
QY	320	LEUVALVALLEUVALASPILEUUMETASPLEUGLYALALEUALARGASNCYSGLIARG	338	
DB	790	CTGGTCCTGCTGTGGACACCTCATGTAGGACCCGGTGTCAACAGACCTGTACACGGC	849	
QY	340	GIUSERATGVALASPVALALALYSSEVALTHRSERGLYLEUGLYTYRMECHISCYSCYS	359	
DB	850	CACAGTGCATACACAGGCGCTGAGTCCACCGAGATTCTGGGCATCTTTCACAGCTGC	909	
QY	360	LEUASNPHEULEUTYRALPHEVALGLYVALYLYSPHEATGGLIARGMETPRMETLEU	379	

Db	910	CTCAACCCCCCTCATCTACGCCCTTCATTGGCCACAGAATTCGCCCATGAGCATCCCTCCAGATT	969
Oy	380	LeuLeuArGLyGLyCysProAsnGlnArGLyLeuGlnArGlnProSerSerSerArg	399
Db	970	CTAGCCACACATGAGCTTGATGACGAAGCACTCCCTGCCAAGACAGACAGCCCTCTT	1029
Oy	400	ArgAspSerSerTrpSerGlnTrsR	408
Db	1030	GTTGGCTCTTCCTTCAGACACACTTCC	1056
RESULT 11			
ABA09268			
XX	ID	ABA09268 standard; cDNA; 1886 BP.	
XX	XX	ABA09268;	
XX	DT	11-JAN-2002 (first entry)	
DE	XX	Human IL-8R B homologue-encoding cDNA, SEQ ID NO:1044.	
XX	XX	Human; cytokine; cell proliferation; cell differentiation; growth factor;	
KW	KW	haematopoiesis regulation; tissue growth; immunomodulator; activin;	
KW	KW	inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;	
KW	KW	proliferation; metastasis; cancer; tumour; haematopoietic disorder;	
KW	KW	myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;	
KW	KW	chronic inflammatory condition; proliferative retinopathy;	
KW	KW	atherosclerosis; coronary heart disease; arterial ischemia;	
KW	KW	bone disorder; osteoporosis; vascular growth disorder;	
KW	KW	tissue regeneration; wound healing; infection; immune disorder;	
KW	KW	cell culture; drug screening; gene therapy; antiinflammatory;	
KW	KW	antasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;	
KW	KW	cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;	
XX	XX	antifungal; vulnerary; antulcer; ss.	
OS	XX	Homo sapiens.	
PN	XX	WO200157188-A2.	
XX	XX	09-AUG-2001.	
PD	XX	05-FEB-2001; 2001WO-US03800.	
XX	XX	03-FEB-2000; 2000US-0496914.	
PF	XX	27-APR-2000; 2000US-0560875.	
PR	XX	(HYSE-) HYSEQ INC.	
PA	XX	Tang YT, Liu C, Drmanac RT;	
PI	XX	WPI: 2001-457740/49.	
DR	XX	P-PSDB: ABB12024.	
XX	XX	Human proteins and DNA encoding sequences useful for preventing,	
PT	XX	treating or ameliorating a medical condition in a mammalian subject	
PT	XX	e.g. arthritis and cancer -	
PS	XX	Claim 1; Page 874; 1963pp; English.	
XX	XX	Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and	
CC	CC	sequences ABA08225-ABA09574 represent nucleic acids encoding them. The	
CC	CC	invention also relates to vectors and recombinant host cells comprising a	
CC	CC	nucleotide of the invention, methods of producing the novel polypeptides,	
CC	CC	antibodies against the polypeptides, methods of detecting the nucleotides	
CC	CC	or polypeptides in a sample, and methods of identifying compounds which	
CC	CC	bind to polypeptides of the invention. Although novel, many of the	
CC	CC	polypeptides of the invention have homology to known proteins, thereby	
CC	CC	giving an insight into their probable biological activities, and hence	
CC	CC	potential therapeutic applications. The polypeptides of the invention may	
CC	CC	have various activities, including cytokine, cell proliferation or cell	
CC	CC	differentiation activities; stem cell growth factor activity;	
CC	CC	haematopoiesis regulatory activity; tissue growth activity;	
CC	CC	immunomodulatory activity; activin- or inhibin-related activities;	
CC	CC	chemotactic or chemokinetic activities; haemostatic, thrombotic or	

CC	thrombolytic activities; receptor or ligand activities; or may be
CC	involved in oncogenesis, cancer cell proliferation or metastasis.
CC	Depending on their biological activities, polypeptides and nucleotides of
CC	the invention are useful for preventing, treating or ameliorating medical
CC	conditions, e.g., by protein or gene therapy. Such conditions include
CC	cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC	disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC	proliferative retinopathy, atherosclerosis, coronary heart disease,
CC	arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC	vascular growth. Polypeptides involved with tissue regeneration and
CC	repair (or nucleic acids encoding them) may be used to promote wound
CC	healing (e.g., of burns, incisions and ulcers), while those with
CC	immunomodulatory activities may be used in the treatment of viral,
CC	bacterial and fungal infections in addition to immune disorders.
CC	Polypeptides with growth factor activity may be used in cell cultures to
CC	promote cell growth. For example, such polypeptides may be used to
CC	manipulate stem cells in culture to give rise to neuroepithelial cells
CC	that can be used to augment or replace cells damaged by illness,
CC	autoimmune disease or accidental damage. The polypeptides, and nucleotides
CC	may also be used in the diagnosis of the above conditions, and in drug
CC	screening techniques. The present sequence represents a cDNA encoding a
CC	novel human polypeptide of the invention.
XX	
XX	Sequence 1886 BP; 428 A; 556 C; 418 G; 484 T; 0 other:
Alignment Scores:	
Pred. NO.:	4,99e-61 Length: 1886
Score:	637.50 Matches: 154
Percent Similarity:	51.09% Conservative: 57
Best Local Similarity:	37.29% Mismatches: 145
Query Match:	29,64% Indels: 57
DB:	22 Gaps: 10
US-09-101-518A-2 (1-415) x ABA09268 (1-1886)	
OY	17 GlyIyAlaAlaGlnSerLySergInThrLySeraSPSerIleThrLyGluPheLeu 36
Db	349 GGAGGTGTCTCAACGCGGAAAC----- 372
OY	37 ProGlyLeuYrThrAlaProSerSerProPhePro---ProSergIValSeraspHis 55
Db	373 -----CCAGCGACCCAGCTCAGGATTAACTTAACCTCAAAATAAGAGATTTT 420
OY	56 GluValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe----- 70
Db	421 AACATGGAGAGTACAC-----TTTGAAGATTTCGGAAGGTGAAT 465
OY	71 SerSerSerLyaspYrGlyGluAsnGluSeraspSerCysCysThrSerProCys 90
Db	466 CTTAGTAAATTACAGTTACAGCTTACCCGCCCTTTCTCTAGATGCCGCCCATGT 525
OY	91 ProGlnAspPheSerIleuAsnPheAspArgAlaPheLeuProAlaLeuYrSerIleu 110
Db	536 GAACCGAGA--TCCTCGGAATCAACACAGTATTTGTGTGCTATTAATGCCCTGGTA 582
OY	111 PheLeuLeuGlyLeuLeuGluYAsnGlyAlaValAlaValLeuLeuSerArgTrpThr 130
Db	583 TTCTCTGCGAGACCGTGGGAAATCCCTCGTATGCTGTGCTATCTTAACGACGAGGTC 642
OY	131 AlaLeuSerSerThrAspThrPheLeuLeuHisIleuAlaValAlaAspThrLeuVal 150
Db	643 GGCGGCTCCGCACTGATGTCTACGCTGGAACCTGAGCTTGCGGACGACTCTTTGCC 702
OY	151 LeuThrLeuProLeuThrAlaValAspAlaAlaValAlaGlnTrpValPheGlySerGlyLeu 170
Db	703 CTGACCTTGCCCACTGTGGCGGCTCCCAAGGTGAATAGCGATTTTGGCACAATTCCTG 762
OY	171 CysLySValAlaGlyAlaLeuPheAsnIleAsnPheTyAlaGlyAlaLeuLeuLeuAla 190
Db	763 TGCAGGTGGTCTCACTCTGAAGGAAAGTCATCTTATAGGAGCATCCCTGCTATGGCC 822
OY	191 CysIleSerPheAspArgTyLeuAsnIleValHisAlaThrGlnLeuTyArgArgGly 210

D	b		823	TGCATCAGTGTGGACCGTTAACTCCGCGCATTTGCCATTCGCACACGC-----	CysLeuA1a	221	867
O	y		211	ProProAlaArgValThrLeuthr-----			
D	b		868	-----ACACTGACCAGAACGCGCTACTTGTCGAATTCAATTCATGTCTCAGC			
O	y		222	ValTrpGlyLeuCysIleuPheAlaLeuProAspPheIlePheLeuSerAlaHisHis			
D	b		913	ATCTGGGGGTGTCTTGGCTCTCGGCCCGCTGCTTAATTTCGAAGAAGCCGTCTAC			
O	y		242	AspGluArgLeuSnaIatThrHisCysGlnTryAsnProGlnValGly-----			
D	b		973	TTCATCCAACTGTATCCCGC---TGC-----TATGAGACAATGGCACAACTTCA			
O	y		259	-----ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu			
D	b		1021	GCAAACTGGCGGATGCTGTACAGGATCTCGCCAGATCCTTGCTTCATCGTGCAC TG			
O	y		276	LeuValMetAlaIArgCysTryAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln			
D	b		1081	CTGATCATCTGCTGTCTGCTACAGGATTCACCCCTGACCGCTTTTAGGCCACATGGGG			
O	y		296	ArgArgLeuArgAlaMetArgLeuValValValValAlaValAlaPheAlaLeuCysTrp			
D	b		1141	CAGAGACACCGGGCCATCGCGGATCTTCTGCTGCTGCTCTCATCTTCTGCTGCTGG			
O	y		316	ThrProTryHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg			
D	b		1201	CTGGCCCTACAACTCGTGCTGCTGGCAGACACCCCTCATGAGGACCCAGTGTATCGAGAG			
O	y		336	AsnCysGlyArgGlnSerArgValAspValAlaIArgSerValThrSerGlyLeuGlyTy			
D	b		1261	ACCGTGTAGCGCCGCAATCATCATCGACCGGCTGTGGATGTCGACGAGATTCTGGCGATC			
O	y		356	MetHisCysCysLeuAsnProLeuLeuTryAlaPheValGlyValIlysPheArgGluArg			
D	b		1321	CTTCACACGCTGCTCTCAACCCCCTCATCTACGCTTCTATTTGGCCAGAACTTTGCCAGTGA			
O	y		376	MetTrpMetLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro			
D	b		1381	CTCTCTCAAGATTCTTACGCTATACATGCGCTTGATGACGACGAAGATCCCTCCCAAAGACACG			
O	y		396	SerSerSerArgArgAspSerSerTrpSerGluThrSer			
D	b		1441	AGGCTTCCTTGTGTGGCTCTCTTCTTCAGGACACTTCC			
			RESULT 12				
			AAS77796				
			ID AAS77796 standard; cDNA; 2785 BP.				
			XX AAS77796;				
			XX AC				
			XX AA577796;				
			DT 13-FEB-2002 (first entry)				
			XX DNA encoding novel human diagnostic protein #13600.				
			XX Human: chromosome mapping; gene mapping; gene therapy; forensic;				
			KW food supplement; medical imaging; diagnostic; genetic disorder; ss.				
			XX Homo sapiens.				
			OS Homo sapiens.				
			PN WO200175067-A2.				
			PD 11-OCT-2001.				
			PF 30-MAR-2001; 2001WO-US08631.				
			XX 31-MAR-2000; 2000US-0540217.				
			PR 23-AUG-2000; 2000US-0649167.				
			XX (HYSE-) HYSEQ INC.				
			PA Dmanac RT, Liu C, Tang YT;				
			PI				

XX WP1: 2001-639362/73.
DR P-PSDB: ABG13609.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 13600; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.

Seq	Sequence	2785 BP	739 A	722 C	629 G	695 T	0 other
	Alignment Scores:						
	Pred. No.:	9,11e-61	Length:	2785			
	Score:	637.50	Matches:	154			
	Percent Similarity:	51.09%	Conservative:	57			
	Best Local Similarity:	37.29%	Mismatches:	145			
	Query Match:	29.64%	Indels:	57			
	DB:	23	Gaps:	10			
US-09-101-518A-2 (1-415) x AAS77796 (1-2785)							
Oy	17 GLYGLVALAALAGINserLeuSerGlnThrIlySerAspserIleThrIlyGluPheLeu	36					
Db	349 GGAGGTGTCCTACAGGTGAAAAGC-----	372					
Oy	37 ProGlyLeuTyThrAlaProSerSerProPhePro--ProSerGlnValSerAspHis	55					
Db	373 -----CCAGCAGCCACGTCAGAGATTAAAGTTAACTTCAAAAATGGAAGATT	422					
Oy	56 GlnValLeuasnAspAlaGluValAlaAlaLeuLeuGluAsnPhe-----	70					
	:::						
Db	421 AACATGAGAGACTGCAGC-----TTTGCAGATTTCTGGAAGAGTGAAGAT	465					
Oy	71 SerSerSerTyraapTyrcIyGluAsnGluSerAspSerScyStnSerProProCys	90					
Db	466 CTTAGTAAATTAACAGTTACAGCTTACCCCTGCCCTTTTCTACTAGATGCCGCCCATGT	522					
Oy	91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrrSerLeuLeu	110					
	:::						
Db	526 GAACCAAGAA---TCCCTGGAAATCAACAAGATTTTGGCGCATTAATCTAAGCCCTGGTA	583					
Oy	111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValaLeuLeuSerArgArgThr	130					
Db	583 TTCCTGCTGACCCGCTGGGAAATCCCTCGTATGCTGCATCTTATACAGCAGGGTC	642					
Oy	131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuVal	150					
Db	643 GAGCGCTCGTCACTGATGCTACTCGTGTGAACCTAGCTGTGGCGAGCACTCTTTGGC	702					

Oy	151	LeuThrLeuProLeuThrAlaValAlaAlaValAlaGlnThrProValPheGlySerGlyLeu	170
Db	703	CTGACCTTGGCCCATCTGGGCGCCTCCAGGTGAATGGCTGGATTTTGGACATCTTCG	762
Oy	171	CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla	190
Db	763	TGCAGAGGTGGTCTCACTCTGTAGAGAACTCAACTTCTTAACTGGATCTCTGTCTGGCC	822
Oy	191	CysIleSerPheAspArgTyrGlyLeuAsnIleValAlaHisAlaThrGlnLeuTyrArgGly	210
Db	823	TGCATCACTGTGGACCGCTTACCTGGCCATTTGTCATGGCACACGCC-----	867
Oy	211	ProProAlaArgValThrLeuThr-----CysLeuAla	221
Db	868	-----ACACTGACCAGAGAGCGCTACTGGTCAAAATTCATATGTCTGTACG	912
Oy	222	ValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHis	241
Db	913	ATCTGGGGTCTGTCTCTCTCTGCTGGCCCTGGCTGTCTTACTTTTCCGAAAGACCGTCTAC	972
Oy	242	AspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGly-----	258
Db	973	TTCATCCATGTATTAGCCGACGC---TGC-----TATGAGACATAGGGCAACAATACA	1020
Oy	259	-----ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuPro	275
Db	1021	GCAAACTGGCGAGTGCCTGTACAGGATCTGCCCAAGTCCCTTGGCTTCATGTCCACTG	1080
Oy	276	LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuAlaSerArgGlyGln	295
Db	1081	CTGATCATGCTGTCTGTCTACGGAATCACCTGGCGTACGCTGTAAAGCCCACTGGGG	1140
Oy	296	ArgArgLeuArgAlaMetArgLeuValValValValValAlaAlaPheAlaLeuCysTrp	315
Db	1141	CAGAAAGCACCGGGCCATGCGGGGTCACTTGTCTGTGTCGTCCATCTTCTGTCTGG	1200
Oy	316	ThrProTyrHisLeuValValLeuValAlaSpIleLeuMetAspLeuGlyAlaLeuAlaArg	335
Db	1201	CTGCCCTTCAACCTGTGTCTCTCTGGCAAGACCCCTCTTAAGAGACCCAGATGTCAGAG	1260
Oy	336	AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr	355
Db	1261	ACCTTGTAGCGCCCGCAATCACATGACCGGGCTCTGGATGCCACCGAGATTTCTGGCATC	1320
Oy	356	MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg	375
Db	1321	CTTCAACACTGCTCCCAACCCCTCATCTACAGCCTTCAATGGCCAGAAAGTTTCCGCATGGA	1380
Oy	376	MetTrpMetLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro	395
Db	1381	CTTCCCAAGATTCATAGCATATCATGGCTGTGATCAGCAAGACCTCCGCCAAGACAGC	1440
Oy	396	SerSerSerArgArgAspSerSerTrpSerLuhTrSer	408
Db	1441	AGGCCCTTCTTGTGTGGCTCTTTCAGGACGACACTTCC	1479
RESULT 13			
AAS16876			
ID	AAS16876 standard; DNA; 12789 BP.		
XX	AAS16876;		
AC			
XX			
DT	14-FEB-2002 (first entry)		
XX			
DE	Human interleukin 8 receptor beta (IL8RB) genomic DNA.		
XX			
KW	Human; interleukin 8 receptor beta; IL8RB; ds; antiinflammatory;		
KW	haployping; haploype pair; single nucleotide polymorphism; genotyping		
KW	gene therapy; drug screening; chronic obstructive pulmonary disease;		
KW	inflammatory disease.		
XX			
OS	Homo sapiens.		
XX			

CC a haplotype or haplotype pair of the IL8RB gene can be identified by
 CC comparing the frequency of the haplotype or haplotype pair in a
 CC population exhibiting the trait with the frequency of the haplotype or
 CC haplotype pair in a reference population, where a higher haplotype
 CC frequency in the trait population indicates the trait is associated with
 CC the haplotype or haplotype pair. IL8RB and its corresponding DNA are used
 CC for studying the expression and function of IL8RB, for use in screening
 CC for candidate drugs to treat diseases related to IL8RB activity, such as
 CC chronic obstructive pulmonary disease and other inflammatory disorders.
 CC The sequences are also useful for studying the effect of variation on the
 CC biological activity of IL8RB as well as on the binding affinity of
 CC candidate drugs targeting IL8RB. This sequence represents genomic DNA
 CC encoding IL8RB.

XX Sequence 12789 BP; 3363 A; 3042 C; 2867 G; 3510 T; 7 other;

Alignment Scores:

Pred. No.:	1,42e-59	Length:	12789
Score:	636.00	Matches:	150
Percent Similarity:	52.81%	Conservative:	57
Best Local Similarity:	38.27%	Mismatches:	139
Query Match:	29.57%	Indels:	46
DB:	24	Gaps:	9

US-09-101-518a-2 (1-415) x AAS16876 (1-12789)

OY 43 ProSerSerProPhPro-----ProSerGlnValSerAspHisGln 56
 DB 9537 CCTTCATCTCTCTCTATAGGTACAGATTTAACTTACCTAAATGAGATTTTAAAC 9586
 OY 57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPh-----Ser 71
 DB 9587 ATGGAGATGACAGC-----TTTGAAGATTCTGGAAGGTGAACATCTT 9631
 OY 72 SerSerTyrrAspTyrrGlyGluAsnGluSerAspSerCysTyrrSerProCysPro 91
 DB 9632 AGTAATTACAGTACAGCTTACCTGCCCTTTCTACTAGATGAGCGCCCATGTGA 9691
 OY 92 GlnAspPheSerLeuAsnPhAspArgAlaPheLeuProAlaLeuTyrrSerLeuPhe 111
 DB 9692 CCAGAA---TCCCTGGGAATCAACAAGATTTTGTGCTATTATCTATGCCCTGATTTC 9748
 OY 112 LeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgThrAla 131
 DB 9749 CTGCTGACCTGCTGCGAAACCTCCCTGATGCTGCTGCTATTTTACAGCAGGCTGCG 9808
 OY 132 LeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 151
 DB 9809 CGCTCCGTCACATGATGCTACTGCTGAACCTAGCTGGCGGACCTACTTGGCCCTG 9868
 OY 152 ThrLeuProLeuThrAlaValAlaValAlaValGlnTTPValPheGlySerGlyLeu 171
 DB 9869 ACCTTGGCCCATCTGGGCGGCTCCCAAGGTGAATGGCTGATTTTGGCACAATTCCTGTGC 9928
 OY 172 LysValAlaGlyAlaLeuPheAsnIleAsnPhetyrAlaGlyAlaLeuLeuLeuLacys 191
 DB 9929 AAGGTGCTCCTACCTCTAAGAGAGTCAACTTCTATAGTGGCATCTGCTACTGGCTGTC 9988
 OY 192 IleSerPheAspArgTyrrLeuAsnIleValHisAlaThrGlnLeuTyrrArgArglyPro 211
 DB 9989 ATCACTGTGACCGCTTACTGCGCATTTGTCATGCCACACGC-----10030
 OY 212 ProAlaArgValThrLeuThr-----CysLeuAlaVal 222
 DB 10031 -----ACACTGACCCAGAGCGCTACTTGTCAAATTGATATGTCTGACGATC 10078
 OY 223 TrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisAsp 242
 DB 10079 TGGGTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 10138
 OY 243 GluArgLeuAsnAlaThrHisCysGlnTyrrAsnPhProGlnValGly-----258
 DB 10139 TCCAAATTGTTAGCCGAGCC---TGC-----TATGAGGACATGGGCAACAATACAGCA 10186

OY 259 -----ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
 DB 10187 AACTGGCGGATCTCTTACGAGTCTGCTGCCAGCTCTTGGCTTATGTGTGCTGCTGCTG 10246
 OY 277 ValMetAlaTyrrCysTyrrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
 DB 10247 ATCATGCTGTGTGCTTACGGATTCACCTGGCTAGCTGTTTAAAGCCACATGGGGCAG 10306
 OY 297 ArgLeuArgAlaMetArgLeuValValValValValValAlaAlaPheAlaLeuCysThrPhe 316
 DB 10307 AAGCACGGGCGCATCGGGGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 10366
 OY 317 ProTyrrHisLeuValValLeuValAlaSerIleLeuMetAspLeuGlyAlaAlaLarArg 336
 DB 10367 CCTTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 10426
 OY 337 CysGlyArgGluSerArgValAlaSerValThrSerGlyLeuGlyTyrrMet 356
 DB 10427 TGTGAGCGCGCGCAATCACATGACCGGGCTCTGATGCCACGAGATTTCTGGCATCTCT 10486
 OY 357 HisCysCysLeuAsnProLeuLeuTyrrAlaPheValGlyValAlaLysPheArgGluArgMet 376
 DB 10487 CACAGCTGCTCAACCCCTCATCTACGCTTCATTTGGCCAGAACTTCCGCCATGGACTC 10546
 OY 377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyGluArgGlnProSer 396
 DB 10547 CTCAGATTTCTGCTATACATGCTGTTGATCAGCAAGACTCCCTGCCAAMAGACAGAG 10606
 OY 397 SerSerArgArgAspSerSerTrpSerGluThrSer 408
 DB 10607 CCTTCTTGTGCTGCTCTTCTTACAGGCGACACTTCC 10642
 RESULT 14
 ABK16596.
 ID ABK16596 standard; DNA; 1068 BP.
 AC ABK16596;
 DT 14-MAR-2002 (first entry)
 XX
 DE DNA encoding rhesus macaque CXCR2 receptor #1.
 XX
 KW Human; baboon; chimpanzee; vervet monkey; rhesus macaque;
 KW orangutan; gorilla; tree shrew; dog; analgesic; antiinflammatory;
 KW bradykinin 1 receptor; CXCR2 receptor; pain; inflammation; ds.
 OS Macaca mulatta.
 XX
 PN W0200190134-AL.
 PD 29-NOV-2001.
 XX
 PF 22-MAY-2001; 2001WO-US16777.
 PR 22-MAY-2000; 2000US-0576160.
 XX
 PA (PHAR-) PHARMACOPEIA INC.
 XX
 PI Horlick R, Zhao J, Swanson R, Webb M, Strohl B, Baldwin JF;
 XX Auld DS;
 XX
 DR WPI; 2002-106172/14.
 DR P-PSDB; AAU80489.
 XX
 PT Identifying modulators of receptor activity using orthologues of human
 PT receptors by contacting a compound with receptors from two species, and
 PT measuring the effect of the compound on the receptors -
 XX
 PS Claim 49; Page 98-99; 108pp; English.
 CC The invention relates to identifying modulators of receptor activity
 CC using orthologues of human receptors by contacting a compound with

CC receptors from two species, and measuring the effect of the compound on
 CC the receptors. Included is an isolated nucleic acid (i) comprising a
 CC nucleotide sequence encoding bradykinin B1 receptor (i); or encoding a
 CC CXCR2 receptor (iii). The method is useful for identifying a compound
 CC having dual specificity to modulate the activity of a desired polypeptide
 CC in two different species. The method is useful for identifying a non-
 CC human animal model for testing compounds with potential efficacy as human
 CC receptor modulators. The method comprises contacting a test compound with
 CC receptors from at least two species; measuring an effect of the compound
 CC on the receptors; and selecting an animal model representing a species
 CC having a receptor that exhibits the desired effect when contacted with
 CC the test compound. Also described is a method for identifying a compound
 CC that modulates (ii) or (iii) activity, where a compound is an agonist,
 CC antagonist, suppressor, inhibitor and inducer, useful in treatment of
 CC pain and inflammation and other receptor related pathologies. ABK16569-
 CC ABK16574 and ABK16589-ABK16599 represent bradykinin 1 and CXCR2 receptor
 CC coding sequences of the invention.

xx Sequence 1068 BP; 216 A; 324 C; 245 G; 283 T; 0 other;

Alignment Scores:

Pred. No.:	3.47e-61	Length:	1068
Score:	635.50	Matches:	146
Percent Similarity:	53.61%	Conservative:	47
Best Local Similarity:	40.56%	Mismatches:	128
Query Match:	29.54%	Indels:	39
DB:	24	Gaps:	7

US-09-101-518A-2 (1-415) x ABK16596 (1-1068)

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QY 68 GUAAnPheSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSer 87
   |||:||||| |||:||||| |||: |||
Db 37 GAAGATTTT--AGTAATTACAGTTACAGCTCTGACCTGCCCTCTCTTACAGATGTC 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 88 PROPCysProGlaAspPheSerLeuAsnPhaSPARGAlaIlePheLeuProAlaLeu 107
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94 GCCCATGTCGACGACGAA---TCCTGGAATCAACAGATATTGTGTGCTATTTCAT 150
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 108 SerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaIleAlaIleValLeuSer 127
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 GCCCTGGATTCCTGCTGAGTGGTGGAAACCTCCCTGATGCTGCTGATCTTACAC 210
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 128 ARGATgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThr 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 211 AGCAGGTCGGCGGCTCCATCATCTACTGATCTACTGAACTGGCCATGGCCGACCTA 270
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 148 LeuLeuValLeuThreProLeuProLeuTrpAlaValaIleAlaValaIleTrpValPheGly 167
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 271 CTGTTGGCCCTGACCTTGGCCCATCTGGGCTGGCCGCAAGGTAATGGCTGGATTTTGGC 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 168 SerGlyLeuCysLysValaIleGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeu 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 331 ACATTCCTGTGCAAGGTGTCACCTCCGGAAGCAACTGTATATAGTGCATCTCG 390
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 188 LeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyr 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 391 CTACGGGCTGATCAGTGTGACGCTTACCTGGCCATTTGCCATGCCACAGC----- 444
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 208 ARGATgGlyProProAlaArgValThrLeuThr----- 218
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 -----ACACTGACCCAGAAAGCCGCTACTGGTCAAGTTTCGTA 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 219 CysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSer 238
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 TGTCACAGATCTGAGTCTATCCTGCTCCGCGCCGCTGCTTACTTTTC----- 534
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 239 AlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhaPro----- 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 -----CGAAGACTGTCTACCTGACCTATATTAGCCAGTGTCTAT 576
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 256 ---GlnValGly-----ArgThrAlaLeuArgValLeuGlnLeuVal 268
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 577 GAGGCAATGGGCAACATACAGCAAAATGGGGATGGTGGGATCTCTGCCCGACGACC 636
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 269 AlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaVal 288
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 637 TTGGGCTTATCTTGGCGCTGATCATCATGCTGTCTGTATGATGATGACCTGGCGAC 696
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 289 LeuLeuValSerArgGlyGlnArgArgLeuArgAlaMetArgValaValaValaVal 308
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 697 CTGTTTAAGGCCACATGGGCGCAAGACCGGGCCATCGGGGTATCTTGTCTGCTGTC 756
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 309 ValAlaPheAlaLeuCysThrPheProTyrHisIleuValaValaValaIleLeuMet 328
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 757 CTGATCTTCTACTCTGCTGGCTCTTACACCTGGTCTCTGACACACCTTCATG 816
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 329 AspLeuGlyAlaLeuAlaArgAsnGlyArgGlnSerArgValaIleAlaLysSer 348
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 817 AGCACCCGGTTATCATCAGACGACCTGTACGGCCGCCCAACATGACACAGCCCTGAT 876
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 349 ValThrSerGlyLeuGlyTyrMethisCysCysLeuAsnProLeuLeuTyrAlaPheVal 368
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 877 GCCACCGAGATTCTGGGCTCTCTCACAGCTGCTCAACCCCTCATCTACGCTTCAAT 936
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 369 GlyValLysPheArgGluArgMetTrpMetLeuLeuArgLeuGlyCysProAsnGln 388
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 937 GCCAGAAAGTTTCGCATGAGACTCTCAAGATTCTAGCCACACATGCTGATCAGCAAG 996
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 389 ARGGLyleuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGlnThrSer 408
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 997 GACTCCCTGCCCCAAGACAGCAGCGCTTCTTGTGGCTCTTCTTTCAGAGGACACTTCC 1056
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 15
 AAQ30012 standard; cDNA; 1106 BP.
 ID AAQ30012 standard; cDNA; 1106 BP.
 AC AAQ30012;
 DT 04-APR-1993 (first entry)
 XX Sequence encoding a low affinity recombinant human Interleukin-8
 DE (IL-8) receptor polypeptide in 4AB.
 DE IL-8 receptor polypeptide; G-protein-coupled receptor; ss.
 KW Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 13..1095
 FT CDS /*tag= a
 FT W09218641-A.
 PN 29-OCT-1992.
 PD 29-OCT-1992.
 XX 10-APR-1992; 92WO-US02977.
 PE 10-APR-1991; 91US-0685101.
 PR 09-JUL-1991; 91US-0726606.
 PR 09-DEC-1991; 91US-0803842.
 XX (REP) REPLIGEN CORP.
 PA (UYBO-) UNIV BOSTON.
 PA Navarro J, Thomas KM, Wilt DP;
 PI WPT: 1992-382123/46.
 DR P-PSDB; AAR28273.
 XX Recombinant mammalian interleukin-8 receptor - used for screening
 PT Interleukin-8 binding antagonists, used to treat inflammation
 XX Disclosure; Fig 2; 71pp: English.
 CC Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to

CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (AAQ30015). This probe was designed based on the
 CC sequence derived from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were
 CC isolated. The insert of one of these plaques, termed F3R was of 2.5
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments. A human
 CC peripheral blood leukocyte lambda gIII cDNA library (5' stretch) was
 CC screened with a 652 bp EcoRI/BamHI fragment (including nucleotides
 CC -27 to 625) of the rabbit F3R clone. After tertiary screening
 CC several human clones which hybridized to the rabbit IL-8 probe
 CC were isolated. The insert of one such clone, termed 4AB was
 CC sequenced (AAQ30012).

XX Sequence 1106 BP; 225 A; 336 C; 251 G; 294 T; 0 other;

Alignment Scores:

Pred. No.:	4.17e-61	Length:	1106
Score:	635.00	Matches:	146
Percent Similarity:	53.56%	Conservative:	57
Best Local Similarity:	38.52%	Mismatches:	136
Query Match:	29.52%	Indels:	40
DB:	13	Gaps:	8

US-09-101-518a-2 (1-415) x AAQ30012 (1-1106)

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QY 50 SerGlnValSerAspHisGlnValLeuAsnAspAlaGlnValAlaAlaLeuLeuGlnAsn 69
   |||:||||: ||| :|||:||||: |||:||||: |||:||||: |||:||||: |||:||||:
DB 7 TCATAAATGGAAGATTTTAACTGAGAGAGTGCAGC-----TTTGAAGAT 51

QY 70 Phe-----SerSerSerTyrAspTyrGlnGlnAsnGlnSerAspSerCys 84
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 52 TTCTGGAAGAGTGAAGATCTTAATTAATACATTACAGTTCACGCTTACCTGCCCTTTTCTA 111

QY 85 CysThrSerProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuPro 104
   |||:||||: ||| :|||:||||: |||:||||: |||:||||: |||:||||: |||:||||:
DB 112 CTAGATGCCGCCCATGTGACACAGAA---TCCCTGGAATCAACAAGTATTTTGTGCTC 168

QY 105 AlaLeuTyrSerLeuLeuLeuLeuGlnGlyLeuGlnGlyAsnGlyAlaValAlaAlaVal 124
   |||:||||: ||| :|||:||||: |||:||||: |||:||||: |||:||||: |||:||||:
DB 169 AATTATCTATGCCCCCTGATATCTGCTGACCTCTGGAAACCTCCCTCGATGCTGCTGCTC 228

QY 125 LeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaVal 144
   |||:||||: ||| :|||:||||: |||:||||: |||:||||: |||:||||: |||:||||:
DB 229 ATCTTATACAGCAGGGGCGCGCTCCGTCACTGATGCTTACCTGCTGAACCTAGCCCTTG 288

QY 145 AlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrp 164
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 289 GCGGACCTACTCTTGGCCCTGACCTGACCTGCGCCGCTCCCAAGGTAATGGCTGG 348

QY 165 ValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAla 184
   |||:||||: ||| :|||:||||: |||:||||: |||:||||: |||:||||: |||:||||:
DB 349 AATTTTGGCACAATCTCGTGAAGGTGCTCACTCCTGAAGGAGTCAACCTCTATAGT 408

QY 185 GlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThr 204
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 409 GGCATCTCTCTAGCTGCGCTGACATGAGCTGAGACCTTACCTGCGCATTTGTCATGCCACA 468

QY 205 GlnLeuTyrArgArgGlyProProAlaArgValThrLeuThr----- 218
   |||:||||: ||| :|||:||||: |||:||||: |||:||||: |||:||||: |||:||||:
DB 469 CGC-----ACACTGACCCAGGAAGCGCTACTTGGTC 498

QY 219 -----CysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIle 235
   |||:||||: ||| :|||:||||: |||:||||: |||:||||: |||:||||: |||:||||:
DB 499 AATTCATATGTCTCTGACATCTGGGCTGTGCTCTGCTGCGCTGCTTACTT 558

QY 236 PheLeuSerAlaHisHisArgLysArgLysAlaThrHisCysGlnTyrAsnPhePro 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 559 TTCCGAAGACCGCTTACATCATCAATGTTAGCCAGCC--TGC-----TATGAG 606
  
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QY 256 GlnValGly-----ArgThrAlaLeuArgValLeuGlnLeuValAla 269
   |||:||||: ||| :|||:||||: |||:||||: |||:||||: |||:||||: |||:||||:
DB 607 GACATGGGCAACAATACAGCAAACTGGCGGATGCTGTACGATCCCGCCAGTCTTT 666

QY 270 GlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu 289
   |||:||||: ||| :|||:||||: |||:||||: |||:||||: |||:||||: |||:||||:
DB 667 GCGTTCACTCTGCGACACTGATCATGCTGTCTGTCAACGAAATTCACCTGCGCTAGCCTG 726

QY 290 LeuValSerArgGlnArgLysArgLysValMetArgLeuValAlaValAlaVal 309
   |||:||||: ||| :|||:||||: |||:||||: |||:||||: |||:||||: |||:||||:
DB 727 TTTAAGGCCACATGGGCGAAGACCGGCGCATGCGGCTCATCTTGTGTCGTCCTC 786

QY 310 AlaPheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAsp 329
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 787 ATCTTCCTGCTTGTGTGGCGCCCTTACCAACCTGGTCTGCTGGCAGACACCTCATGAGG 846

QY 330 LeuGlyAlaLeuAlaArgAsnCysGlyArgGlnSerArgValAspValAlaLysSerVal 349
   |||:||||: ||| :|||:||||: |||:||||: |||:||||: |||:||||: |||:||||:
DB 847 ACCCAGGTGATCCAGGAGACCTGTGAGCGCGCATTCATCATGACCGGCTCTGATGCC 906

QY 350 ThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGly 369
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 907 ACCGAGATTCGTGGGATCTTCAACAGCTGCTCAACCCCTCATCTACGCTTCAATGGC 966

QY 370 ValLysPheArgGlnArgMetTrpMetLeuLeuValLeuGlnGlyCysProAsnGlnArg 389
   |||:||||: ||| :|||:||||: |||:||||: |||:||||: |||:||||: |||:||||:
DB 967 CAGAAGTTTGCCATGAGACCTCTCAAGATTCATAGCTATACATGGCTTGATCAGCAAGGAC 1026

QY 390 GlyLeuGlnArgGlnProSerSerArgArgAspSerSerTyrPheGlnThrSer 408
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1027 TTCCTGCCCAAGACAGCAGGCTTCTTGTGTGGCTCTTCTTCAAGGACACACTTCC 1083
  
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Search completed: November 2, 2002, 12:19:15
 Job time : 242 secs

This Page Blank (uspto)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: November 2, 2002, 12:27:35 ; Search time 1693 Seconds

(Without alignments)
3308.468 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGA.....SSSRDSSWSETSEASVSGL 415

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE-frame+ .p2n.model -DEV-xlh
-O/cgnt_1/uspro.spool/US09101518/runat_29102002_091103_98/app_query.fasta-1.583
-DB-EST -QPMT-fastlap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPL=0 -LOOEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=blsum62 -TRANS-human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09101518_6CGN_1_1_763_etunat_29102002_091103_98 -NCP=6 -ICPU=3
-NO_XLPXY -NO_MMAR -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FPGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estbta:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estr:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1251.5	58.2	851	10	B1768435
2	1236.5	57.5	864	10	B1911171

3	1153	53.6	749	10	B1821147
4	730	36.7	578	10	B1975807
5	739	34.4	471	9	AM655246
6	576	26.8	971	9	AU091121
7	549.5	25.5	468	10	BF452722
8	522	24.3	511	10	BE589641
9	514	23.9	3005	11	AK019478
10	507	23.6	993	12	CNS04381
11	506	23.5	935	9	AL531903
12	475.5	22.1	871	10	B1653693
13	466	21.7	392	9	AM354767
14	460	21.4	944	10	AL523112
15	452.5	21.0	910	9	B1762229
16	433	20.1	907	9	AL552677
17	417.5	19.4	875	10	B1765157
18	413	19.2	905	10	B1754094
19	411.5	19.1	798	9	AU240364
20	411.5	19.1	841	9	AL558854
21	411	19.1	708	10	BF453946
22	408	19.0	827	10	B1761664
23	403.5	18.8	857	10	BG682791
24	392	18.2	891	10	B1824663
25	391.5	18.2	866	12	CNS02RNL
26	382.5	17.8	674	10	BM251350
27	382.5	17.8	750	10	BG613352
28	381	17.7	913	10	BM051973
29	380.5	17.7	676	9	AJ398841
30	380.5	17.7	746	10	B1917014
31	371.5	17.3	501	10	BG407320
32	371.5	17.3	782	10	BG685901
33	367.5	17.1	702	10	B1761118
34	366.5	17.0	914	10	B1823179
35	366	17.0	733	9	A1959485
36	366	17.0	938	9	AL543359
37	363	16.9	728	9	AU117058
38	362.5	16.9	658	10	B1835125
39	362.5	16.9	703	10	B1765768
40	362.5	16.9	742	10	B1597875
41	361	16.8	671	10	BG025793
42	359	16.7	573	10	B1395190
43	353	16.4	765	10	BM387369
44	351	16.3	853	9	AL561603
45	348	16.2	561	10	BF591285

ALIGNMENTS

RESULT 1	B1768435	851 bp	MRNA	Linear	EST 25-SEP-2001
LOCUS	603053902P1 NIH-MGC_122	Homo sapiens	cdna	clone	IMAGE:5203512 5'
DEFINITION	B1768435	851 bp	MRNA	Linear	EST 25-SEP-2001
ACCESSION	B1768435	851 bp	MRNA	Linear	EST 25-SEP-2001
VERSION	B1768435	851 bp	MRNA	Linear	EST 25-SEP-2001
KEYWORDS	B1768435	851 bp	MRNA	Linear	EST 25-SEP-2001
SOURCE	B1768435	851 bp	MRNA	Linear	EST 25-SEP-2001
ORGANISM	B1768435	851 bp	MRNA	Linear	EST 25-SEP-2001
REFERENCE	B1768435	851 bp	MRNA	Linear	EST 25-SEP-2001
AUTHORS	B1768435	851 bp	MRNA	Linear	EST 25-SEP-2001
TITLE	B1768435	851 bp	MRNA	Linear	EST 25-SEP-2001
COMMENT	B1768435	851 bp	MRNA	Linear	EST 25-SEP-2001

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC http://mgs.nci.nih.gov/.
Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LIML1510 row: c column: 01

High quality sequence stop: 801.

FEATURES
source

```
1..851
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5203512"
/lab_host="NIH_MGC_112"
/ab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site:1: NotI; Site:2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
BASE COUNT 128 a 305 c 240 g 178 t
ORIGIN
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Alignment Scores:
Pred. No.: 5 24e-114 Length: 851
Score: 1251.50 Matches: 262
Percent Similarity: 92.61% Conservative: 1
Best Local Similarity: 92.25% Mismatches: 14
Query Match: 58.18% Indels: 9
DB: 10 Gaps: 1

US-09-101-518a-2 (1-415) x B1768435 (1-851)

```
QY 41 ThrAlaProSer-----SerProPheProSerGlnValSerAspHisGln 56
||| ||||| ||||| :||| ||||| |||||
Db 7 ACACACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 66
57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheserSerrtyrAsp 76
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 GTGCTAAATGAGCCGAGGTTGCCGCCCTCGGAGAACTTCAGCTTCCTATGACTAT 126
77 G1yGluAsnG1SerAspSerCysThrSerProProCysProGlnAspPheSerLeu 96
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 127 GGAGAGAAAGAGAGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 186
QY 97 AsnPhesPArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGluLeu 116
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 AACTTCGACCGGGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246
QY 117 G1yAsnG1yAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerThrAsp 136
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 GGCAACGGGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 306
QY 137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeu 156
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 ACCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
QY 157 AlaValAspAlaAlaValGlnTrpValPheG1ySerG1yLeuCysLysValAlaG1yAla 176
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 367 GCAGTGAAGAGCGCTCCAGTGGGCTTTGGCTGGCTGGCTGGCAAGTGGCAGGTGG 426
QY 177 LeuPheAsnIleAsnPhetyrAlaG1yAlaLeuLeuAlaCysIleSerPheAspArg 196
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 427 CTTCTTCACATCACTTCACAGAGAGCCCTCGTGGCTGCTGATCAGCTTTGACCC 486
QY 197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgG1yProProAlaArgValThr 216
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 487 TACCTGACATGATGTCATGACCCAGCCTTACCGCGGGGGGCCCGCGCGTGAGCC 546
QY 217 LeuThrCysLeuAlaValTrpG1yLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 547 CTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
QY 237 LeuSerAlaHisHis-AspG1yArgLeuAsnAlaThrHisCysGlnTyrAsnPhetProG1 256
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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```
Db 607 CTGTGGGCCCCACAGCAGCAGCGCTCAACGCCACCCACCTGCATACACTCCACA 666
QY 256 nValG1yArgThrAlaLeuArgValLeuGlnLeuValAlaG1y-PheLeuLeuProLeu 276
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 667 GGTGGGCCCCACAGCGCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 726
QY 276 euValMetAlaTyrCysTyrAlaHisIleLeuAla-ValLeuLeuValSerArgG1yGln 295
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 727 TGGTATGCGCTACTTGATGATGCCACATCGCTGGCTGCTGCTGCTGCTGCTGCTG 786
QY 296 ArgAlaG1yLeuAlaMetArgLeuValValValValAlaPheAlaLeuCysTrp 315
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 787 CGGCGCTGCGGGC-ATGCGGCT-GTGGGTGAGGACAGTGTGCTTGCCTGTGTGG 844
QY 316 ThrPro 317
||| |||||
Db 845 ACCCCC 850
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```
RESULT 2
LOCUS B1911171 864 bp mRNA linear EST 16-OCT-2001
DEFINITION 603062744P1 NIH_MGC_118 Homo sapiens cdna clone IMAGE:5212066 5',
mRNA sequence.
ACCESSION B1911171
VERSION B1911171.1 GI:16174778
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 864)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1M11532 row: g column: 11
High quality sequence start: 3
High quality sequence stop: 788.
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FEATURES
source

```
1..864
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5212066"
/lab_host="NIH_MGC_118"
/tissue_type="leukocyte"
/ab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
BASE COUNT 133 a 306 c 246 g 179 t
ORIGIN
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Alignment Scores:
Pred. No.: 1.66e-112 Length: 864
Score: 1236.50 Matches: 259
Percent Similarity: 92.61% Conservative: 4
Best Local Similarity: 91.20% Mismatches: 16
Query Match: 57.48% Indels: 8
DB: 10 Gaps: 1

```

US-09-101-518a-2 (1-415) x B1911171 (1-864)
OY 41 ThrAlaProSer-----SerProPheProProSerGlnValSerAspHisGln 56
Db 17 ACACCAACCCAGCAGCCAGACACACACCCAGCCAGCTCTTGTAGTGCACACCAA 76
OY 57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheserSerSerTyraSptyr 76
Db 77 GTCCTAAATGAGCGCGAGTTCGCCGCCCTCTGAGAACTTCAGCTCTTCATATGACTAT 136
OY 77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
Db 137 GGAGAAACGAGAGTACTGCTGCTTACTCTCCGCCCTCCGCCACAGACTTCACACCTG 196
OY 97 AsnPhaAspArgAlaPheLeuProAlaLeuTyrserLeuPheLeuLeuGlyLeuLeu 116
Db 197 AACTTCGACGGGCGCTTCTGCGACGCCCTCTACAGCCTCTCTTCTGTGGCGTGGCG 256
OY 117 GlysnglyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
Db 257 GGCACACGGCGCGTGGCAGCCGCTGCTGACCGCGGACACCCCTGACACACCGAC 316
OY 137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
Db 317 AACTTCCTGCTCCACTTACTGTAAGACAGACAGCTGCTGCTGCTGCTGCTGCTGCTG 376
OY 157 AlaValAspAlaValAlaGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
Db 377 GCAGTGGAGCGCGCTCCAGTGGGCTTGTGGCTGCGCTGCGCTGCGCTGCGCTGCG 436
OY 177 LeuPheAsnAlaAsnPhetyrAlaGlyAlaValLeuLeuLeuAlaCysLysSerPheAspArg 196
Db 437 CTCTTCACATGACACTTCTACGACGAGACGCCCTGCTGCTGCTGCTGCTGCTGCTG 496
OY 197 TyrLeuAsnLysValHisAlaThrGlnLeuTyrsArgArgGlyProProAlaArgValThr 216
Db 497 TACCTGAAACATGATTCATGCCACCCAGCTCTACCGCGGGGCGCGCGCGCTGACCC 556
OY 217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheLeuPhe 236
Db 557 CTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 616
OY 237 LeuSerAlaHisHisAspArgLeuArgLeuAsnAlaThrHisCysGlnTrpAsnPhetProGln 256
Db 617 CTGTGGGCGCCACGACGACGACGCGCTCAACGCCAC-CACTGCCAATACAACTTCCACAG 675
OY 257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
Db 676 GTGGGCGCGCAGCGCTGCGGGGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 735
OY 277 ValMetAlaTrpCysTyraAlaHisLysLeuAlaValLeuLeuValSerArgGlyGlnArg 296
Db 736 GTCATGCGCTACTGCTATGTC-CACATCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTG 794
OY 297 -ArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpTh 316
Db 795 GCGCTGCGCAGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 853
OY 316 rProTyHis 319
Db 854 CCCTATTATAC 863

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```

RESULT 3
LOCUS B1821147 749 bp mRNA linear EST 04-OCT-2001
DEFINITION 603053991 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176136 5',
ACCESSION B1821147
VERSION B1821147.1 GI:15932697
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

```

```

REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bts-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11438 row: n column: 09
High quality sequence stop: 747.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5176136"
/clone_11b="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pcmw-SpOrt6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH-MGC Library."
BASE COUNT 121 a 274 c 201 g 153 t
ORIGIN
Alignment Scores:
Pred. No.: 2 67e-104 Length: 749
Score: 1153.00 Matches: 233
Percent Similarity: 94.35% Conservative: 1
Best Local Similarity: 93.95% Mismatches: 7
Query Match: 53.60% Indels: 7
DB: 10 Gaps: 1
US-09-101-518a-2 (1-415) x B1821147 (1-749)
OY 41 ThrAlaProSer-----SerProPheProProSerGlnValSerAspHisGln 56
Db 6 ACACCAACCCAGCAGCCAGACACACCCAGCCAGCTCTTGTAGTGCACACCAA 65
OY 57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheserSerSerTyraSptyr 76
Db 66 GTCCTAAATGAGCGCGAGTTCGCCGCCCTCTGAGAACTTCAGCTCTTCATATGACTA 125
OY 76 rGlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
Db 126 TGGAGAAACGAGAGTACTGCTGCTACTCTCCGCCCTGCGCCACAGACTTCAGCCT 185
OY 96 AsnPhaAspArgAlaPheLeuProAlaLeuTyrserLeuPheLeuLeuGlyLeuLeu 116
Db 186 GAACTTCGACCGCGGCTTCTGCGACCCCTCTACAGCCTCTCTTCTGCTGCGGCTGCT 245
OY 116 uGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAs 136
Db 246 GGGCAACGCGCGGCTGCGAGCGTCTGCTGAGCGCGCGAGACGCCCTGAGCAGCAGA 305
OY 136 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTr 156
Db 306 CACCTTCCTGCTCCACTGCTGTAGCAGACAGCGCTGCTGCTGCTGCTGCTGCTGCTG 365
OY 156 pAlaValAspAlaAlaValAlaGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAl 176

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Db 366 GGCAGTGGACGCTGCCGTCACATGGGTCTTTGGCTCTGGCCTCTGCAGAAAGTGCCAGGTGC 425
QY 176 aleupheasnllaeasnphetyrAlaGlyAlaLeuLeuLeuAlaCysllaserpheaspar 196
|||||
Db 426 CCTCTTCAACATCAACTTCTACGACAGAGCCCTCCGTGGTGGCTGATCATGCTTTGACCG 485
QY 196 gTyrLeuasnllValAlaHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValTh 216
|||||
Db 486 CTACCTGACACATAGTTCATGACGCCACCCAGCTCTACGCCCGGGGGCCCCCGGCCGCGTGAC 545
QY 216 rleuThrCysleuAlaValThrGlyLeuCysleuLeuPheAlaLeuProAspPheleper 226
|||||
Db 546 CCGCACCTGCTGCTGTGGGGGGCTGCTGCCCTTTTGGCCCTCCAGACTTCATCTT 605
QY 236 eleuSerAlaHisHisAspGlnArgLeuAsnAlaThrHisCysGlnTyrAsnProgi 256
|||||
Db 606 CCGTGGGGCCACACAGACAGAGGCGCTCAACGCCACCTGCATACACTTCCACCA 655
QY 256 nValGlyArgThrAlaLeuArg-ValleuGlnLeuValAla-GlyPheLeuLeuProleu 275
|||||
Db 666 GGTGGGCCCCACAGCGCTGCTGGGGGCTGCTGCAGCTGGTGGCTTCTGCTGCCCGCTG 725
QY 276 leuValMetAlaTyrCys 281
|||||
Db 726 CTGGTCATGGCTAACTGT 743

RESULT 4
BI975807 578 bp mRNA linear EST 23-OCT-2001
LOCUS
DEFINITION 484335 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BI975807
VERSION BI975807.1 GI:16350212
KEYWORDS
SOURCE EST.

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 578)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Pettea,G., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE
COMMENT 21180013
Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross-match with the -minscore 18
and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACACCTATGACCAT
BACKWARD: GTTTCCACATCAGCAGC
Plate: 110 row: A column: 16
Seq primer: ATTAGGTGACCTATGAC.
Location/Qualifiers

FEATURES
source 1..578
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/issue_type="pooled"
/lab_host="PH10B"
/note="Vector: pCMV SPORF6; Site_1: XbaI; Site_2: XhoI;
library made from pooled tissue from testis, thymus,
semilendonsus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

BASE COUNT 92 a 199 c 152 g 135 t
ORIGIN
Alignment Scores:
Pred. No.: 2,19e-68 Length: 578
Score: 790.00 Matches: 153
Percent Similarity: 87.77% Conservative: 12
Best Local Similarity: 81.38% Mismatches: 21
Query Match: 36.73% Indels: 2
DB: 10 Gaps: 1

US-09-101-518A-2 (1-415) x BI975807 (1-578)

QY 44 SerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAspAlaGluVal 63
:::||||| :|||||
Db 20 ACCAGGCCAGCTATGGTCCCTGATGATGAGCAAGCCAAAGTCCACACCTCCGATTTT 79
QY 64 AlaAlaLeuLeuGlnAsnBheSerSerSerTyrAspTyrGlyGlnAsnGlnSerSer 83
||| |||||
Db 80 GCCTACCTCTCGGAAAC-----TCTTCATGACTACGAGAAATAGACTACTTC 133
QY 84 CysCysThrSerProProCysProGlnAspBheSerLeuAsnBheAspArgAlaPheLeu 103
|||||
Db 134 TGCTGACTTCCCGACCCCTGCACAGACTTCAGCTCAACTCGACCGACCTTCG 193
QY 104 ProAlaLeuTyrSerLeuLeuPheLeuGlyLeuLeuGlyAsnGlyAlaValAlaAla 123
||| |||||
Db 194 CCGGCTCTACAGCCTCCTCTTTGTGTGGGGCTTCTGGTAAATGCGATCGTGGCAGTC 253
QY 124 ValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAla 143
|||||
Db 254 GTGCTCTGAGCCAGAGAGGGGGCTGAGCAGACCGACACTTCTGCTGCACCTTGGCT 313
QY 144 ValAlaAspThrLeuLeuValLeuThrLeuProLeuThrAlaValAspAlaValGln 163
|||||
Db 314 GTGGCCGATGACATGCTGTGGTGGACACTCCCTTGAGCAGTGAATGCAGCATCAG 373
QY 164 TrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnLleasnPhetyr 183
|||||
Db 374 TGGGCTTTGGCTGTGGCTGTGCACAAAGTGGGGGTGCACTCTTCACATCAACTCTAC 433
QY 184 AlaGlyAlaLeuLeuLeuAlaCysllaserpheasparTyrLeuAsnllValAlaHisAla 203
|||||
Db 434 GCAGGGGCCCTCTGCTGCTGTATACACTTCGATCGGTACTGCTGCTGTCGACCTTGGC 493
QY 204 ThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeuAlaValTrp 223
Db 494 ACCAGCTCTACCGCGGGGCCCCCGGACTCGCGTGGCCCTACCTGTGGCAGTCTGG 553
QY 224 GlyLeuCysLeuLeuPheAlaLeu 231
Db 554 GGGCTGTGTGCTGCTTTGGCGCTC 577

RESULT 5
AM655246 471 bp mRNA linear EST 25-APR-2001
LOCUS
DEFINITION 106015 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AM655246
VERSION AM655246.1 GI:7421144
KEYWORDS
SOURCE EST.

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 471)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Pettea,G., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL
MEDLINE
COMMENT

Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smilh TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smilhemall.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTACAGAGC
Plate: 86 row: D column: 24
Seq primer: ATTAGGACACATATAG.
Location/Qualifiers
1..471
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1B0Y"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

BASE COUNT 72 a 152 c 148 g 99 t
ORIGIN

Alignment Scores:
Pred. No.: 1.88e-63 Length: 471
Score: 739.00 Matches: 141
Percent Similarity: 95.48% Conservative: 7
Best Local Similarity: 90.97% Mismatches: 7
Query Match: 34.36% Indels: 0
DB: Gaps: 0

US-09-101-518a-2 (1-415) x AW655246 (1-471)

Oy 244 ArgLeuAsnAlaThrHisCysGlyTyrAsnProGlnValGlyArgThrAlaLeuArg 263
|||||
Db 5 CGCCTCAATGCCACCCACTGCGACGATCACTTCCACAGAGGGCCACACAGCTCTGGCC 64

Oy 264 ValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAla 283
:::|||||
Db 65 ATCCGCGACGCTGGGCGAGGCTTCTGCTGCCCTGCTGCTATGCTATGCTATGCTCC 124

Oy 284 HisLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAlaMetArgLeu 303
|||||
Db 125 CGCATCCGCTGCTGCTGCTGCTGCCAGGGGCCAGCGGGCTCAGAGCCATGCGGCTG 184

Oy 304 ValValValValValValAlaPheAlaLeuCysTyrPheProTyrHisLeuValValLeu 323
|||||
Db 185 GTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 244

Oy 324 ValAspIleLeuMetAspLeuGlyValAlaLeuAlaArgAsnGlyArgGlnSerArgVal 343
|||||
Db 245 GTGACACACCTCATGAGCTGGGGCCCTTACGCCCTTAATCTGGGACAGAGAGAGCTGTG 304

Oy 344 AspValAlaIleValSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeu 363
:::|||||
Db 305 GACATAGCAAGTCGTCACGCTCGGGCATGGGCTATGATGCACTGCTCAACCCACTG 364

Oy 364 LeuTyrAlaPheValGlyValValPheArgGlnArgMetTyrPheLeuLeuLeuArgLeu 383
|||||
Db 365 CTCATGCTCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 424

Oy 384 GlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSer 398
|||||
Db 425 GCGTGGCTGACGACAGAGTGGCCACAGCGGACGACCATGACCTTCC 469

RESULT 6
A0091121

LOCUS A0091121 971 bp mRNA linear EST 23-JAN-2001
DEFINITION A0091121 lambda ZAPit-Con A stimulated leukocytes Paralicthys
olivaceus cDNA clone JFconA882F forward similar to Galus gallus
Chemokine receptor-like protein (24122324), mRNA sequence.
ACCESSION A0091121
VERSION A0091121.1 GI:12391161
KEYWORDS EST.
SOURCE A0091121.1
ORGANISM Paralicthys olivaceus
basterd halibut.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorphi; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralicthysidae; Paralicthys.
REFERENCE 1 (bases 1 to 971)
AUTHORS Nam, B., Hirano, I. and Aoki, T.
TITLE Identification of expressed genes from Japanese flounder
(Paralicthys olivaceus) leukocytes stimulated with Con A/PMA
unpublished (2000)
JOURNAL
COMMENT Laboratory of Genetics and Biochemistry
Tokyo University of Fisheries
Konan 4-5-7, Minato-ku, Tokyo 108, Japan
Email: hirono@tokyo-u-fish.ac.jp.
Location/Qualifiers
1..971
/organism="Paralicthys olivaceus"
/db_xref="taxon:825"
/clone_lib="JFconA882F"
/clone_lib="lambda ZAPit-Con A stimulated leukocytes"
/cell_type="leukocytes"
/dev_stage="adult"

BASE COUNT 205 a 248 c 221 g 297 t
ORIGIN

Alignment Scores:
Pred. No.: 9.13e-47 Length: 971
Score: 576.00 Matches: 125
Percent Similarity: 55.83% Conservative: 57
Best Local Similarity: 38.34% Mismatches: 108
Query Match: 26.78% Indels: 36
DB: Gaps: 8

US-09-101-518a-2 (1-415) x A0091121 (1-971)

Oy 70 PheSerSerSerTyrAspTyrGlyGlnGlnGlnSerAspSerCysCysThrSerProPro 89
|||||
Db 12 TTTTCACGCGCCACACGACTACGAGAAATATGAGATGACACA----- 53

Oy 90 CysProGlnAspPheSer----- 95

Db 54 -----GACTATAGTCAACAGAACGTCCTCCGACTCCGACTATATCTGTGAAGAA 104

Oy 96 -----LeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
|||||

Db 105 GAAGAGAGGCGGCTGCACAGCCCTGGCACCTGCTCCAGCCGTGTTGACAGCTTGATC 164

Oy 111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaValLeuLeuSerArgArgThr 130
|||||
Db 165 TTCTGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 224

Oy 131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
|||||
Db 225 CTCCTGCCCATCACTGAAATATATCACTTCACTCGCCCTGGCTGGACTCATGCTCTT 284

Oy 151 LeuThrLeuProLeuThrPAlaValAlaValAlaValGlnTyrPvalPheGlySerGlyLeu 170
|||||
Db 285 TTAAGCTTCCCTTGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 344

Oy 171 CysIysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuAla 190
|||||
Db 345 TGCAGGCTGATGGCGCTGATGAACATCAATCTCTCTGGGAGATTCTCTTTACT 404

Oy 191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210

Db	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment	
Db	405	TGCAATTTGGTTGATCGGATATTGGCTATCGTTCATGCCATTCGCCATCCAGCATGGCAATTCGG	464	ProphetaargValThrLeuThrCysLeuAlaValTrrpGlyLeuCysLeuDeuPheAla	230	CGTCCGAGAGCATGCATCATGATACCTTTCATTTACTGTGGCTGTCTGTGGTTTATCA	524	LeuProAspPheIlePheLeuSerLanHisAspGly--ArgLeuAsnAlaThrHis	249
Db	211	ProphetaargValThrLeuThrCysLeuAlaValTrrpGlyLeuCysLeuDeuPheAla	230	CGTCCGAGAGCATGCATCATGATACCTTTCATTTACTGTGGCTGTCTGTGGTTTATCA	524	LeuProAspPheIlePheLeuSerLanHisAspGly--ArgLeuAsnAlaThrHis	249	CGTCCGAGAGCATGCATCATGATACCTTTCATTTACTGTGGCTGTCTGTGGTTTATCA	524
Db	465	CGTCCGAGAGCATGCATCATGATACCTTTCATTTACTGTGGCTGTCTGTGGTTTATCA	524	LeuProAspPheIlePheLeuSerLanHisAspGly--ArgLeuAsnAlaThrHis	249	CGTCCGAGAGCATGCATCATGATACCTTTCATTTACTGTGGCTGTCTGTGGTTTATCA	524	LeuProAspPheIlePheLeuSerLanHisAspGly--ArgLeuAsnAlaThrHis	249
Db	231	LeuProAspPheIlePheLeuSerLanHisAspGly--ArgLeuAsnAlaThrHis	249	CGTCCGAGAGCATGCATCATGATACCTTTCATTTACTGTGGCTGTCTGTGGTTTATCA	524	LeuProAspPheIlePheLeuSerLanHisAspGly--ArgLeuAsnAlaThrHis	249	CGTCCGAGAGCATGCATCATGATACCTTTCATTTACTGTGGCTGTCTGTGGTTTATCA	524
Db	525	GCTCAAAATTTTGTGTCTTCTGTGTGTGAGAGAGGACAAACTTACACATCCAGCCTCTAC	584	CysGlnTyrAsnProGlnVal--GlyArgThrAlaLeu-----ArgValLeu	265	TGCTCTCTATATCATCATGATCATCCATCCATGACACCAACTGGGTTTTCACCAACAGAGTCTTC	644	GlnLeuValAlaGlyPheLeuDeuProLeuLeuValMetAlaTyrCysTyrAlaHisIle	285
Db	266	GlnLeuValAlaGlyPheLeuDeuProLeuLeuValMetAlaTyrCysTyrAlaHisIle	285	GATCATCATTTTC--TTTTCGTACCTCTGGCTGCATGAGAGTACTGTCACACAGAGTG	701	LeuAlaValLeuLeuValSer--ArgGlyGlnArgGlyLeuAlaGlyAlaMetArgLeuVal	304	GATCATCATTTTC--TTTTCGTACCTCTGGCTGCATGAGAGTACTGTCACACAGAGTG	701
Db	266	GlnLeuValAlaGlyPheLeuDeuProLeuLeuValMetAlaTyrCysTyrAlaHisIle	285	GATCATCATTTTC--TTTTCGTACCTCTGGCTGCATGAGAGTACTGTCACACAGAGTG	701	LeuAlaValLeuLeuValSer--ArgGlyGlnArgGlyLeuAlaGlyAlaMetArgLeuVal	304	GATCATCATTTTC--TTTTCGTACCTCTGGCTGCATGAGAGTACTGTCACACAGAGTG	701
Db	702	GATCATCATTTTC--TTTTCGTACCTCTGGCTGCATGAGAGTACTGTCACACAGAGTG	701	LeuAlaValLeuLeuValSer--ArgGlyGlnArgGlyLeuAlaGlyAlaMetArgLeuVal	304	GATCATCATTTTC--TTTTCGTACCTCTGGCTGCATGAGAGTACTGTCACACAGAGTG	701	LeuAlaValLeuLeuValSer--ArgGlyGlnArgGlyLeuAlaGlyAlaMetArgLeuVal	304
Db	305	ValValValValValAlaPheAlaLeuCysTrrpThrProTyrHisLeuValValLeuVal	324	TTACTTTCATCATCTGTCTTTTTCCTCTGTGTGGCTCCCATATTAACATCATCCTTACTGTGTA	821	AspIleLeuMetAspLeuGlyAlaLeu--AlaArgAsnCysGlyArgGlnSerArgVal	343	ValValValValValAlaPheAlaLeuCysTrrpThrProTyrHisLeuValValLeuVal	324
Db	762	TTACTTTCATCATCTGTCTTTTTCCTCTGTGTGGCTCCCATATTAACATCATCCTTACTGTGTA	821	AspIleLeuMetAspLeuGlyAlaLeu--AlaArgAsnCysGlyArgGlnSerArgVal	343	ValValValValValAlaPheAlaLeuCysTrrpThrProTyrHisLeuValValLeuVal	324	TTACTTTCATCATCTGTCTTTTTCCTCTGTGTGGCTCCCATATTAACATCATCCTTACTGTGTA	821
Db	325	AspIleLeuMetAspLeuGlyAlaLeu--AlaArgAsnCysGlyArgGlnSerArgVal	343	ValValValValValAlaPheAlaLeuCysTrrpThrProTyrHisLeuValValLeuVal	324	TTACTTTCATCATCTGTCTTTTTCCTCTGTGTGGCTCCCATATTAACATCATCCTTACTGTGTA	821	AspIleLeuMetAspLeuGlyAlaLeu--AlaArgAsnCysGlyArgGlnSerArgVal	343
Db	822	AAACTCTGTGACCTGTGGAGGTATCCACATGTAACACTGTGCAAACTTTTCCCTGCTG	881	AspValAlaIlySerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeu	363	CGAGCGCGCTTCGATGATCTCCCTGATGCTGGGATCTTACACTGTGCTGCAACCCCTTC	941	LeuTyrAlaPheValGly	369
Db	344	AspValAlaIlySerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeu	363	CGAGCGCGCTTCGATGATCTCCCTGATGCTGGGATCTTACACTGTGCTGCAACCCCTTC	941	LeuTyrAlaPheValGly	369	CGAGCGCGCTTCGATGATCTCCCTGATGCTGGGATCTTACACTGTGCTGCAACCCCTTC	941
Db	882	CGAGCGCGCTTCGATGATCTCCCTGATGCTGGGATCTTACACTGTGCTGCAACCCCTTC	941	LeuTyrAlaPheValGly	369	CGAGCGCGCTTCGATGATCTCCCTGATGCTGGGATCTTACACTGTGCTGCAACCCCTTC	941	LeuTyrAlaPheValGly	369
Db	942	CTTATGCTTCATTTGGG	959	LeuTyrAlaPheValGly	369	CTTATGCTTCATTTGGG	959	LeuTyrAlaPheValGly	369
RESULT 7	BF452722								
LOCUS	BF452722								
DEFINITION	BF452722	468 bp	mRNA	linear	EST 01-DEC-2000				
ACCESSION	BF452722								
VERSION	BF452722.1								
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
REFERENCE	Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
TITLE	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.								
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),								
COMMENT	Tumor Gene Index								
	Unpublished (1997)								
	Contact: Robert Strausberg, Ph.D.								
	Email: cgaaps-remail.nih.gov								

```

/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAACATCTGAAGGGGAGCGGCGCGGTCTTTTCTTTTCTTTTCTTTT
3') double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73D vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT      90 a      143 c      119 g      116 t
ORIGIN

Alignment Scores:
Pred. No.:      1,28e-44      length:      468
Score:          549.50      Matches:      112
Percent Similarity: 87.50%      Conservative: 7
Best Local Similarity: 82.35%      Mismatches: 16
Query Match:      25.55%      Indels: 1
DB:              10      Gaps: 1

US-09-101-518A-2 (1-415) x BF452722 (1-468)
OY      51      GlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGlnAsnPhe 70
      :::::::::::|:::::::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      61      GAGGTATTAGAACGCTCAAGTGTCTAGATGGCTGGAGCTTGGCTTCTTCTTGGAANAACAGC 120
OY      71      SerSerSerTyrAspTyrGlyGlnAsnGluSerAspSerGlyCysGlyThrSerProCys 90
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      121     ACCCTCTCCCTACGATTATAGGGGAAACAGACAGACGAC---TTCTCTGACCTCCCGCCCTGC 177
OY      91      ProGlnAspPheSerLeuAsnAspPheAspArgAlaPheLeuProAlaLeuTyrSerLeu 110
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      178     CCACAGGATTTTACGCTGACTTATACAGAACCTTCTGCGACGCCCTTACAGCTTCTC 237
OY      111     PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      238     TTCTGTGGGGCTGCTAGGCAATGGGGGGGGCTGCTGTCTGCTACTGATGATCAGCGCACT 297
OY      131     AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAlaAspThrLeuVal 150
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      298     GCCCTGACACGACGACGACCTTCTGCTGCCACCTGGCTGTAAGCGAGTTCCTGCTGGTG 357
OY      151     LeuThrLeuProLeuThrAlaValAspAlaAlaValAlaGlnThrValPheGlySerGlyLeu 170
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      358     TTTACTCTTCCCTTTGTGGGCAGTGGATGCTGTCGCCAGTGGGTTTGTGGCCCTTGCCCTC 417
OY      171     CysTysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAla 186
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      418     TGCANAAGTGGCAAGCGCCTTGTTCACAACATTATTAATGAAGGCC 465

RESULT 8
BE589641      511 bp      mRNA      linear      EST 28-AUG-2000
BE589641      BE589641
LOCUS      BE589641
DEFINITION      195994 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION      BE589641
VERSION      BE589641.1 GI:9842680
KEYWORDS      EST.
SOURCE      COW.
ORGANISM      Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE      1 (bases 1 to 511)
AUTHORS      Sonstegard,T.S., Capucio,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
TITLE      Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
JOURNAL      unpublished (2000)
COMMENT      Contact: Sonstegard TS
USA, ARS, Beltsville Agricultural Research Center

```


JOURNAL	freshwater pufferfish Tetraodon nigroviridis
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 993) Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Benoit,A., Fitzmes,C., Winkler,P., Brotier,F., Quetier,F., Saurin,W. and Weissenbach,J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence Unpublished
TITLE	3 (bases 1 to 993)
JOURNAL	Genoscope.
REFERENCE	Direct Submission
AUTHORS	Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
JOURNAL	This sequence is a single read and was generated as part of a large scale clone-and sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
COMMENT	Location/Qualifiers
FEATURES	location=993
SOURCE	/organism="Tetraodon nigroviridis" /db_xref="taxon:99883" /clone="080013" /clone_11p="G" /note="Genoscope sequence ID : COHG080AH07SP1-end : PUC-Ori"
BASE COUNT	223 a 275 c 232 g 258 t 5 others
ORIGIN	
Alignment Scores:	
Pred. NO. :	6.84e-40 Length: 993
Score:	507.00 Matches: 123
Percent Similarity:	51.08% Conservative: 43
Best Local Similarity:	37.85% Mismatch: 84
Query Match:	23.57% Indels: 79
DB:	12 Gaps: 5
US-09-101-518A-2 (1-415) x CNS043RI (1-993)	
OY	135 ThisArphrPhleuleuHnlsleuAlavalAsprhtleuleuValleuthyPro 154 : : :::
Dd	7 ACAGCAGCTTCATGCCTCCACGTGGCGGCGTGAGTTAGTGTGGTGGTCCC 66
OY	155 leutrralavaleasralavalaln-----trvalPheglyserglyLeucyllys 172 ::
Dd	67 ACTTGCGGCCGACAGCACCCAG-GATAGGGGTGGACTTCGGCAGCCTGTGCAG 125
OY	173 ValAlaglyAlaleuPhe- - - - - 178 ::: :
Dd	126 ATCAACGGAGCTGTTTTATTGTGAAGAAGTCAGACGTAGAAATACTCAGCAAGGTT 185
OY	178 ----- 178
Dd	186 TAACTTCATCATGATGAGACATTTTAACAATCCTTTAACCTCAATCAAAA 245
OY	179 -----Asn 179
Dd	246 TGAAATATATGCATTTTAGGTCACCATTAAAGATATATGTTTCTATGCATCA 305
OY	180 -lleasnPhetyrAlaglAlaleuleuHnlsylearPheaspargtyrleus 199 :::
Dd	306 GGTCACACTTCTACTGTGGGATTTTCTCTGGCTGCATCGATTTCGACCGGTACTGTC 365
OY	199 ntlevalHnlsAlathrglnleutyArgdglyProforAlatryValIthrleuthcy 219
Dd	366 TATGTCTCATGCSACACCATGTACTCTCCACAGAAAGCCGTGGGCAATTCGGATCAGTGTG 425
OY	219 sleudAlatlrrllyleucysleuleurPheAlaleuproAspheileupeSerAl 239 ::: :::::: ::
Dd	426 CATGCTCCCTCCGGCTTTTCTCTCCCTACTGTCTCATGTACAACTCGGTCTTCAAGAC 485
OY	239 AHNshIsprgluartryleuasndlatrhnlscysglntrytansrpheroglnval---- 257 :
Dd	486 TTGTGAGCATATGACATGAGAACCGACAACTGTCTTCGTAACATATTT-AATGTTCAACA 544

QY	258	-----	-GlyArgThrIalaLe	262
Db	545	AGCAATCCGAGAGTTTCAACCCGACGGCTTAATTCAGACGAGTTAACTGGACAGCTGGCAATC	604	...
QY	262	uargvalleuglnleuValAlaGlyPheLeuDeuProLeuValMetAlaTyCysTy	282	...
Db	605	GGGGCTGATCTTACCAACCAAGTGGTTTCTCTCTCTGCGCCACAGCCGCAATGCTTGTGCTA	664	...
QY	262	ralahisileuValaValleu---LeuValSerArgGlyGlnArgGluArgAlaIle	301	...
Db	665	CACCGCATCCCGCTCGCGCTGAGCGTGCAGCGCCGACGGGCGCTTCAAAAGACAGAGCTAT	724	...
QY	301	targLeuValaValaValaValaValaPheAlaLeuCysTrpPrrProTyHisLeuVa	321	...
Db	725	CAGGGTGAATCATCGCTGTGTGGGCGCGGTGTTTCTCTGTGGAGCGCCCTPACAATAGT	784	...
QY	321	lvalleuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSe	341	...
Db	785	CCCTCTGGTGACACGTTTACTCTCCACAGTGC---AGTGATAGTGAGGAATGCACAC	841	...
QY	341	rArgValaSpValAlaLysSerValThSerGlyLeuGlyTyMetHisCysCysLeuAs	361	...
Db	842	AACATATGAGAAAGGCTTCAGCTGACCTCCCTCGGTGATTACCTCCACATGAGGCTCA	901	...
QY	361	nProLeuLeuTyAlaPheValaGlyValLysPheArgGlyLuarGlyMetTrpMetLeuLe	381	...
Db	902	CCCCATCTCTGATGCTTCGTGGGGGTAA-TTACAGGCGTCACTCTGTGCC-GTCTGTAG	959	...
QY	381	uargLeuGlyCys	385	...
Db	960	GTCTCTGGGCTGT	972	...
RESULT 11				
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DEFINITION	AL531903 LTI_NFL001_NB04	935 bp	mRNA	linear
ACCESSION	AL531903	935 bp	mRNA	linear
VERSION	AL531903	935 bp	mRNA	linear
KEYWORDS	AL531903.1	GI:12795396		
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.			
JOURNAL	Full-length cDNA libraries and normalization			
COMMENT	Unpublished (2001)			
FEATURES	Contact: Genoscope			
SOURCE	Genoscope - Centre National de Sequencage			
	BP 191 91006 Evry cedex - France			
	Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.			
	Location/Qualifiers			
	1..935			
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	/db_xref="taxon:9606"			
	/clone="CS0DM003YH06"			
	/clone_lib="LTI_NFL001_NB04"			
	/sex="male"			
	/tissue_type="neuroblastoma cells"			
	/lab_host="DH10B"			
	/note="Organ: brain; Vector: PCMVSPORT 6; 1st strand cDNA			
	was primed with a NotI-oligo(5') primer. Five prime end			
	cloned, double-stranded cDNA was digested with Not I and			
	cloned into the Not I and Eco RV sites of the PCMVSPORT 6			
	vector. Library was normalized. Library was constructed			
	by Life Technologies. Contact: Feng Liang Life			
	Technologies, a division of Invitrogen 9800 Medical Center			
	Drive Rockville, Maryland 20850, USA Fax : (1) 301 610			
	8371 Email : filiang@life-tech.com URL :			
	http://fulllength.invitrogen.com			
BASE COUNT	191 a	261 c	232 g	250 t
				1 others

ORIGIN

Alignment Scores:
 Pred. No.: 7,84e-40 Length: 935
 Score: 506.00 Matches: 119
 Percent Similarity: 51.69% Conservative: 34
 Best Local Similarity: 40.20% Mismatches: 97
 Query Match: 23.52% Indels: 46
 Gaps: 7

US-09-101-518A-2 (1-415) x AL531903 (1-935)

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QY 78 GUASGUGLSERASPERYSCYTHRSRPRPPOCYSPROGLNASPHE---SERLEU 96
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Db 50 GAAAGTGAAGAGACATGTCAAATATATACAGATCCACAGATGGAGTTTGTATGATCTTA 109
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 97 AASPHE-----ASPARGALAPHELEUPROLAEU-----106
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Db 110 AATTTCTAGTGCATGCCACCTGCAGATGAGATTACAGCCCTGTATGCTAGAACTGAG 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 107 -----TYRSEULEUPHELEUENGLYLEUEN 116
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 170 ACACATCAACAGATGTGTGATCATGCCCTATGCCCTAGTGTCTGCTGAGCCGTCTG 229
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QY 117 GYAASNGLYALAVAlAAlAVAlLEUUSERATGATGTALALEUSERSERTHASP 136
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Db 230 GGAACACTCCCTGGTGTGCTGGTCATCTTATACAGTAGGCGCGCTCCCTCATCTGAT 289
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QY 137 THRPHELEUENHISLEUALAVAlAASPPTHLEUENVALLEUTHRIEUPROLEUTP 156
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Db 290 GTCTACCTGCTGACAGCTGGCTGGCGACCTACTCTTTGCCCTGACCTTGGCCATCTG 349
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QY 157 ALAVAlASPLAAlAAlAVAlGINTTPVALPHEGLYSERGLYSEUSLYSVALAGLYALA 176
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Db 350 GCCGCGCTCCAGAGTGAATGGCTGGATTTTGGCACATCTGTGCAAGGTGCTCAGTC 409
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QY 177 LEUPHEASNIIEASPHETRYRALAGLYALALEUENLEUALCYSILSESPHEASPAR 196
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Db 410 CTGAAGGAAGTCAACTTCTACACAGTGCATCCGTGTTGGCTGCATCAGTGGAGCCGT 469
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QY 197 TYTLEASNIIEVALHISALATHRGINLEUTYARGARGLYPROPROLAEATGVALTPR 216
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Db 470 TACCTGGCCATTGTCTCATGCCACACGC-----ACA 499
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QY 217 LEUTHR-----CYLLEUALAVAlTPRGLYLEUCYSLEU 227
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Db 500 CTGACCCAGACAGCGTCACTTGGTCAAGTTTGTCTTGGCGTGGGGAGCTGTATG 559
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QY 228 LEUPHEALALEUPROASPHETIIEPHELEUSERALAHISISPGLUATRGLEUASNALA 247
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Db 560 AATCTGTGCTCCCTCTTCTCTTCTTCCCGCAGGCTTACCATCAAAAC-----AATTC 613
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QY 248 THRIHISCYGLINTYR-----ASPHEPROGLNVALGIVARGRHRALEUATG 263
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Db 614 AGTCCAGTTTGCATAGAGTCTGGGAATGACACAGCAAAATGGGGATGGGTGGCG 673
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QY 264 VALLEUGINLEUVALAAGLYPHELEUENPROLEUENVALMETALYRYSYTRALA 283
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 674 ATCTGTCCTACACACCTTGGCTTACATCGTGGCGCTGTTGTCATGCTGTCTGATGGA 733
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QY 284 HISLIELEUALAVAlLEUENVALSERATGILNATGARGLEUATRGALAMEATRGLEU 303
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Db 734 TTTCACCTCTGACACTGTTTAAGGCCCAATGGGGCAGAACACACCGACCCATGAGGGTTC 793
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 304 VALVALVALVALVALVALALAPHEALALEUCYSTTRPTHRPTYTHHISLEUVALLEU 323
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Db 794 ATCTTGTGCTGTCTCTCACTTCTTCTGCTTGTGCTGCTGCCCTACCACTGGTCTGCTG 853
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QY 324 VALASPILEULEUMETASPLEUENGLYALALEUALATGASNSCYGLYARG 339
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Db 854 GCAGACACCTCATATGAGGACCCAGGATGATCAAGAGACCTGTGAGGCG 901
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B1653693
LOCUS B1653693 871 bp mRNA linear EST 12-SEP-2001
DEFINITION 603300354F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5340828 5',
RNA sequence.
ACCESSION B1653693
VERSION B1653693.1 GI:15567929
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 871)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1M11865 row: 1 column: 13
High quality sequence stop: 835.
Location/Qualifiers
1. 871
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5340828"
/clone_lib="NIH_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-Sport6; Site_1: NCI;
Site_2: Salt; Cloned unidirectionally. Primer: Oligo dt.
Average insert 2 kb. Library constructed by Life
Technologies, catalog #12017-018. Investigators providing
samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference
for transgenic model: Xu et al., Nature Genetics 22, 37-43
(1999). Note: this is a NCI_CGAP Library."
BASE COUNT 164 a 274 c 221 g 212 t
ORIGIN
Alignment Scores:
Pred. No.: 7.57e-37 Length: 871
Score: 475.50 Matches: 105
Percent Similarity: 56.58% Conservative: 54
Best Local Similarity: 37.37% Mismatches: 115
Query Match: 22.11% Indels: 8
DB: Gaps: 3
US-09-101-518A-2 (1-415) x B1653693 (1-871)
QY 135 THRASPPTHRIEULEUENHISLEUALAVAlAASPPTHLEUENVALLEUTHRIEUPRO 154
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Db 1 ACGGATACCTACTGCTCAACTGGCGCGGACAGACATCTTCTCCTCATCTTCTGCC 60
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QY 155 LEUTHRALAVAlASPLAAlAAlAGINTTPVALPHEGLYSERGLYSEUSLYSVALALA 174
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Db 61 TTCTGGGCTTACAGCAGCAAGTCTGTGATCTTGGGCTGTACTGTGTAAGGGCATC 120
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QY 175 GLYALALEUPHEASNIIEASPHETRYRALAGLYALALEUENLEUALCYSILSESPHE 194
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Db 121 TTTCGATCTATTAAGTTAAGCTTCTTACAGCGGATGCTGCTCTATGCATGACATT 180
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QY 195 ASPATGTYTLEASNIIEVALHISALATHRGINLEUTYARGARGLYPROPROLAEATG 214
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GACCGCTACGATGACATCTGCCAGCGCGTGGCGCTCATCGCCAC-----CGCGCCGC 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 215 VAL-----THRLEUTHRCYSLEUALAVAlTPRGLYLEUCYSLEUENLEUPHEALA 230
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 235 GTGCTTCTCATGACGAAGCTGTCTGTGGGCACTGTGATGCTGCGCTTCTCTCTCC 294
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OY	231	LeuproasphePheleuseSerAlahShiAsqGluArgLeuSsnAatThrHtScys	250
		:	
Db	295	ATCCCGAGACCTCCTTACAGCGGCCTCCAGAAGMACGGCGGAGACACCGCTGAGATTC	354
OY	251	GlnTyraSnpheprOgInVal--GlyArgrThralaleuArgValleuGlnleuValala	269
Db	355	TCACTGGTCAGTGCCCAATGGAGGCCCTTGATCACCATTCACAATGGCCCCAGATGTTTT	414
OY	270	GlyPheleuLeuProleuLeuValMetalaTYRcystylAlahisIleleualavalLeu	289
		:	:
Db	415	GGGTTCCTAAGTCCCTAATGCTGGCTATGAATTCTCTACTCATTAATCTCCGTACTTG	474
OY	290	LeuValSerArGlYglinarGrleuArGlaMetArGleuValValalValalValal	309
			:
Db	475	CITCCAGGCGACCGAACTTTAGCGGAACAAGCGCATCAAGTATCATCTCCGTGGTGA	534
OY	310	AlapheaIaleuCysTrpThrProTyrlHisleuValleuValaspileuMetasp	329
			:
Db	535	GTCCTCAATAGTCTTCCAGCTGCCCTTCACAAATGGGGGTGTCCTGGCAGACGGTGGCAAC	594
OY	330	LeuGLyAlalaLeuAlaArgasnysglYargGluserArGvalAspValAlalysserval	349
			:
Db	555	TTCAACATTCACCAATAGACGCTGCCAAMACCAACCAAGCACCTCAACATTCCTATGACGTC	654
OY	350	TherSerGlyleuGLYrmetHisCysCysleuasnsProleuleuTyralaPheValgly	369
			:
Db	655	ACCTACAGCTGGCTCCGCTCGCTGCTGCTGCGTCAACCCTTTTGTATGCCCTTCATCGGC	714
OY	370	VallYsphearGlgularGmetrlrmetleuleuLeuArgleuGLYCysProasnlgArG	389
			:
Db	715	GTCCAGTTTCCGACGAGCACTCTTCACAACTCTTCAA-GGACTTGGGGCGTGTACAGCAG	773
OY	390	GlyleuGlnArGlnProSerSerSerArgrArGaSpSerSetrtipserCluthrserGlu	409
			:
Db	774	AACGGCTCCCGCACTGCTCTTCGCGGCAATGATGACMAAGCGTCGTGGTAGCATTTGAG	833
OY	410	Ala 410	
Db	834	CGC 836	
RESULT_13			
LOCUS	AM354767	392 bp	mRNA linear EST 25-APR-2001
DEFINITION	36685 MARC IBOV Bos taurus cDNA 5', mRNA sequence.		
ACCESSION	AM354767		
VERSION	AM354767.1 GI:6853757		
KEYWORDS	EST.		
SOURCE	cow,		
ORGANISM	Bos taurus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
	Bovidae; Bovinae; Bos.		
REFERENCE	1 (bases 1 to 392)		
AUTHORS	Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,		
	Cesari,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,		
	G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G.,		
	Petee,G., Holt,I., Karamycheva,S., Liang,F., Quekenbush,J. and		
	Keele,J.W.		
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA		
	libraries and construction of a gene index for cattle		
JOURNAL MEDLINE COMMENT	Genome Res. 11 (4), 626-630 (2001)		
	21180013		
	Contact: Smith TPL		
	USDA, ARS, US Meat Animal Research Center		
	PO Box 166, Clay Center, NE 68933-0166, USA		
	Tel.: 402 762 4366		
	Fax: 402 762 4390		
	Email: smith@email.marc.usda.gov		
	Single pass sequencing. Bases called and trimmed with phred		
	v0.980904.e. Vector identified by cross-match with the -mismscore 200		
	and_mismatch 12 options.		
	PCR primers		

FEATURES					
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Seq primer:	ATTAGTGACACTATG.				
Location/Qualifiers					
BASE COUNT	70 a	131 c	102 g	89 t	
ORIGIN					
Alignment Scores:					
Pred. No.:	1.95e-36	Length:	392		
Score:	466.00	Matches:	95		
Percent Similarity:	80.00%	Conservative:	9		
Best Local Similarity:	73.08%	Mismatches:	20		
Query Match:	21.66%	Indels:	6		
DB:	9	Gaps:	2		
US-09-101-518A-2 (1-415) x AM354767 (1-392)					
Oy	41 ThrAlaProSer-----SerProPheProSerGlnValSerAspHisGln	56			
Db	8 ACGGGGCCAGACGCAGCCGTACACGCCAGCATATGCTCCGAGATGATGACGCCAA	67			
Oy	57 ValLeuAsnAspAlaGluValAlaValLeuGluGluAsnPheserSertyrAspyr	76			
Db	68 GAGTTCGAAGCCTCGATTGCTCACTACCCTCGGAAMC-----TCTTCATGACTAC	121			
Oy	77 GlyGluAsnGluSerAspserCysThrThrSerProProcysProGlnAspHeserLeu	96			
Db	122 GGAGAAATGACAACCTACTTCTGCTGTAATTTCCCACCTGCCACAGGACTTCACCTC	181			
Oy	97 AsnPhasParAlaPheLeuProAlaLeuTyrrSerLeuPheLeuGlyLeuLeu	116			
Db	182 AACTTCGACCGCACCTCTCTGCCCGCTCCTACAGCTCTCTTTGTGCGGGCTTCG	241			
Oy	117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgatgThralaLeuSerThrAsp	136			
Db	242 GGTAAATGGCATCGTGGCAGTCTGCTGCAGACCCAGAGGGCGCCCTGAGCACCGAC	301			
Oy	137 ThrPheLeuHisLeuAlaValAlaAspTrpLeuValLeuThrLeuProLeuTrp	156			
Db	302 ACCTTTCTGCTCACCTTGGCTGTGGCGATGCACGTGTGCTGACACATCCCTCTGG	361			
Oy	157 AlaValAspAlaAlaValAlaGlnTrpValPhe	166			
Db	362 GCAGTGGATGCAGCATCGACGTGGTCTT	391			
RESULT 14					
LOCUS	AL523112	944 bp	mRNA	linear	EST 13-FEB-2001
DEFINITION	AL523112 LTI.NFL003.NBC3 Homo sapiens cDNA clone CSDDC001YB09.5				
ACCESSION	AL523112				
VERSION	AL523112.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
TITLE	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.				
JOURNAL	Full-length cDNA libraries and normalization				
COMMENT	Unpublished (2001)				
	Contact: Genoscope				
	Genoscope - Centre National de Sequencage				

Best Local Similarity:	36.33%	Mismatches:	109
Query Match:	21.04%	Indels:	12
DB:	10	Gaps:	5

US-09-101-518A-2 (1-415) x BI762229 (1-910)

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OY	77	---GlyGUASngJUserAspSerCysThrSerProCysProGlnAspPheSer	95
Db	119	ATGGGCTCAGGGGACTATGACTCC-----ATGAAGGAACCCGTGTTCCGGAGAAAT	172
OY	96	LeuAsnPhleAspArgAlaPhleuProAlaLeuYSerLeuLeuPhleuLeuGlyLeu	115
Db	173	GCTAAATTCATAAATCTCTCGCCACCATCAGTCATCAACATCTCTTAACGGCATT	232
OY	116	LeuGlyAsnGlyAlaValAlaAlaAlaLeuSerArgThrAlaLeuSerSerThr	135
Db	233	GTGGGCATGGATGGTGTCATCTCGTGTATGGGTTACAGAAAGAACTGAGAACGATACG	292
OY	136	AspThrPhleuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeu	155
Db	293	GACACAGTCACAGCTGCACCTTCAGTAGTGCCAGCCCTCTTGTCATCAGCTCTCCCTTC	352
OY	156	TrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysIysValAlaGly	175
Db	353	TGGGCACTGATGCCCGGCGCAACTGGACTGTGGAAATTCCTATGCAAGGCAAGTCAT	412
OY	176	AlaLeuPheAsnIleAsnPhleYTrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAsp	195
Db	413	GTCATCTCACAGTCACCACTTACAGCAGGTGCTCATCTCGGCTTCATCAGCTCGAC	472
OY	196	ArgGlyLeuAsnIleValAlaHisAlaThrGlnLeuYTrArgArgGlyProProAlaArgVal	215
Db	473	CGCTACCTGGCCATCGTCCAGCCACACAGTCAGAGGCCAAGGAAGCTGTGGCGAA	532
OY	216	ThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuPheuPheAlaLeuProAspPheIle	235
Db	533	AAGGGGCTATGTGGCGCTGGATGCCCTGCTCTGCTGACTATGCCGACTTCATC	592
OY	236	PheLeuSerAlaHisHisAspArgLeuAsnAlaThrCysGlnYTrAsnPhePro	255
Db	593	TTT-----GCCAACGTCAGAGGAGGACAGATGACAGATATGTGTGACCCGCTTCACCC	646
OY	256	---GlnAlaGlyArgThrAlaLeuArgValLeuGlnIleuValAlaGlyPhleLeuPro	274
Db	647	AATACATTGGCGGTGGTGTGTACCACTTTACAGACATCATGGTGGCCCTTATCTGCGCT	706
OY	275	LeuLeuValMetAlaTrpCysTrpAlaHisIleLeuAlaValLeuLeuValSerArgGly	294
Db	707	GGATGTGTCATCCGTCCTGTGATATGATATATCTTCCAAAGCTGTACACTCAAGGG	766
OY	295	GlnArgArgLeuArgAlaMetArgLeuValValValValAlaPhe-AlaLeuY	314
Db	767	CACCAAGAGGCGCCAGGCCCTCCAGACACAGTCATCTCATCTGCGTTCTTGGCGCTG	826
OY	314	StrThrProYTrHisLeuValValLeuValAspIleLeuMetAspLeuGly	331
Db	827	TTGGCTGCTTACTACTTGGGATGACCATCGAATTCCTTTACCTCCATCCTCGGA	878

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Job time : 1706 secs

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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 2, 2002, 12:19:26 : Search time 2890 Seconds
(without alignments)
3106.742 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRRKYGRGLAGTIGGAA.....SSSRDSSWSGPTSEASVSGL 415

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 21979536 seqs, 10817449327 residues
Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Pending_Patents_NA_Main -QFMT=fastap -SUFFIX=p2n.inpm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100
-THR.MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09101518.ecgn_1_1.1201_etunatc_29102002_091059_29959
-NCPU=6 -ICPU=3 -NO_KLAPT -NO_MAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_Main:

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6: /cgn2_6/ptodata/1/pna/US082.COMB.seq:*
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Print. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	DB ID	Description
1	2142	99.6	1876	1	PCT-US96-00499-1
2	2142	99.6	1876	1	PCT-US96-00499A-1
3	2142	99.6	1876	15	US-09-101-518-1
4	2136	99.3	1877	1	PCT-US00-265248-2115
5	2116	98.4	6604	64	US-60-258-773-3
6	2073	96.4	1293	14	US-09-016-434-1052
7	2073	96.4	1293	36	US-09-960-706-962
8	1897	88.2	1670	14	US-09-023-655-980
9	1897	88.2	1670	24	US-09-624-594-1
10	1897	88.2	1670	24	US-09-633-541-1
11	1897	88.2	1670	26	US-09-663-702-1
12	1897	88.2	1670	26	US-09-663-799-1
13	1897	88.2	1670	33	US-09-880-107-3833
14	1891	87.9	1107	15	US-09-170-496-19
15	1891	87.9	1107	15	US-09-170-496C-19
16	1891	87.9	1107	15	US-09-170-496D-19

OY	341	SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTYrMetHisCysCysLeu	360
Db	1193	AGCAGGGAGACGCGGCCCAAGTGGTCACCTCCAGGCGCTGGGCTACATGACGACTGGCTTC	1252
OY	361	AsnProLeuLeuTYrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu	380
Db	1253	AACCCGGCTGCTATAGCTTTGTAGGGGGTCAAGTTCGGGGACGGATGGATGGCTGGCTC	1312
OY	381	LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg	400
Db	1313	TTGGGCGTGGGCTGCCCAACACAGAGAGGGCTTCAGAGGACACCATCGCTTCCGCCGG	1372
OY	401	AspSerSerTYrSerGlnThrSerGluAlaSerTYrSerGlyLeu	415
Db	1373	GATTCATCTCTGTCTGAGACCTCAGAGGCGCTCTACTCGGGCTTG	1417
RESULT 3			
US-09-101-518-1			
; Sequence 1, Application US/09101518			
; GENERAL INFORMATION:			
; APPLICANT: Li, Yi			
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSAT068			
; FILE REFERENCE: PF218PCT.US			
; CURRENT APPLICATION NUMBER: US/09/101,518			
; CURRENT FILING DATE: 1998-12-21			
; PRIOR APPLICATION NUMBER: PCT/US96/00499			
; PRIOR FILING DATE: 1996-01-11			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 1876			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (173)..(1420)			
US-09-101-518-1			
Alignment Scores:			
Pred. NO.: 2,14e-191			
Score: 2142.00			
Percent Similarity: 99.76%			
Best Local Similarity: 99.76%			
Query Match: 99.58%			
DB: 15			
Gaps: 0			
US-09-101-518A-2 (1-415) x US-09-101-518-1 (1-1876)			
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Db	173	ATGAGATTGAGGAAGTACGGCCCTGGAGACTGGCGGGAGCAGTTATAGAGGACTCT	232
OY	21	GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTYr	40
Db	233	CAGAGTAAATACAGACTAATATCAGACTCAATCACAAAAGACTTCTCCAGGCGCTTAC	292
OY	41	ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnSP	60
Db	293	ACAGCCCTCTCTCCCGGTTCGCCCTCACAGGTAGTAGACCAACCAAGTGTAAATGAC	352
OY	61	AlaGluValAlaAlaLeuLeuGlnAsnPheSerSerSerTYrAspTYrGlyGluAsnGlu	80
Db	353	GCGCAGGTGGCGGCCCTCCGAGAACTTCAGTCTTCTTAAGACTATAGCAAAACGAG	412
OY	81	SerAspSerCysTYrSerProProCysProGlnAspPheSerLeuAsnPheAspArg	100
Db	413	AGTACTCTGCTGTACTCTCCGCCCTGCACACAGACTTCAGGCTGAACTTGACCGG	472
OY	101	AlaPheLeuProAlaLeuTYrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla	120
Db	473	GCTTCTCTGCCAGCCCTCAACAGACCTTCCTTTCTGTGGGCTCTGGGCAAGCGCGCG	532

QY 121 VALIAAALAVALEULEUSERARGRGRHRALEUSERSETHASPTHPhELEULEU 140
 DB 533 GTGGACGGCTGCTCTGAGCGGCGAGACGCCCTGACAGACCGAACCTTCCTGCTC 592
 QY 141 HSLLEUALAVAIASPHRPREULEUVALLEUTHRLEUPROLEUTRALAVALASPLA 160
 DB 593 CACCTTAGCTTAGACAGACACGCTGCTGGTGGTGAACACTGCCCTTGGGAGTGGACGCT 652
 QY 161 ALAVAGLINTRPVALPHEGLYSERGLYSEUCSYLSVALAIGLYALALEUPHEASNILE 180
 DB 653 GCCGTCACAGTGGGTCTTTGGCTCTGAGCCTCGCAAGTGGAGAGTGGCCCTCTCAACATC 712
 QY 181 ASNPHEYTRALAGLYALALEULEUALACYSILLESERPHASPARTRYLEUASNILE 200
 DB 713 AACCTTCACGAGGAGGCCCTCTGCTGGCTGACACACCTTTGACCGCTTACCTGACATTA 772
 QY 201 VALHLSAIAATHGILEUTHYRARGRGLYPROPOLIAARGVALTHLEUTHCYSEU 220
 DB 773 GTTCATGCCACCAAGCTTACCGCGGGGGGCCCGGGGCCGGTACCTACCTGCTG 832
 QY 221 ALAVATRPGLYLEUCSYSEULEUPHEALALEUPROASPHLEIAPHELEUSERALHIS 240
 DB 833 GGTGCTGGGGGCTCTGGCTGCTTTCCGCCCTCCAGACTTCATTTCTGTCGGGCCAC 892
 QY 241 HISASPGIUAIGLEUASNAIATHRHSYSGINTYRASNPHPROGLINVALIYARGTHR 260
 DB 893 CACGACGAGCGGCTTACGCGCCACCTGCCAATCAACTTCCACAGTGGCGCGCAGC 952
 QY 261 ALALEARGVALLEGLILEUVALAIGLYPHELEULAEUPROLEULEUVALMETALATYR 280
 DB 953 GCTTCCGGGGTCTCTGACGTGGTGGCTTCTTCTGCTGCCCTCTGCTGATGGCTTAC 1012
 QY 281 CYSYTRALHSLILEUVALALEULEUVALSERARGIYGLINARGRLEUARGLA 300
 DB 1013 TCGTATGCCCAATCGCTGGCGGTGCTGCTGGTTCCAGAGGGGACAGCGCGCTGGGGCC 1072
 QY 301 METARGLEUVALVALVALVALVALAIPHEALALEUCSYTRPTHRPROTYHISLEU 320
 DB 1073 AAGCGGCTGGTGGTGGTGGTCTGCTGGCGCTTGGCCCTCTGCTGACCCCTCATCACTG 1132
 QY 321 VALVALLEUVALASPILEULEUMETASPLEUGLYALALEUVALARGASNSYGLIYARGLU 340
 DB 1133 GTGGTCTGGTGGATCCTCATGGACCTTGGCGCTTGGCCCGCAACTGTGGCCGAGAA 1192
 QY 341 SERARGVALASPVALLALYSSEVALTHRSERGILEUGLYTYRMEHISCYSCYLEU 360
 DB 1193 ACCAGGGTAGAGCTGGCCAGTGGCTACACTGAGCCCTAGGCGTATCATCTGCGCTC 1252
 QY 361 ASNPROLEULEUTYRALAPHEVALIGLYVALYLSPHEARGIUAIRGMEETRPMELEULEU 380
 DB 1253 AACCGGCTGCTTACGCTTGTAGGGGTCAAGTCCCGGAGCGGATGGATGCTGCTC 1312
 QY 381 LEUARGLEUGLYCYSPROASNGIARGGLYLEUGLINARGIINPROSESESERARGARG 400
 DB 1313 TTGGCCCTGGGGCTGGCCCAACAGAGAGGGCTCCAGAGGCCATCGCTTCCTCCGGCGG 1372
 QY 401 ASPSERSETRPSERGLIUTHSERGIUALASERTYRSEGLYLEU 415
 DB 1373 GATTATCTCTGCTGAGACCTCAGAGGCGCTTACTGCGGGCTTG 1417
 RESULT 4
 PCT-US00-26524B-2115
 ; Sequence 2115, Application PC/TUS0026524B
 ; GENERAL INFORMATION:
 ; APPLICANT: Birste et. al.
 ; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
 ; FILE REFERENCE: PA050PCT
 ; CURRENT APPLICATION NUMBER: PCT/US00/26524B
 ; CURRENT FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 60/157,137
 ; PRIOR FILING DATE: 1999-09-29
 ; PRIOR APPLICATION NUMBER: 60/163,280
 ; PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 2115
 LENGTH: 1877
 TYPE: DNA
 ORGANISM: Homo sapiens
 PCT-US00-26524B-2115

Alignment Scores:

Pred. No.:	7.89e-191	Length:	1877
Score:	2136.00	Matches:	413
Percent Similarity:	99.52%	Conservative:	0
Best Local Similarity:	99.52%	Mismatches:	2
Query Match:	99.30%	Indels:	0
	1	Gaps:	0

US-09-101-518a-2 (1-415) x PCT-US00-26524B-2115 (1-1877)

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QY 1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
DB 173 ATGGAGTTGAGGAATACAGCCCTCGAAGACTGGCGGGAGACGTTATAGAGAGAGCTGCT 232
QY 21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
DB 233 CAGAGTAATACAGACTAAATCAGACTCAATCACAAGAGTTCCTGCGAGGCTTTAC 292
QY 41 ThrAlaProSerSerProPheProPheProSerGlnValSerAspHisGlnValLeuAsnAsp 60
DB 293 ACAGCCCTTCCTCCCTCCGCTCCGCTCCACAGAGTACAGACCACTGCTAAATGAC 352
QY 61 AlaGluValAlaAlaLeuLeuGluAsnPheserSerSerTyrAspTyrGlyGluAsnGlu 80
DB 353 GCCGAGGTGGCGCCCTCTCGAGAACTTCACTCTTCTATGACTATGAGAAAACGAG 412
QY 81 SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheserArg 100
DB 413 AGTGAMTGTGCTGTAACCTCCCGCCCTGCGCCACAGAGACTTCACTGCACTTCGACCGG 472
QY 101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGlyLeuLeuGlyGlnGlyAla 120
DB 473 GCTTCTGCTGCGCCCTCACAGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 532
QY 121 ValAlaAlaValAlaLeuLeuSerArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
DB 533 GTGGCAGCGCTGCTGCTGAGCGGGGAGACGCCCTGAGAGACCGACGACTTCTCTGCTC 592
QY 141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAla 160
DB 593 CACCTAGCTGTAGCAGACACRGTGCTGGTGCAGACTGCCCTGCGGCACTGGACGCT 652
QY 161 AlaValGlnTrpValPheGlySerGlyLeuGlyLysValAlaGlyAlaLeuPheAsnIle 180
DB 653 GCCGTCCAGTGGCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 712
QY 181 AsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
DB 713 AACTCTACGCGAGGAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 772
QY 201 ValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeu 220
DB 773 GTTCATGCCACCACAGCTGTACCGCGGGGCGCCCGCGGCTGACCTCTACCTGCTGCTGCT 832
QY 221 AlaValTrpGlyLeuGlyLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
DB 833 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892
QY 241 HisAspGlnArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValAlaGlyArgThr 260
DB 893 CACGACGAGCGCGCTCAACGCCACGCCACATGCAATCACTTCCACAGAGTGGCGCGGACG 952
QY 261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
DB 953 GCTTGGCGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1012
  
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QY 281 CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla 300
DB 1013 TCGTATGCCCCACATCTGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1072
QY 301 MetArgLeuValValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeu 320
DB 1073 ATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1132
QY 321 ValValLeuValAspIleLeuMetAspLeuGlyAlaValAlaArgAsnCysGlyArgGlu 340
DB 1133 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1192
QY 341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
DB 1193 ACAGAGGTAGCTGCGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1252
QY 361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 380
DB 1253 AACCGCTCTCTATGCTCTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGATGCTGCTC 1312
QY 381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerArgArg 400
DB 1313 TTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1372
QY 401 AspSerSerTrpSerGlnThrSerGlnAlaSerTyrSerGlyLeu 415
DB 1373 GATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1417

RESULT 5
US-60-258-273-3/C
; Sequence 3, Application US/60258273
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
; TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1001042-PROV
; CURRENT APPLICATION NUMBER: US/60/258,273
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6604
; TYPE: DNA
; ORGANISM: Human
; US-60-258-273-3

Alignment Scores:
Pred. No.: 3.07e-188 Length: 6604
Score: 2116.00 Matches: 414
Percent Similarity: 99.28% Conservative: 0
Best Local Similarity: 99.28% Mismatches: 1
Query Match: 98.37% Indels: 2
DB: 64 Gaps: 0

US-09-101-518a-2 (1-415) x US-60-258-273-3 (1-6604)

QY 1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
DB 3700 ATGGAGTTGAGGAATACAGCCCTCGAAGACTGGCGGGAGACGTTATAGAGAGAGCTGCTG 3641
QY 20 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
DB 3640 TCAGAGTAATACAGACTAAATCAGACTCAATCAACAAAAGAGTTCTCTGCGAGGCTTTTA 3581
QY 40 ThrAlaProSerSerProPheProPheProSerGlnValSerAspHisGlnValLeuAsnAsp 60
DB 3580 CACAGCCCTTCTCCCTCCGCTTCCGCTCACAAGGTGAGTGAACCAAGTCTTAATATGA 3521
QY 60 PalGluValAlaAlaLeuLeuGluAsnPheserSerSerTyrAspTyrGlyGluAsnGlu 80
DB 3520 CGCCGAGGTGGCGCCCTCTGAGAACTTCAAGCTTCTTCTGACTATGAGAAAACGA 3461
  
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QY      80  uSerAspSerCysCysThrSerProCysProGlnAspPheSerLeuAsnPhaSpaR 100
      |||
      3460 GAGTGCAGCTGCTGCTGACCTCCCCGCTGCCCCACAGAGACTTCAGCTGAACTTCGACCG 3401
QY      100  gAlaPheLeuProAlaLeuTyrrSerLeuPheLeuGlyLeuGlnGlyAl 120
      |||
      3400 GGGCTTCTGCTCCAGCCCTTACAGCTCTCTTCTGCTGGGCTCTGCGGCAACGCGCC 3341
QY      120  aValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 140
      |||
      3340 GGTGGAGCGCTGCTGCTGAGCGGGGAGAGCGCTGAGAGACAGCAGCAGCTTCTGCT 3281
QY      140  uHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrrAlaValAspAl 160
      |||
      3280 CCACCTAGCTGTAGCAGACACGCTGCTGGGTGAGACACTCCGCTCGGGCAGTGGACGC 3221
QY      160  aAlaValGlnTrrValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 180
      |||
      3220 TGGCTTCAGTGGGCTGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3161
QY      180  eAsnPhaTyrrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrrLeuAsn 200
      |||
      3160 CAACCTTCAGCGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3101
QY      200  eValHisAlaThrGlnLeuTyrrArgArgGlyProProAlaArgValThrLeuThrCys 220
      |||
      3100 AGTTCATGCGCACCCAGCTACCGCGGGGGCGCGCGCGCGCGCTGACCTGACCTGCGCT 3041
QY      220  uAlaValTrrGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaH 240
      |||
      3040 GGGTGTCTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2981
QY      240  sHisAspGluArgLeuAsnAlaThrHisCysGlnTyrrAsnPhaProGlnValGlyArgTh 260
      |||
      2980 CCACGAGAGCGCGCTCAGCGCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2921
QY      260  rAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAla 280
      |||
      2920 GGGCTGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2861
QY      280  rCysTyrrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArg 300
      |||
      2860 CTGCTATGCGCCACATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2801
QY      300  aMetArgLeuValValValValValValAlaPheAlaLeuCysTrrThrProThrHis 320
      |||
      2800 CATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2741
QY      320  uValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArg 340
      |||
      2740 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2681
QY      340  uSerArgVal-AspValAlaValSerValThrSerGlyLeuGlyTyrrMetHisCysCys 360
      |||
      2680 AAGCAGAGGAGTACAGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2621
QY      360  eAsnProLeuLeuTyrrAlaPheValGlyValLysPheArgGluArgMetTrrMetLeu 380
      |||
      2620 TCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2561
QY      380  eLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArg 400
      |||
      2560 TCTTGGGCTGCGGCTGCCCAACAGAGAGGGGCTCAGAGGAGGAGGAGGAGGAGGAGG 2501
QY      400  rAspSerSerTrrPrrSerGlyThrSerGlnAlaSerTyrrSerGlyLeu 415
      |||
      2500 GGGATTTCATCTGCTGCTGAGACCTAGAGGCTCTCTACTCTGGGCTTGG 2454

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RESULT 6
 US-09-016-434-1052
 ; Sequence 1052, Application US/09016434
 ; GENERAL INFORMATION:

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? APPLICANT: Janice Au-Young
? APPLICANT: Jeffrey J. Seilhamer
? TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
? TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
? NUMBER OF SEQUENCES: 1490
? CORRESPONDENCE ADDRESS:
? ADDRESS: INCYTE PHARMACEUTICALS, INC.
? STREET: 3174 PORTER DRIVE
? CITY: PALO ALTO
? STATE: CALIFORNIA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/016,434
? FILING DATE: HEREWITH
? CLASSIFICATION:
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Zeller, Karen J.
? REGISTRATION NUMBER: 37,071
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (650) 855-0555
? TELEFAX: (650) 845-4166
? INFORMATION FOR SEQ ID NO: 1052:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1293 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: GENBANK
? CLONE: g1002740
? US-09-016-434-1052

Alignment Scores:
Pred. No.: 4,33e-185 Length: 1293
Score: 2073.00 Matches: 400
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.37% Indels: 0
DB: 14 Gaps: 0

US-09-101-518a-2 (1-415) x US-09-016-434-1052 (1-1293)
QY      16  lIeGlyGlyAlaAlaGlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPhe 35
      |||
      1  ATAGAGGAGAGCTGCTCAGAGTAAATCAGACTAAATCAGACTCAATCAAAAGAGTTG 60
QY      36  LeuProGlyLeuTyrrThrAlaProSerSerProPheProProSerGlnValSerAspHis 55
      |||
      61 CTGCCAGGCGCTTACACACCCCTTCTCCCGCTCCCGCTCCCGCTCCAGGTGAGTACAC 120
QY      56  GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGlnAsnPhaSerSerSerTyrrAsp 75
      |||
      121 CAAGTCTAAATAGACCGCCAGGTGGCGGCTGCTGAGAACTTCAGCTTCTTCTATGAC 180
QY      76  TyrrGlyGlnAsnGlnSerAspSerCysTyrrSerProProCysProGlnAspPheSer 95
      |||
      181 TATGAGAAAGAGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY      96  LeuAsnPhaAspArgAlaPheLeuProAlaLeuTyrrSerLeuLeuPheLeuLeuGlyLeu 115
      |||
      241 CTGAACCTTGACCGGCGCTTCTGCCAGGCCCTTCTACAGCTCTCTTCTGCTGGGCGTG 300

```


STREET: Two Millita Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/663,702
FILING DATE: 15-Sep-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/829,839
FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TK196-01A
TELEPHONE: (617) 861-9540
TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1670 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown

FEATURE:
NAME/KEY: CDS
LOCATION: 69..1172
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-663-702-1

Alignment Scores:
Pred. No.: 2,47e-168 Length: 1670
Score: 1897.00 Matches: 369
Percent Similarity: 97.63% Conservative: 1
Best Local Similarity: 97.36% Mismatches: 5
Query Match: 88.19% Indels: 4
Gaps: 1

US-09-101-518a-2 (1-415) x US-09-663-702-1 (1-1670)

Qy 41 ThrAlaProSer-----SerProPheProProSerGlnValSerAspHisGln 56
Db 36 ACACCAACCCAGAGCCAGACGACACGACGATGCTTCCTGAGGTGATGACCA 95

Qy 57 ValLeuAsnAspAlaGlnValAlaAlaLeuGlnValAsnPheSerSerSerTyrAspTyr 76
Db 96 GTGCTAAATGAGCGCCGAGGTGCGCCCTCTCGGAGAACTTCAGCTTCCTCATGACTAT 155

Qy 77 GlysGlnAsnGluSerAspSerCysThrSerProProCysProGlnAspPheSerLeu 96
Db 156 GGAGAAACAGAGAGTACTGCTGCTGACTGCCGCCCTGCCACAGACTTCACGCTG 215

Qy 97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGlnLeuLeu 116
Db 216 AACTTCGACCGGGGCTTCCTGCGACCCCTTCACGCTTCCTTCCTGCTGGGGCTG 275

Qy 117 GlysAsnGlyAlaValAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
Db 276 GGCAACGGGGGGGGGAGCGGCTGCTGAGCCGCGAGACGCTGAGCAGCAGCCGAC 335

Qy 137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTyr 156
Db 336 ACCTTCCTGCTCCACCTGACTGCTGACAGACAGCTGCTGCTGCTGCTGCTGCTG 395

Qy 157 AlaValAspAlaAlaValGlnTyrValPheGlySerGlyLeuCysLysValAlaGlyAla 176
Db 396 GCAGTGAAGAGCTGCGCTCAGTGGGCTCTTGGCTGCGCTCTGCAAGTGGCAGGTGCC 455

Qy 177 LeuPheAsnIleAsnPheTyrAlaGlnValAlaLeuLeuAlaCysIleSerPheAspArg 196
Db 456 CTCTTACATCACTACTTCTACACGAGACGCTCTCTGCTGCTGCTGCTGCTGCTG 515

Qy 197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
Db 516 TACCTGACATGATGTCATGCCACACCGACTCTACCGCGGGGGGGGGGGGGGGGGG 575

Qy 217 LeuThrCysLeuAlaValTrrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
Db 576 CTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 635

Qy 237 LeuSerAlaHisHisAspGlnValArgLeuAsnAlaThrHisCysGlyIleTyrAsnPheProGln 256
Db 636 CTGTGCGCCGACGACGAGCGGCTCTAAGCGCACCCGCTGCTGCTGCTGCTGCTG 695

Qy 257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
Db 696 GTGGGGCGGACGCGCTGCGGGGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTG 755

Qy 277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
Db 756 GTCATGCGCTACTGCTATGCCACATCCTGCGCGCTGCTGCTGCTGCTGCTGCTG 815

Qy 297 ArgLeuArgAlaMetArgLeuValValValValValValValValValValValValVal 316
Db 816 CGCCTGCGGGCCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 875

Qy 317 ProTyrHisLeuValValValValValValValValValValValValValValValVal 336
Db 876 CCTATACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 935

Qy 337 CysGlyArgGluSerArgValAlaValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
Db 936 TGTGGCCGAGAAAGCAGGCTAGACGCGCAAGTGCCTCAGGCTGCGGCTGCTGCT 995

Qy 357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
Db 996 CACTGCTGCTCAACCGGCTGCTATGCTTGTGAGGGGCTCAAGTCCGGGAGCGGAG 1055

Qy 377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgInProSer 396
Db 1056 TGGATGCTGCTCTTGGCGCTGCGCTGCCCAACAGAGAGGCTCCAGAGGACCATGG 1115

Qy 397 SerSerArgArgAspSerSerTrpSerGlnThrSerGlnAlaSerTyrSerGlyLeu 415
Db 1116 TCTTCCCGCGGAGTTCATCTGCTGCTGAGACCTCAGAGGCTCTCATACGCGCTTG 1172

RESULT 12
US-09-663-799-1
Sequence 1, Application US/09663799
GENERAL INFORMATION:
APPLICANT: Loetscher, Marcel
Moser, Bernhard
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
NUCLEOTIC ACIDS, AND METHODS OF USES THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P. C.
STREET: Two Millita Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/663,799
FILING DATE: 15-Sep-2000

```
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/709,838
  FILING DATE: <Unknown>
  ATTORNEY/AGENT INFORMATION:
    NAME: Brook Esq., David E.
    REGISTRATION NUMBER: 22,592
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (617) 861-6240
    TELEFAX: (617) 861-9540
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1670 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: unknown
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 69..1172
  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-663-799-1
```

```
Alignment Scores:
Pred. No.: 2,47e-168 Length: 1670
Score: 1897.00 Matches: 369
Percent Similarity: 97.63% Conservative: 1
Best Local Similarity: 97.36% Mismatches: 5
Query Match: 88.19% Indels: 4
DB: Gaps: 1
```

US-09-101-518a-2 (1-415) x US-09-663-799-1 (1-1670)

```
QY 41 ThrAlaProSer-----SerProPheProSerGlnValSerAspHisGln 56
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 36 ACACCAACCCAGCAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 95
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheserSerTyraSpr 76
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 96 GTGCTAAATGACGCCGAGGTGCCGCCCTCGAGAACTTCAGCTTCCTATGACTAT 155
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 77 GtGtGluAsnGluSerAspSerCysThrSerProProCysProGlnAspHisSer 96
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 156 GGAGAAACGAGAGTACCTGCTGTACCTCCGCCCTCCACAGGACTTCACACCTG 215
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 97 AsnPhaAspArgAlaPheLeuProAlaLeuTySerLeuPheLeuGluGlyLeuLeu 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 216 AACTTCGACGGGCGCTCTGCCACGCCCTTACAGCTCTCTTCTGCTGGGCGTGTG 275
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 117 GtGluAsnGtAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerThr 136
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 276 GGCAACGGCGCGGTGGCAGCCGTGCTGAGACCGCGGAGACGCTGAGCAGCAG 335
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuPro 156
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 336 ACCCTTCCTGCTCCACTTACTCTTACAGCAGCAGCTGCTGTGACACTGCGCTG 395
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 157 AlaValAspAlaAlaValAlaGlnTrpValPheGlySerGlyLeuCysLysVal 176
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 396 GCAGTGGAGCGTCCGCTCCAGTGGGCTTGTGCTGTGCTTGCCTGCAAAATGG 455
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 177 LeuPheAsnIleAsnPheTyraGlyAlaLeuLeuLeuAlaCysIleSerPheAsp 196
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 456 CTCTTCACATCATCACTTACACGAGAGCCCTCGCTGGCTGCATCATGTTGAC 515
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 197 TyrLeuAsnIleValHisAlaThrGlnLeuTyraArgGlyProProAlaArgVal 216
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 516 TACCTGAACATGATCATGCTCCACAGCTTACCCGCGGGGCGCCCGCGCGAG 575
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 217 LeuThrCysLeuAlaValTrpArgLysLeuLeuPheAlaLeuProAspPheIle 236
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 576 CTCACCTGCTGGCTGTCTGGGGGCTGCTGCTTTCGCTCCACAGCTTCATCTTC 635
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
QY 237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyraAsnProGln 256
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 636 CTGTGGCCACACAGCAGCAGCGCTCAACGCCACACCCATGCCAATATCACTCCACAG 695
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 276
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 696 GTGGGCGGACGCTCTGGGGGTGCTGACGTGGGTGGCTTCTGTGCCCCCTGCTG 755
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 277 ValMetAlaTyrcysTyraAlaHisIleLeuAlaValLeuLeuValSerArgLys 296
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 756 GTCATGCGCTACTGCTATGCCACATCCCTGCGCGCTGCTGCTTCACAGGGCCAG 815
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 297 ArgLeuArgAlaMetArgLeuValValValValAlaValAlaPheAlaLeuCysTrp 316
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 816 CGCTGCGGGCCATGCGGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 875
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 317 ProTyHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 336
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 876 CCTATCACCTGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 935
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTy 356
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 936 TGTGGCCGGAAGACAGGCTAGACGTGGCCAGTGGCTACCTCAGGCTGGGCTTAC 995
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 357 HisCysCysLeuAsnProLeuLeuTyraAlaPheValGlyValLysPheArgGlu 376
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 996 CACTGCTGCTCAACCCGCTGCTTATGCTTGTAGGGGTCAAGTTCGGGAGCGGATG 1055
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgL 396
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1056 TGGATGCTGCTCTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1115
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 397 SerSerArgArgAspSerSerTrpSerGluTrpSerGluAlaSerTySerGlyLeu 415
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1116 TCTTCCCGCGGGATTCATCTGCTGTGAGACCTCAGAGGCTCTACTGCGGCTTG 1172
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 13

```
US-09-880-107-3833
; Sequence 3833, Application US/09880107
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Iwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatencIn Ver. 2.1
; SEQ ID NO 3833
; LENGTH: 1670
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. X95876
US-09-880-107-3833
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Alignment Scores:
Pred. No.: 2,47e-168 Length: 1670
Score: 1897.00 Matches: 369
Percent Similarity: 97.63% Conservative: 1
Best Local Similarity: 97.36% Mismatches: 5
Query Match: 88.19% Indels: 4
DB: Gaps: 1
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US-09-101-518a-2 (1-415) x US-09-880-107-3833 (1-1670)

QY 41 ThrAlaProSer-----SerProPheProSerGlnValSerAspHisGln 56

```

36 ACACACACGAGGAGAGACACACGAGGATGCTTGTAGGTGAGTGCACACAA 95
57 VALLEAAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheserSertYrAspYr 76
96 GTGCTAAATGAGCGGAGGTGGCGGCTTCGGAGAACCTTCAGCTTCATATGACTAT 155
77 GLYGLuAsnGluSerAspSerCysThrSerProCysProGlnAspPheserLeu 96
156 GGAGAAAGAGAGAGTACTGCTGCTTACCTCCCGCTGCCACAGACTTCACCTTG 215
97 AsnPheserPArgAlaPheLeuProAlaLeuYrSerLeuLeuPheLeuGluLeu 116
216 AACTTCGACCGGCGCTTCCTGCACAGCCTCTACAGCCTCTTCTGCTGGGGGCTG 275
117 GLYAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerThrAsp 136
276 GGCAAGGGGCGGTGGACCGGCTGAGCGGGGAGACCCCTGAGCAGCAGCGAG 335
137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
336 ACCTTCCTGCTCACCCTGACTGTAGCAGACAGCCTGCTGCTGACACTGGCGCTCTGG 395
157 AlaValAspAlaAlaValAlaGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
396 GCAGTGGAGCGTCCGCTCCAGTGGGCTTTGGCTTGCGCTCGCAAGTGGCAGGTGGC 455
177 LeuPheAsnIleAsnPhenylrAlaGlyAlaLeuLeuAlaCysIleSerPheAspArg 196
456 CTTCTCAACATCACTTCACGAGAGAGCCCTTCGCTGGCTGCACTTCAGCTTGCACCGC 515
197 TyrLeuAsnIleValHisAlaThrGlnLeuYrArgArgGlyProProAlaArgValThr 216
516 TACGTGAACATAGTTCATGCTCACCACGCTTCACCGCGGGGGCGCCCGCGCTGAGC 575
217 LeuThrCysLeuAlaValAlaTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
576 CTCACCTGCTGGCTGCTGGGGGCTCTGCTGCTTTGCGCCCTCCACAGACTTCATCTTC 635
237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTrpAsnPhenProGln 256
636 GTGTGGGCGCCACGACGAGCGGCTCAACGCGCCTGCGCAATCAACACTTCGCCACG 695
257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
696 GTGGGCGGACGCTCTGGGGGCTGCTGCTGCTGCTGCTTCTTCTGCTGCCCTGCTG 755
277 ValMetAlaTrpCysTrpAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
756 GTCATGGCTACTGCTATGCTCCACATCCTGGCGCTGCTGCTGCTGCTGCTGCTGCTG 815
297 ArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrpThr 316
816 GCGCTGGCGGCGCATGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 875
317 ProYrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaAsn 336
876 CCGTATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 935
337 CysGlyArgGluSerArgValAlaValAlaLysSerValThrSerGlyLeuGlyTrpMet 356
936 TGTGGCGGAGAAAGCAGGTAGACGTGGCCAGTGGTCAACGTCAGGCGTGGGCTCATG 995
357 HisCysCysLeuAsnProLeuLeuTrpAlaPheValGlyValLysPheArgGluArgMet 376
996 CACTCTGCTGCTAACCGGCTGCTATGCTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055
377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnTrpGlnProSer 396
1056 TGGATGCTCTCTTGGCGCTGGGCTGCTGCCAACAGAGAGGGCTCCAGAGGCGCATG 1115
397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTrpSerGlyLeu 415
|||||
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```

DB 1116 TCCTCCCGCGGAGTTTCATCTGTGCTGAGACTTCAGAGCCTCTCATCTGGGCTTG 1172
RESULT 14
US-09-170-496-19
; Sequence 19, Application US/09170496
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupl
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496-19

Alignment Scores:
Pred. No.: 5,36e-168 Length: 1107
Score: 1891.00 Matches: 364
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.73% Mismatches: 0
Query Match: 87.91% Indels: 0
DB: 15 Gaps: 0

US-09-101-518a-2 (1-415) x US-09-170-496-19 (1-1107)
QY 51 GlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPh 70
DB :|||
DB 10 GAGTAGTGACCAACAGTCTAAATGAGCGCGAGAGTGGCCCTCTCGAGAACTTTC 69
QY 71 SerSerSerTrpArgGlyGluAsnGluSerAspSerCysThrSerPropCys 90
DB :|||
DB 70 AGCTCTTCATATGATGAGAAAGAGAGTACTGCTGCTGATCTCCCGCCCTGC 129
QY 91 ProGlnAspPheSerLeuAsnPheserPArgAlaPheLeuProAlaLeuYrSerLeuLeu 110
DB :|||
DB 130 CCACAGACTTCAGCTGAACTTCGACCGGCGCTTCCTGCGACCGCTTCACACTCTC 189
QY 111 PheLeuLeuGlyLeuLeuGlnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
DB :|||
DB 190 TTTCTGCTGGGCTGCTGGGCAACGGCGGTGGCGGCTGCTGCTGCTGCTGCTGCTG 249
QY 131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
DB :|||
DB 250 GCCCTAGCAGCAGCAGCAGCTTCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 309
QY 151 LeuThrLeuProLeuTrpAlaValAlaAspAlaValAlaGlnTrpValPheGlySerGlyLeu 170
DB :|||
DB 310 CTGACACTGCGGCTGGGAGTGGAGCGCTGCGCTCAGTGGGTCTTTGGCTCTGGCCTC 369
QY 171 CysLysValAlaAlaValAlaLeuPheAsnIleAsnPhenylrAlaGlyAlaLeuLeuAla 190
DB :|||
DB 370 TGCAAAGTGGCAGGTGCTCTTCAACATCACTTTCAGCAGAGACCCCTCCGCTGGCC 429
QY 191 CysIleSerPheAspArgTrpTrpLeuAsnIleValHisAlaThrGlnLeuYrArgArgGly 210
DB :|||
DB 430 TGCATAGCTTTTACCGCTTACCTGAAACATATGTTCAATGCCACCCAGCTTACCGCGGG 489
QY 211 ProProAlaArgValThrLeuThrCysLeuAlaValAlaTrpGlyLeuCysLeuLeuPheAla 230
DB :|||
DB 490 CCGCGCGCGCGGTGACCTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549
QY 231 LeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCys 250
DB :|||
DB 550 CTCGCCAGCTTTCATCTTCGTTGGGCGCCACAGAGAGCGGCTCAACGCCACCTCC 609
QY 251 GlnTrpAsnPhenProGlnValGlyArgThrAlaLeuArgValLeuLeuValAlaGly 270
|||||
```



```
|||||
Db 610 CAAATACAACTTCCACAGAGTGGGCGCCAGCGCTGCGGGTGGCTGACGTGGGTGGCTGGC 669
Oy 271 PheLeuLeuProLeuLeuValMetalatYrCysTYrAlaHisIleLeuAlaValLeuLeu 290
Db 670 TTTCTGCTGCCCCCTGCTGGTCACTGGCTTACTGCTATGCCACATCCTGGCCGCTGCTG 729
Oy 291 ValSerArgGlyGlnArgArgLeuAlaMetArgLeuValValValValValValAla 310
Db 730 GTTTCAGAGGGGCGAGCGGCGCTGCGGCGCATGCGGCTGCTGGTGGTGGCGTGGGCGC 789
Oy 311 PheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAlaPheLeuMetAspLeu 330
Db 790 TTTGGCCCTGTGCGACCCCTATACCTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 849
Oy 331 G1yAlaLeuAlaArgAsnCysGlyArgGlnSerArgValAlaPvalAlaLysSerValThr 350
Db 850 GCGGCTTGGCCCGCAACTGTCGCGCCAGAAAGCAGAGGTAGACGTGGCCAAAGTCGTCACC 909
Oy 351 SerGlyLeuGlyTYrMetHisCysCysLeuAsnProLeuLeuTYrAlaPheValGlyVal 370
Db 910 TCAGGCTTGGGCTACATGACACTGCTCTCAACCCGCTGCTATGCTTTGTAGGGGCTC 969
Oy 371 LysPheArgGlnArgMetTrpMetLeuLeuArgLeuGlyCysProAsnGlnArgGly 390
Db 970 AAGTTCCGGGAGCGGAGTGGATGCTGCTTGGCGCTGGGCTGGCCCAACGAGAGGG 1029
Oy 391 LeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGlnThrSerGlnAla 410
Db 1030 CTCACAGAGCAGACGATCGTCTTCCCGCGGATTCCTCTGCTAGACCTCAGAGGCC 1089
Oy 411 SerTYrSerGlyLeu 415
Db 1090 TCCTACTCGGCGCTTG 1104

RESULT 15
US-09-170-496C-19
; Sequence 19, Application US/09170496C
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496C
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496C-19

Alignment Scores:
Pred. No.: 5,36e-168 Length: 1107
Score: 1891.00 Matches: 364
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.73% Mismatches: 0
Query Match: 87.91% Indels: 0
DB: 15 Gaps: 0

US-09-101-518A-2 (1-415) x US-09-170-496C-19 (1-1107)
Oy 51 GlnValSerAspHisGlnValIleuAsnAspAlaGlnValAlaAlaLeuLeuGlnAsnPhe 70
Db 10 GAGGTGAGTGACCACTCAAGTCTAAATGAGCGCGAGGTTGGCCGCTCTGTGAGAACTTC 69
Oy 71 SerSerSerTYrAspTYrGlyGlnAsnGlnSerAspSerCysCysThrSerProPocYs 90
Db 70 AACTCTCTCTATGACTATGAGAGAAACGAGAGTGACTGCTGCTACTTCCTCCCGCCCTGC 129
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Oy 91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTYrSerLeuLeu 110
Db 130 CCACAGAGCTTAGCCTTAAGCTTCGACCGGCGCTTCTCTCCAGCCCTCTACAGCTCTC 189
Oy 111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgGlyThr 130
Db 190 TTTCTGCTGGGCGTGGGCAACGGCGGCGGCGCGCTGCTGGTGGTGGTGGTGGTGGTGG 249
Oy 131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
Db 250 GCCCTAGCAGCAGCAGCAGCAGCTTCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGG 309
Oy 151 LeuThrLeuProLeuTYrAlaValAlaAspAlaAlaValGlnTYrValPheGlySerGlyLeu 170
Db 310 CTGACACCTGCGCTGGGCGAGTGAGCGCTGCCGTCACTAGGAGGCTTTGGCTTGCGCTC 369
Oy 171 CysLYsValAlaGlyAlaLeuPheAsnIleAsnPheTYrAlaGlyAlaLeuLeuAla 190
Db 370 TGCAAAGTGGCAGAGTCCCTTTCACATCACTTCTACGCAAGAGCCCTCTGCTGGCC 429
Oy 191 CysIleSerPheAspArgTYrLeuAsnIleValIleAlaThrGlnLeuTYrArgArgGly 210
Db 430 TGCATACGCTTTGACCGCTACCTGAACATAGTTCAATGCCACCCAGCTCTACCGCGGGG 489
Oy 211 ProProAlaArgValThrLeuThrCysLeuAlaValTYrGlyLeuCysLeuLeuPheAla 230
Db 490 CCCCCGCGCGCGTACCCTCACTGCTGGCTGTGTGGGGGCTGCGCTTGGCTTTGGCC 549
Oy 231 LeuProAspPheIlePheLeuSerAlaHisHisAspGlnArgLeuAsnAlaThrHisCys 250
Db 550 CTCGCCAGCTTCACTCTCTGTCGGGCCACGAGAGAGAGCGGCTCAACCCACCACTGC 609
Oy 251 GlnTYrAsnPheProGlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGly 270
Db 610 CAAATACAACTTCCACAGAGTGGGCGCCAGCGCTCTGCGGCTGCTGAGCTGGTGGCTGC 669
Oy 271 PheLeuLeuProLeuLeuValMetalatYrCysTYrAlaHisIleLeuAlaValLeuLeu 290
Db 670 TTTCTGCTGCCCCCTGCTGGTCACTGGCTTACTGCTATGCCACATCCTGGCCGCTGCTG 729
Oy 291 ValSerArgGlyGlnArgArgLeuAlaMetArgLeuValValValValValValAla 310
Db 730 GTTTCAGAGGGGCGAGGGGCGCTGCGGCGCATGCGGCTGGTGGTGGTGGTGGTGGG 789
Oy 311 PheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAlaPheLeuMetAspLeu 330
Db 790 TTTGGCCCTGCTGCGACCCCTATACCTGCTGCTGGTGGTGGTGGTGGTGGTGGTGG 849
Oy 331 G1yAlaLeuAlaArgAsnCysGlyArgGlnSerArgValAlaPvalAlaLysSerValThr 350
Db 850 GCGGCTTGGCCCGCAACTGTCGCGCCAGAAAGCAGAGGTAGACGTGGCCAAAGTCGTCACC 909
Oy 351 SerGlyLeuGlyTYrMetHisCysCysLeuAsnProLeuLeuTYrAlaPheValGlyVal 370
Db 910 TCAGGCTTGGGCTACATGACACTGCTCTCAACCCGCTGCTATGCTTTGTAGGGGCTC 969
Oy 371 LysPheArgGlnArgMetTrpMetLeuLeuArgLeuGlyCysProAsnGlnArgGly 390
Db 970 AAGTTCCGGGAGCGGAGTGGATGCTGCTTGGCGCTGGGCTGGCCCAACGAGAGGG 1029
Oy 391 LeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGlnThrSerGlnAla 410
Db 1030 CTCACAGAGCAGACGATCGTCTTCCCGCGGATTCCTCTGCTAGACCTCAGAGGCC 1089
Oy 411 SerTYrSerGlyLeu 415
Db 1090 TCCTACTCGGCGCTTG 1104
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Search completed: November 2, 2002, 13:15:40
Job time : 2919 secs


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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-101-518a-2 (1-415) x US-09-101-518a-1 (1-1876)
OY 1 MetGluleuAArgLysTyrGlyProGlyAArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
Db 173 ATGGAGTTGAGGAAGTACGGCCCTGGAGAGACTGGCGGGAGACGTTATAGAGAGACTGCT 232
OY 21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
Db 233 CAGAGTAATATCACAGACATAATACAGCTCAATCACAAAAGATTCTCGCAGGCGCTTTAC 292
OY 41 ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
Db 293 ACAGGCCCTTCTCTCCCGCTTCCCGCTCACAGGTGAGTGAACACCAAGTGTAAATGAC 352
OY 61 AlaGluValAlaAlaLeuLeuGlnAsnPheSerSerSerTyrAspTyrGlyLysGlnGlu 80
Db 353 GCCGAGTTGGCCGCCCTCTGGAGAACTTCAGCTCTCTATAGACTATGAGAGAAAACGAG 412
OY 81 SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
Db 413 AGTGACTGCTGCTGTAACCTCCCGCCCTGCCACAGAGACTTCAGCTGAACCTGCACCGG 472
OY 101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGlyLeuLeuGlyAsnGlyAla 120
Db 473 GCCTTCCTGCGCCAGCCCTCTACAGCTCTCTTCTGCTGGGCTGCTGGGCAACGGCGG 532
OY 121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
Db 533 GTGGCAGCGCTGCTGCTGAGCGCGGACAGCCCTGAGAGACAGCAGCACTTCTGCTG 592
OY 141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuThrAlaValAspAla 160
Db 593 CACCTAGCTGTAGCAGACACGCTGCTGCTGAGACATGCCCTTGCGCACTGAGACGT 652
OY 161 AlaValGlnTrrPValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle 180
Db 653 GCCGTCCAGTGGGCTTGGCTGCTGCTGCTGCAAAAGTGGCGCCCTCTTCAACATC 712
OY 181 AsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
Db 713 AACTTCTACGCGAGAGACCTCTGCTGCTGCTGATCAGCTTGCACGCTTGAACATA 772
OY 201 ValHisAlaThrGlnLeuTyrArgArgLysProProAlaArgValThrLeuThrCysLeu 220
Db 773 GTTCATGCCACCCAGCTCTACCGCGGGGGGCCCGCGCGCTGACCTCTACCTGCGCTG 832
OY 221 AlaValTrrPglyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
Db 833 GCTGCTCGGGGGCTGCTGCTGCTTTCGCCCTCCAGACTTCATCTTCTCTGCGGCCAC 892
OY 241 HisAspGluAArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr 260
Db 893 CAGCAGCGAGCGCTCAACGCCACCTGACCAATACAACTTCCACAGGTGGCGCGCAG 952
OY 261 AlaLeuAArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
Db 953 GCTTGGCGGGTCTCAGCTGCTGCTGCTGCTTTCGCTGCTGCTGCTGCTGCTGCTGCT 1012
OY 281 CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla 300
Db 1013 TGCTATGCCACATCTCTGCGCTGCTGCTGCTTTCAGAGGGGCGACGGCGCTGCGGGCC 1072
OY 301 MetArgLeuValValValValValAlaPheAlaLeuCysTrrPThrProTyrHisLeu 320
Db 1073 ATGCGGCTGGTGGTGGTGGTGGTGGTGGCTTTCCTGCTGAGACCCCTATACACCTG 1132
OY 321 ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlu 340
Db 1133 GTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1192
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OY 341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
Db 1193 AGCAGGTAGACGTGGCCCAAGTGGCTACCTAGGCTCGGGCTATCATGCACTGCGCTC 1252
OY 361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluAArgMetTrrPMetLeuLeu 380
Db 1253 AACCCGCTGCTCTATGACCTTTCCTAGGGGTCAAGTTCCGGAGCGGATGCTGATGCTGCT 1312
OY 381 LeuArgLeuGlyCysProAsnGlnAArgGlyLeuGlnAArgGlnProSerSerArgArg 400
Db 1313 TTGCGCTTGGCTGCCCAACAGAGAGGGCTCCAGAGCAAGCTTCTTCCGCGG 1372
OY 401 AspSerSerTrrPserGluThrSerGluAlaSerTyrSerGlyLeu 415
Db 1373 GATTATCTGCTGTGAGACCTCAGAGCGCTCTCTAGTGGGCTTG 1417

RESULT 2
US-10-106-698-2125
; Sequence 2125, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106, 698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157, 137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163, 280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 2125
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-2125

Alignment Scores:
Pred. No.: 4,53e-189 Length: 1877
Score: 2136.00 Matches: 413
Percent Similarity: 99.52% Conservative: 0
Best Local Similarity: 99.52% Mismatches: 2
Query Match: 99.30% Indels: 0
Gaps: 0

US-09-101-518a-2 (1-415) x US-10-106-698-2125 (1-1877)
OY 1 MetGluleuAArgLysTyrGlyProGlyAArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
Db 173 ATGGAGTTGAGGAAGTACGGCCCTGGAGAGACTGGCGGGAGACGTTATAGAGAGACTGCT 232
OY 21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
Db 233 CAGAGTAATATCACAGACATAATACAGCTCAATCACAAAAGATTCTCGCAGGCGCTTTAC 292
OY 41 ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
Db 293 ACAGGCCCTTCTCTCCCGCTTCCCGCTCACAGGTGAGTGAACACCAAGTGTAAATGAC 352
OY 61 AlaGluValAlaAlaLeuLeuGlnAsnPheSerSerSerTyrAspTyrGlyLysGlnGlu 80
Db 353 GCCGAGTTGGCCGCCCTCTGGAGAACTTCAGCTCTCTATAGACTATGAGAGAAAACGAG 412
OY 81 SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
Db 413 AGTGAMTGTGCTGTAACCTCCCGCCCTGCCACAGAGACTTCAGCTGAACCTGCACCGG 472
OY 101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGlyLeuLeuGlyAsnGlyAla 120
Db 473 GCCTTCTGCGCCAGCCCTCAGACGCTCTCTTTCGCTGCGGCTGCTGCGCAACGGCGG 532
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QY 121 ValAlaAlaValLeuLeuSerArgArghrAlaLeuSerSerThrAspThrPheLeuLeu 140
 |||||
 Db 533 GTGGCAGCCGCTGCTGACGCCGGGAGCAGCCCTGACACAGCCAGACACTTCTGCTTC 592
 QY 141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuThrPAlaValaAspAla 160
 |||||
 Db 593 CACCTACGCTGACGACACACRGTGCTGGTGCAGACACTGCCGCTCTGGGAGTGGAGCT 652
 QY 161 AlaValGlnTrpValPheGlySerGlyLeuGlySlyValAlaGlyAlaLeuPheAsnIle 180
 |||||
 Db 653 GCCGTCGAGTGGGCTCTTGGGCTCTGGCTTCGCAAAAGGGAGGAGGCCCTTTCACACATC 712
 QY 181 AsnPheTrpAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
 |||||
 Db 713 AACCTTCAGCAGAGAGGCCCTCTGCTGGCTGCATCAGACTTTGACCGCTACTGACACTA 772
 QY 201 ValHisAlaThrGlnLeuLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeu 220
 |||||
 Db 773 GTTCATGCCACACAGACTTCACCGCCGGGGGGCCCCCGGCCCGTGGACCTCACCTGCTG 832
 QY 221 AlaValTrpGlyLeuGlyLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
 |||||
 Db 833 GCTGCTCGGGGCTCTGCTGCTCTTTCCCTCCAGACTTCATCTTCCTCTGCGGCCAC 892
 QY 241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValAlaGlyThr 260
 |||||
 Db 893 CACGACGAGGCCCTCAAGCCACCCACCTGCCAATACACTTCCACAGAGTGGCGGCACG 952
 QY 261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
 |||||
 Db 953 GCTCTCGGGGCTGCTGACGCTGGTGGCTCTTCTGCTGCGCCCTGCTGTCATGGCTTAC 1012
 QY 281 CysTrpAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla 300
 |||||
 Db 1013 TGCATGCCCCACATCTCGGCGGCTGCTGCTGGTTCACAGGGGCCACGGGCGCTGGGGGCC 1072
 QY 301 MetArgLeuValAlaValAlaValAlaPheAlaLeuCysTrpThrProTyrHisLeu 320
 |||||
 Db 1073 ATGGGGCTGGTGGTGGTGGTGGTGGCTTTGGCCCTCTGCTGACGCCCTATCACCTG 1132
 QY 321 ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlu 340
 |||||
 Db 1133 GTGGTGGCTGGGAGCATCTCATGAGACTGGCGGCTTTGGCCCGCACTGGTGGCCGAATA 1192
 QY 341 SerArgValaAspValAlaIAspSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
 |||||
 Db 1193 AGCAGGCTAGACGCGGCCAATCGCTCACCTGACGCCCTGAGCTCATCTGCTGCTC 1252
 QY 361 AsnProLeuLeuTyrAlaPheValGlyValAlaLysPheArgGluArgMetTrpMetLeuLeu 380
 |||||
 Db 1253 AACCCGCTGCTCATGCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGATGCTGCTC 1312
 QY 381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerArgArg 400
 |||||
 Db 1313 TTGGCGCTGGGCTCCCCAACACAGAGGGCTCCACAGAGGCCCATCTCTTCCCGCCGG 1372
 QY 401 AspSerSerTrpSerGlnThrSerGlnAlaSerTyrSerGlyLeu 415
 |||||
 Db 1373 GATTCACTCTGCTGTGAGACTCTCAGAGGCTCTCTACTCGGAGCTTG 1417
 RESULT 3
 PCT-US02-30182-962
 : Sequence 962, Application PC/TUS0230182
 : GENERAL INFORMATION:
 : APPLICANT: Gene Logic, Inc.
 : APPLICANT: Munger, William E.
 : APPLICANT: Kulkarl, Prakash
 : APPLICANT: Getzenberg, Robert H.
 : APPLICANT: Maga, Iwao
 : APPLICANT: Yamamoto, Jun
 : TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
 : TITLE OF INVENTION: Gene Expression Profiles

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FILE REFERENCE: 44921-5029-01-WO
CURRENT APPLICATION NUMBER: PCT/US02/30182
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: 09/960,706
PRIOR FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 962
LENGTH: 1293
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. U32674
PCT-US02-30182-962

Alignment Scores:
Pred. No.: 2.08e-183 Length: 1293
Score: 2073.00 Matches: 400
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.37% Indels: 0
DB: 2 Gaps: 0

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US-09-101-518A-2 (1-415) x PCT-US02-30182-962 (1-1293)

QY	16	IleelgylalalalaglnserlysserclnThlyssersperllThlysglupl	35
Db	1	ATAGAGAGAGCTGCTCAGAGTAATATCAACACTAATACACTATCAACAAAGATTG	60
QY	36	LeuProglyLeuYrThrAlaProSerSerProphabProbrosclnValSeraspHis	55
Db	61	CTCGACGAGCCCTTTCACAGGCCCTTCCTCCCTCCGCTCCGCTCACAGGTGATGCAC	120
QY	56	GlnValLeuasnAspAlaGluValAlaAlaLeuLengLunAsnpheserSertYrAsp	75
Db	121	CAAGTCTTAATGACGCCGAGATTGCCGCCCTCTGAGACTTCAGCTTCTTAATGAC	180
QY	76	TyrIglyLunsglnSeraspSerCysCysThrSerProCysbProGlnAspPheSer	95
Db	181	TATGAGAGAAAACGAGAGTGAAGCTGTCGTACCTCCCGCCGCTCCACAGGACTTCAC	240
QY	96	LeuasnPhespAspAlaAlaPheLeuProAlaLeuYrSerLeuLeuPheLeuLengLyu	115
Db	241	CTGAAGCTTCGACGGGGCTTCTGTCACGCCCTCTACAGCTCTCTTCTGCTGGGGCTG	300
QY	116	LeuLysnGlyAlaValAlaAlaValLeuLeuSerArgYrThrAlaLeuSerSertThr	135
Db	301	CTGGGCAACGGCCGGGTGGCAGCGTGTCTGTAGCCGGCGGACACCTCGAGACACAC	360
QY	136	AspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeu	155
Db	361	GACACCTTCCTGCTCCACCAAGCTGTATGACAGACACCTGTGTGCTGACACTGCCGCTC	420
QY	156	TyrAlaValAspAlaAlaValAlaGlnTyrValPheGlySerGlyLeuCysLysValAlaGly	175
Db	421	TGGGCACTGAGACGCTGCCGCTCCAGATGGGTCTTTGGCTGTGGCTCTGCAAAAGTGCAGGT	480
QY	176	AlaLeuPheasnIleasnPheYrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheasp	195
Db	481	GCCCTCTTCAACAATCAACTCTTACGCGAGAGGCCCTCTGCTGGCTGCATACACTTTGAC	540
QY	196	ArgYrLeuasnIleValIleAlaThrGlnLeuYrArgArgGlyProProAlaArgVal	215
Db	541	CGCTACTCGAACAATGATTCATATGCCACCACTCTTACCGCGGGGGGCCCCCGCCGCGTG	600
QY	216	ThrLeuThrCysLeuAlaValTyrGlyLeuCysLeuLeuPheAlaLeuProAspPheIle	235
Db	601	ACCTCACTACGTGCGGTGCTGGGGGCTCTGCTGCTTTTGGCCCTCCACAGACTTCAC	660
QY	236	PheLeuSerAlaHisHisAspGluThrGluLeuAsnAlaThrHisCysGlnTyrAsnPhePro	255
Db	661	TTTCTGTGTGGGCCCAACGACGAGAGCGCTCTACAGCCACACCTGCGCAATACACTTCCCA	720

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Oy 256 GlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 275
Db 721 CAGGTGGGCGGCGAGGCTCTGGCGGTGCTGCAGCTGGTGGCTGGCTTCTGTCGCCCTG 780
Oy 276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgIlyGln 295
Db 781 CTGGTCATGGCCCTACTGCTATGCCCCACATCCGCGCGCTGCTGTTCCAGGGGCGCAG 840
Oy 296 ArgArgLeuArgAlaMetArgLeuValValValAlaValAlaPheAlaLeuCysTrp 315
Db 841 CGGCGCCCTGGCGGCGCATGCGGCTGGTGGTGGTGGTGGTGGCTTGGCTTGGCTGG 900
Oy 316 ThrProTyrHisLeuValValLeuValAlaPheLeuMetAspLeuGlyAlaLeuAlaArg 335
Db 901 ACCCCCTATACACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
Oy 336 AsnGlyGlyArgGlnSerArgValAlaAlaLysSerValThrSerGlyLeuGlyIlyr 355
Db 961 AACTGTGGCCGAGAAAGAGGAGGTAGACGTGGCCAAAGTCGTCACCTCAGGCGCTG 1020
Oy 356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValIlyPheArgGlyIlyr 375
Db 1021 ATGCACCTGCTGCTCAACCCGCTGCTATGCTTGTAGGGGTCAAGTTCGGGAGCGG 1080
Oy 376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgInPro 395
Db 1081 ATGTGATGCTGCTCTTGGCGCTGGGCTGCCCAACAGAGGCGCTCCAGAGCGACCA 1140
Oy 396 SerSerSerArgArgAspSerSerTrpSerGlnTrpSerGlnAlaSerTyrSerGlyLeu 415
Db 1141 TCGTCTTCCCGGGGATTCACTCTGCTGTGAGACCTCAGAGCGCTCCACTACGCGGCTTG 1200

RESULT 4
PCT-US02-18947-620
: Sequence 620, Application PC/TUS0218947
: GENERAL INFORMATION:
: APPLICANT: Kosetta Pharmaceuticals
: TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
: FILE REFERENCE: 9301-175-228
: CURRENT APPLICATION NUMBER: PCT/US02/18947
: CURRENT FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: 60/380,770
: PRIOR FILING DATE: 2002-05-14
: NUMBER OF SEQ ID NOS: 2699
: SEQ ID NO 620
: LENGTH: 1670
: TYPE: DNA
: ORGANISM: Homo sapiens
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: NM_001504
: DATABASE ENTRY DATE: 2001-06-18
: PCT-US02-18947-620

Alignment Scores:
Pred. No.: 7.04e-167 Length: 1670
Score: 1897.00 Matches: 369
Percent Similarity: 97.63% Conservative: 1
Best Local Similarity: 97.36% Mismatches: 5
Query Match: 88.19% Indels: 4
DB: 2 Gaps: 1

US-09-101-518a-2 (1-415) x PCT-US02-18947-620 (1-1670)
Oy 41 ThrAlaProSer-----SerProPheProProSerGlnValSerAspHisGln 56
Db 36 ACACCAACCAGCAGCAGCAAGCAGCCAGCCAGCTGCTTGAAGTGAGTACACCA 95
Oy 57 ValLeuAsnAspAlaGlyValAlaAlaLeuLeuGlnAsnPheSerSerSerTyrAspTyr 76
Db 96 GTGCTAAATGAGCGCGAGGTGGCGCCCTCCGAGAACTTCAGCTTCCATGACTAT 155
Oy 77 GlyIlyuAsnGlnSerAspSerCysThrSerProProCysProGlnAspPheSerLeu 96
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Db 156 GGAGAAAAGAGAGTACTGCTGCTGACTCTCCCGCCCTGCGCCACAGACTTCAGCCTG 215
Oy 97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuGlyLeuLeu 116
Db 216 AACTTGAACGGGCGCTTCTGCGAGCCCTCTACAGCCTCTCTCTTCTGCTGGGCTGCTG 275
Oy 117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
Db 276 GGCAACGGGCGGCTGGCGAGCGGTGCTGAGCGCGGAGACGCCCTGACAGCAGCAGAC 335
Oy 137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
Db 336 ACCCTCTGCTCTCCACTGACTGTACAGACAGCGCTGTGGCTGTGACACTGCGCTGCG 395
Oy 157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysIlyValAlaGlyAla 176
Db 396 GAGTGAAGCGCTGGCGTCCAGTGGGTCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 455
Oy 177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
Db 456 CTCTTCACATCACTTCTACGCAAGAGCCCTCGCTGGCTGCTGATCAGCTTTGACCGC 515
Oy 197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProAlaArgValThr 216
Db 516 TACCTGAACATAGTTCATGCCACCCAGCTTACCGCGGGGCGCCCGCGCGCTGAC 575
Oy 217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheLePhe 236
Db 576 CTCACCTGCTGGGCTGTGTGGGGCTGTGCTGCTTGTGGCTTCCAGACTCTCACTTTC 635
Oy 237 LeuSerAlaHisHisAspGlnArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
Db 636 CTGTGGCGCCACACAGAGAGGCGCTCAAGCGCACCCACTGCGATACACTTCCACAG 695
Oy 257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
Db 696 GTGGGCGCCAGCGCTCTCGGGTGTGCTGACGTGGGCTGTGCTCTGCTGCTGCTGCTG 755
Oy 277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyValArg 296
Db 756 GTCATGGCTTACTGCTATGCCCCACATCTCGGCGGTGCTGCTGCTGCTGCTGCTGCTG 815
Oy 297 ArgLeuArgAlaMetArgLeuValValValValValAlaAlaPheAlaLeuCysTrpThr 316
Db 816 CGCGTGGGCGCATGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 875
Oy 317 ProTyrHisLeuValValLeuValAlaPheLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
Db 876 CCGTATCACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 935
Oy 337 CysGlyArgGlnSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
Db 936 TGTGGCCGAGAAAGCAGGCTGACGTGGCCANAGTGGTACCTCAGGCGCTGAGCTACATG 995
Oy 357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValIlyPheArgGlyIlyrMet 376
Db 996 CACTGCTGCTCAACCCGCTGCTATGCTCTTGTAGGGGTCAAGTTCGGGAGGAGATG 1055
Oy 377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgInProSer 396
Db 1056 TGGATGCTGCTCTTGGCGCTGGGCTGGCCCAACAGAGAGGCTTCCAGAGCAGCAGCAT 1115
Oy 397 SerSerArgArgAspSerSerTrpSerGlnTrpSerGlnAlaSerTyrSerGlyLeu 415
Db 1116 TCTTCCCGCGGGATTCACTCTGCTGTGAGACTTCAGAGGCTCTACTCGGGCTTG 1172

RESULT 5
PCT-US02-25766-2790
: Sequence 2790, Application PC/TUS0225766
: GENERAL INFORMATION:
: APPLICANT: GENE LOGIC, INC.
: APPLICANT: MUNGER, William E
: APPLICANT: FAULK, Ronald
```

```
; APPLICANT: SUN, Hongwei
; APPLICANT: SASAI, Hitoshi
; APPLICANT: WAGA, Iwao
; APPLICANT: YAMAMOTO, Jun
; TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
; FILE REFERENCE: 44921-5068-WO
; CURRENT APPLICATION NUMBER: PCT/US02/25766
; PCT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/311,837
; PRIORITY FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 13946
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 2790
; LENGTH: 1670
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. X95876
PCT-US02-25766-2790

Alignment Scores:
Pred. No.: 7,04e-167 Length: 1670
Score: 1897.00 Matches: 369
Percent Similarity: 97.63% Conservative: 1
Best Local Similarity: 97.36% Mismatches: 5
Query Match: 88.19% Indels: 4
DB: 2 Gaps: 1

US-09-101-518a-2 (1-415) x PCT-US02-25766-2790 (1-1670)
QY 41 ThrAlaProSer-----SerPropeProProSerGlnValSerAspHisGln 56
Db 36 ACACACCCAGAGAGCCAGAGCAGCAGCCAGCCAGCCAGCTTCCTTGTAGAGTGCATCACCACCA 95
QY 57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnAspSerSerSerTyrAspTyr 76
Db 96 GTGCTAAATGAGCGCCGAGCTTCCCTCCCTCGAGAACTTCAGCTCTCTATGACTAT 155
QY 77 GlyGluAsnGluSerAspSerCysThrSerProProCysProGlnAspHisSerLeu 96
Db 156 GGAGAAACGAGAGTACTCGTGTACTCTCCGCCCTCCAGAGACTTCAGACCTG 215
QY 97 AsnAspAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
Db 216 AACTTCGACCGGGCTTCCTGCACCCCTTCACCTCTCTTCTGCTGGGCTGCTG 275
QY 117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgTyrAlaLeuSerSerThrAsp 136
Db 276 GGCAACGGCGGGGTGGCAGCCGCTGCTGAGCCGGGAGACGCCCTGAGCAGCACCGAC 335
QY 137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTyr 156
Db 336 ACCTTCCTGCTCCACCTGCTGCTAGACAGACGCTGCTGCTGCTGCTGCTGCTGCTG 395
QY 157 AlaValAspAlaAlaValAlaGlnTyrValPheGlySerGlyLeuCysLysValAlaGlyAla 176
Db 396 GCAGTGGAGCGGCGGCTGCAGTGGGCTTTGGCTGCTGCGCTTCGCAAGTGGCAGTGGC 455
QY 177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuAlaCysIleSerPheAspArg 196
Db 456 CTTTCACATCACTACCTTCTAGCAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 515
QY 197 TyrLeuAsnIleValAlaIleAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
Db 516 TACCTGAACATATGTTCAATGCCACCCAGCTTACCCCGGGGGCCCCCGGCGCTGAC 575
QY 217 LeuThrCysLeuAlaValTyrGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
Db 576 CTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 635
QY 237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
Db 636 CTGTGCGCCACACGAGAGAGGCTTCAACGCCACCTGCTCAATATACACTTCCACAG 695
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QY 257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
Db 696 GTGGGCCGACAGGCTTGGCGGGCTGCGACGCTGGTGGCTGCTTTCCTGCCCTGCTG 755
QY 277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
Db 756 GTCATGGCTTACGCTATGCCACATCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 815
QY 297 ArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTyrPhe 316
Db 816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 875
QY 317 ProTyrHisLeuValValValValValValValValValValValValValValValVal 336
Db 876 CCTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 935
QY 337 CysGlyArgGluSerArgValAlaValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
Db 936 TGTGGCCGAGAAAGCAGGCTAGACGTGGCCAGTGGCTACCTCAGCCCTGGGCTACATG 995
QY 357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
Db 996 CACTGCTGCTCAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1055
QY 377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
Db 1056 TGGATGCTGCTCTTGGCGCTGGGCTGCCCAACACAGAGGGCTCCAGAGGCACCATCG 1115
QY 397 SerSerArgArgAspSerSerTyrPheSerGluThrSerGluAlaSerTyrSerGlyLeu 415
Db 1116 TCTTCCCGCGGGATTTCATCCTGCTGTGAGACTCAGAGGCTCTCTACTGGGCTTG 1172

RESULT 6
US-10-172-118-620
; Sequence 620, Application US/10172118
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; PRIORITY FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIORITY FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 620
; LENGTH: 1670
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001504
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-620

Alignment Scores:
Pred. No.: 7,04e-167 Length: 1670
Score: 1897.00 Matches: 369
Percent Similarity: 97.63% Conservative: 1
Best Local Similarity: 97.36% Mismatches: 5
Query Match: 88.19% Indels: 4
DB: 12 Gaps: 1

US-09-101-518a-2 (1-415) x US-10-172-118-620 (1-1670)
QY 41 ThrAlaProSer-----SerPropeProProSerGlnValSerAspHisGln 56
Db 111 TCTTCCCGCGGGATTTCATCCTGCTGTGAGACTCAGAGGCTCTCTACTGGGCTTG 1172
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Db 36 ACACACCCAGCAGCCAGACACCCAGCCAGCCAGCTTGGAGGTGAGTGACCAACCA 95
QY 57 ValLeuAsnAspAlaGluValAlaAlaLeuGluAsnPhseSerSertYrAspTyr 76
Db 96 GTGCTAAATGAGCCGAGGTTGCCCTCTGGAGAACTTGACCTTCTGTAAT 155
QY 77 GlyGluAsnGluSerAspSerCysCysThrSerProCysProGlnAspPheSerLeu 96
Db 156 GGAGAAAGAGAGTGTACTGTGCTGTACCTCCCGCCCTGGCCACAGACTTCAGCCTG 215
QY 97 AsnPhseAspArgAlaPheLeuProAlaLeuTyrSerLeuPheLeuGlyLeuLeu 116
Db 216 AACTTGACCGGGGCTTCTGGCCAGCCCTCTACAGCCTCTTCTGTGGGGCTGTG 275
QY 117 GlysAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSertHrasp 136
Db 276 GGCAACGGGGCGGTGGACCCGTGCTGAGCCGGGACACCCCTTGAGCAGACCCGAC 335
QY 137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTyr 156
Db 336 AACTTCTGCTCCACCTGACTGAGCAGACAGCCTGCTGTGCTGACACTGGCCGCTCTGG 395
QY 157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
Db 396 GGAGTGGAGCGCTGCGTCCAGTGGGCTTTGGCTGTGGCTTGCAGAGTGGAGGTGCC 455
QY 177 LeuPheAsnIleAsnPhetYrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
Db 456 CTCTTCAACATCATCACTTTCACGAGAGAGGCCCTCTGCTGGCCGCACTGACCTTTGACCCG 515
QY 197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
Db 516 TACCTGGAACATGATGTCATGCCACCCAGCTCTACCGCGGGGGGCCCGCCGCTGTGACC 575
QY 217 LeuThrCysLeuAlaValAlaTrpGlyLeuCysLeuPheLeuProAspPheIlePhe 236
Db 576 CTCACCTGCTGCTGCTGTGGGGGCTCTGCTGCTTTTGCCCTCCAGACTTCATCTTC 635
QY 237 LeuSerAlaHisAspGlnArgLeuAsnAlaThrHisCysGlnTrpYrAsnPhseProGln 256
Db 636 CTGTGGGCCACACAGCAGAGCGGCTCAAGCCCACTGGCAATACAACTTCCACAG 695
QY 257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
Db 696 GTGGGGCCGACGCTCTGGGGGTGCTGACGTGCTGTGCTGTGCTGCTGCTGCTGCTG 755
QY 277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
Db 756 GTCATGGCTTACTGTATGCCCCACATCTGGCCGTGCTGTGTTCCAGGGGCCAGCGG 815
QY 297 ArgLeuArgAlaMetArgLeuValValAlaValAlaPheAlaLeuCysTrpThr 316
Db 816 CGCCTGCGGGCCATGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 875
QY 317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
Db 876 CCTATACACTGTGTGTGTGGTGGACATCTCATGACCTGGGCCCTTGTGGCCCAAC 935
QY 337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
Db 936 TGTGGCCGGAAGAGAGGTAGTGGCCAAAGTGGTCACTCAGGCGCTGGGCTACATG 995
QY 357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGlnArgMet 376
Db 996 CACTGTGCTCAACCGGTGCTATGCTTGTATGGGGTCAAGTCCGGAGGCGGATG 1055
QY 377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
Db 1056 TGGATGCTGCTCTTGGCTGGGCTGCCCAACACAGAGGGGCTCCAGAGGACGACATCG 1115
QY 397 SerSerArgArgAspSerSertTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
Db 1116 TCTTCCCGCGGGATTCACTGTGGTCTGAGACCTCAGAGGCGCTCTCACTCGGGCTTGG 1172

RESULT 7
US-10-251-686-1
; Sequence 1, Application us/10251686
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Margel
; Moser, Bernhard
; Qin, Shixin
; Mackay, Charles R.
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
; ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/251,686
; FILING DATE: 20-Sep-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,839
; FILING DATE: 31-MAR-1997
; APPLICATION NUMBER: US 08/709,838
; FILING DATE: 10-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David F.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: TK196-01A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1670 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 69..1172
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-251-686-1

Alignment Scores:
Pred. No.: 7,04e-167 Length: 1670
Score: 1897.00 Matches: 369
Percent Similarity: 97.63% Conservative: 1
Best Local Similarity: 97.36% Mismatches: 5
Query Match: 88.19% Indels: 4
Gaps: 1

US-09-101-518a-2 (1-415) x US-10-251-686-1 (1-1670)
QY 41 ThrAlaProSer-----SerProPheProSerGlnValSerAspHisGln 56
Db 36 ACACACCCAGCAGCCAGACACCCAGCCAGCATGTGCTGAGGTGAGTGACCAACCA 95
QY 57 ValLeuAsnAspAlaGluValAlaAlaLeuGluAsnPhseSerSertYrAspTyr 76
Db 96 GTGCTAAATGAGCCGAGGTTGCCCTCTGGAGAACTTGACCTTCTGTAAT 155
QY 77 GlyGluAsnGluSerAspSerCysCysThrSerProCysProGlnAspPheSerLeu 96
Db 156 GGAGAAAGAGAGTGTACTGTGCTGTACCTCCCGCCCTGGCCACAGACTTCAGCCTG 215

	:	TITLE OF INVENTION:	Protein-Coupled
	:	TITLE OF INVENTION:	Receptors
	:	FILE REFERENCE:	AREN-0040
	:	CURRENT APPLICATION NUMBER:	US/10/251,385
	:	CURRENT FILING DATE:	2002-09-20
	:	PRIOR APPLICATION NUMBER:	US/09/170,496
	:	PRIOR FILING DATE:	1998-10-13
	:	NUMBER OF SEQ ID NOS:	294
	:	SOFTWARE:	PatentIn version 3.1
	:	SEQ ID NO 19	
	:	LENGTH:	1107
	:	TYPE:	DNA
	:	ORGANISM:	Homo sapiens
	:	US-10-251-385-19	
	:	Alignment Scores:	
	:	Pred. No.:	1,52e-166
	:	Score:	1891.00
	:	Percent Similarity:	100.00%
	:	Best Local Similarity:	99.73%
	:	Query Match:	87.91%
	:	DB:	11 gaps: 0
US-09-101-518A-2 (1-415) x US-10-251-385-19 (1-1107)			
Oy	51	GlnValSerAspHisGlnIvalLeuAsnAspAlaGluValAlaAlaLeuGluAsnPhe	70
	::::		
Db	10	GAGGGACGTGAACCAACAGTCTTAATATACCCCGACAGTGCGGCCCTCTCGAACAATTG	69
Oy	71	SerSerSerTYRASPTRYGLYGLUASNGLUSeRSASPsercysCYTHrSerProCys	90
Db	70	AGCTCTTCCTATGACTATAGGAAACAGACGATGACTGTGCTTACTCTCCCGCCCTGC	129
Oy	91	ProGlnAspPheSerLeuAsnPhaspargylAphLeuProAlaLeuTYRSerLeuLeu	110
Db	130	CCACAGGACTTCAGCCTTAACATTGACCGGGCTTCCTGCCAGCCCTCTACAGCCTCTC	188
Oy	111	PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr	130
Db	190	TTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCACCGCTGCTGAGCGCGGAC	249
Oy	131	AlaLeuSerSerThrAspThrPheLeuLeuHISLeuAlaValAlaAspThrLeuLeuVal	150
Db	250	GCCCGTAGACAGACCGAACCTTCCTGCTCCACTTACTGTAGCAGACAGCTGTCTGTG	309
Oy	151	LeuThrLeuProLeuTrpAlaValAlaAspAlaAlaValGlnTrpValPheGlySergLYleu	170
Db	310	CTGACACGCGCGCTCTGGGCAAGTGAGCGCTGCCCTCCAGTGGCTTTGGCTCTGGGCTC	368
Oy	171	CysLYSValAlaGlyAlaLeuPheAsnLLeasnPheTYRAlaGlyAlaLeuLeuAla	190
Db	370	TGCAAAAGTGGAGGCGCCCTCTCAACATCAACTTCAACGAGGAGGCCCTCTGCTGGCC	429
Oy	191	CysLieserPheAspARGTYRLeuAsnLLeaHISLarThrgLnLeuTYRARGArgLY	210
Db	430	TGCATCAGCTTTGACCGCTTACTTGAACATAATTATGTCACACCAAGCTCTACCGCGGGGG	488
Oy	211	ProProAlaArgValThrLeuThrCysLeuAlaValATrpGlyLeuCysLeuLeuPheAla	230
Db	490	CCCCGGCGCCCGTAGACCTCATCGCTGCTGCTGTGGGGGCTCTGCTGCTTTTGGCC	549
Oy	231	LeuProAspPheIlePheLeuSerAlaHISLHSAspGLuarGluAsnAlaThrHIScys	250
Db	550	CTCCACAGCTTCATCTCTCTCTGTGGCCACACACAGCAGCGCCCAACGCCACCCACTGC	609
Oy	251	GlnTYRAsnPheProGlnValGlyARGThrAlaLeuArgValLeuGlnLeuValAlaGly	270
Db	610	CAATACACACTTCCCACAGGTGGCGCCGACGGCTTGGGGGTGCTGACGTGTGGTGGCGC	669
Oy	271	PheLeuLeuProLeuLeuValMetAlaTYRCysTYRAlaHISLLeuAlaValLeuLeu	290
Db	670	TTTTCTGCTGGCCCTGCTGTGTCATGCGCTACTGCTATGCTCCACATCTCGCGGCTGTGCTG	729


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; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1409
; LENGTH: 34570
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(448)
; OTHER INFORMATION: "n" at positions 1 thru 448 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6032)..(6550)
; OTHER INFORMATION: "n" at positions 6032 thru 6550 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (29960)..(29979)
; OTHER INFORMATION: "n" at positions 29960 thru 29979 can be any base
US-10-035-832-1409

Alignment Scores:
Pred. No.: 6 446-49 Length: 34570
Score: 648.00 Matches: 157
Percent Similarity: 52.88% Conservative: 63
Best Local Similarity: 37.74% Mismatches: 166
Query Match: 30.13% Indels: 30
DB: 13 Gaps: 9

US-09-101-518a-2 (1-415) x US-10-035-832-1409 (1-34570)
QY 4 ArgLysTYrGLyProGLyArgLeuAlaGLyThrValILleGLyAlaAlaInserLys 23
   ::::::::::: |||||
DB 21978 AAAAAGCATTAAGCTGGAGG---ACAGGAAACCTCAGAGTGCGACCTTCCTCAGAG 22034
QY 24 SerGlnThrLysSerAspSerIleThrLysGluPhelLeuProGLyLeuTYrThrAlaPro 43
   :::::
DB 22035 GAAAAAAGAGAGAGAGAGAGAGAGAGAGAGATAT-----GCTATCTCTTTTCAT 22085
QY 44 SerSerProPhaProProSerGlnValSerAspHisGlnValLeuAsnSprAlaGluVal 63
   ||| ||| |||
DB 22086 TTCTCTTTCTTTTGGCTTACAGTACAGAA-----22118
QY 64 AlaAlaLeuGlnAsnPheserSerTYrAspTYrGlyGlnAsnGlnSerAspSer 83
   ||| :::::::::::
DB 22119 -----CTGGCCTTCTACAGTACAGCAGGAGATTCCCTACAGGACGATACCTTC 22169
QY 84 CysCysThrSerProProCysProGlnAspPheserLeuAsnPhesAspAlaPhelLeu 103
   ||| |||
DB 22170 TCTCTTAC-----GTCGAGGAGCCTTACTGACGCTCTTTTAAGCGGTATTCATG 22220
QY 104 ProAlaLeuTYrSerLeuLeuPhelLeuGlyLeuGlyValAsnGlyAlaValAlaAla 123
   ||| |||||
DB 22221 CCTGGGCTTACAGCTCATCTTCTCTGGGTATGATGGAAACATCCTGGGTGCTGA 22280
QY 124 ValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPhelLeuHisLeuAla 143
   ::::: |||
DB 22281 ATCTGGAGAGCAGCAGCAGCAGCAGCTGAGCTCAGCAGGACCTCTGTTCCACCTCGCA 22340
QY 144 ValAlaAspThrLeuLeuValLeuThrLeuProLeuThrAlaValAlaValAlaGln 163
   ||||| |||||
DB 22341 GTAGCGGACCTTCTCTTACTTCTTACCTCTTTTGACAGTGCGGCGGCTCTGCGGT 22400
QY 164 TrpValAlaPheGLySerGLyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPhetYr 183
   ||||| ||::: |||||
DB 22401 TGGGTCTTAGGACCTTCTCTTGCAAAACTGTGATGCTCTGACAAAGATTCATTTCTAC 22460
QY 184 AlaGlyAlaLeuLeuAlaCysIleSerPheAspArgTYrLeuAsnIleValHisAla 203
   ::::: |||||

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DB 22461 TGCAGACCGCTGCTGGCTGATAGCTGTAGACCGGATACCATGTCATAGCT 22520
QY 204 ThrGlnLeuTYrArgArgGLyProProAlaArgValThrLeuThrCysLeuAlaValTrp 223
   |||||
DB 22521 GTTCAGCGCTACCGCGCGCTGACCTCTCCATCCATCCATCCATCCATCCATCCAT 22580
QY 224 GlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAla-----His 240
   |||||
DB 22581 CTGGCGGCTTCTCTGCTTACCGGAACTCTCTTTTCCCAAGGTGGCCAACTCAT 22640
QY 241 HisAspGlnArgLeuAsnAlaThrHisCysGlnTYrAsnPhelProGlnValGlyArgThr 260
   ::::: |||
DB 22641 AACACGACCTCTTA-----CCACAGTGCACCTTCTCCACAGGAAAAAGAGGAAACT 22694
QY 261 -----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuProLeuLeu 276
   ||| |||
DB 22695 AGAGCTGTTCACCTCCCTTTCTCTTACACATCGGGGGCTCTTACACGATGCTT 22754
QY 277 ValMetAlaTYrCysTYrAlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGln 295
   |||||
DB 22755 GTGATGGATGTGTTRACGTGGGCTGTGTCACAGGCTACTGCAAGCCCGGCGCT 22814
QY 296 ArgArgLeuArgAlaMetArgLeuValAlaValAlaValAlaAlaPheAlaLeuCysTrp 315
   :::::
DB 22815 CACGGGAGAGGCGGTACAGGTGGCCATTTTAGTGACAAAGATTTTCTCTGCTGTG 22874
QY 316 ThrProTYrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaAlaAlaArg 335
   ::::: |||
DB 22875 TCCGCTTACACATTTGTATCATCTTCTAGATATCATCTGAGAGAGCTGAGAGCTGGAATAGC 22934
QY 336 AsnCysGLyArgGlnSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTYr 355
   ::::: |||||
DB 22935 AGCTGGAGCTGAGTGCTATCTCTGTGGCCATCATCTTGTCGTAATTCCTGGGCTG 22994
QY 356 MetHisCysCysLeuAsnProLeuLeuTYrAlaPheValGlyAlaLysPheArgGluArg 375
   |||||
DB 22995 GCACACTGCTGTCTCATCCATGCTCTACCTGCTGCGTAAAGTCCGCAAGTAC 23054
QY 376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
   ::::: |||||
DB 23055 CTCTCTGCTGTGTGACCAAGCTGGCTGTGCTGGCCGCGCTCTCT---TGCCAACTT 23111
QY 396 SerSerSerArgArgAspSerSerTrpSerGlnuThrSerGlnuLaser 411
   ::::: |||||
DB 23112 TTCCCAACTGCGCGCAAGATAGTCTCTGAGTCAAGAAATGCTACT 23159

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; Sequence 1411, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1411
; LENGTH: 1125
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-035-832-1411

Alignment Scores:
Pred. No.: 4 796-50 Length: 1125
Score: 640.00 Matches: 143
Percent Similarity: 56.29% Conservative: 54
Best Local Similarity: 40.86% Mismatches: 139

```

```

RESULT 11
US-10-035-832-1411
; Sequence 1411, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1411
; LENGTH: 1125
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-035-832-1411

Alignment Scores:
Pred. No.: 4 796-50 Length: 1125
Score: 640.00 Matches: 143
Percent Similarity: 56.29% Conservative: 54
Best Local Similarity: 40.86% Mismatches: 139

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Query Match:	29. 75%	IndeIs:	14
DB:	13	Gaps:	6
US-09-101-518A-2 (1-415) x US-10-035-832-1411 (1-1125)			
QY 70 pheserSerSerTyrAspTyrGlyGluAsnGlyAspSerScyscysThrSerProPro			89
Db 76 TACAGTACACACAGGAGATTCCTCCCTACAGACAGTAACTTGGCTCTACA-----			126
QY 90 CysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeu			109
Db 127 GTCCAGGAGACCTTACTAGAGCTGTCTTAAGGCGGTATTCATGCTGTGGCTACAGACCTC			186
QY 110 LeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArg			129
Db 187 ATCTTCCTCCCTGGGTATAGTGGGAACATCTGGTGTGTATCTGTGAACCTGGAGGACCGG			246
QY 130 ThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeu			149
Db 247 CACACGTGGAGCTCAACCGAGACCTTCCTGTCCACCTGGAGTACCGACCTCTCTTA			306
QY 150 ValLeuThrLeuProLeuTrrAlaValAlaAspAlaAlaValGlnTrrValPheGlySerGly			169
Db 307 GTCTTCATCTCCCTTTTGGCAGTGGGTGGAGGGCTGTGGTGGTGGCTTACAGCTCACTTC			366
QY 170 LeuScyLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeu			189
Db 367 CTCTGCACAAACTGTGATCGCTGTGCACACAGATTAATTTCTACGCGACGACCTGCTGTG			426
QY 190 AlaScyLLeSerPheAspArgTyrGlyLeuAsnIleValHisAlaThrGlnLeuTyrArgArg			209
Db 427 GCCTGTATAGCTGTAGACCGGTACCTAGCATGCTGCATGCTGTTCACGCTACCGCGGC			486
QY 210 GlyProProAlaArgValIleThrLeuThrCysLeuAlaValIleTrrGlyLeuCysLeuPhe			229
Db 487 CCGCGACTCTCTCCATCCATCCATCACCTACCTACGCGCATTTGGCTGGCGCTTCCTGTTC			546
QY 230 AlaLeuProAspPheIlePheLeuSerAla-----HisIAspGlnArgLeuAsn			246
Db 547 GCCTTACCGGAACTCCCTTTGGCAGAGTGGGCCAACCTCATACACAGACTCTCTTA---			603
QY 247 AlaThrIscysGlnTyrAsnPheProGlnValGlyArgThr-----AlaLeu			262
Db 604 --CCACAGTGCACCTTCTCCGAGAAACGAAGCGGAACATAGACCTGTTCACTCC			660
QY 263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyr			282
Db 661 CGTTTCTCTTACACATTCGGGGGCTTCTCTAATCCGATCTTGTATGGATGGGTATAC			720
QY 283 AlaHisIleLeuAlaValLeuLeu--ValSerArgGlyGlnArgArgLeuTrrAlaMet			301
Db 721 GTGGGCGGCGHCCACAGGTACTAGCAGGCCACGCGCGCTCAGCGGAGAAAGCGGTC			780
QY 302 ArgLeuValValValAlaValAlaPheAlaPheAlaLeuCysTrrPThrProTrrHisLeuVal			321
Db 781 AGGGGCGCATTTTATAGACAMACATTTTCTCTCTGCTGGCTGCACACATTTGTC			840
QY 322 ValLeuValAspIleLeuMetAspSerGlyAlaLeuAlaArgAsnCysGlyArgGluSer			341
Db 841 ATCTTCTCTAGTACACTGGAGAGGCTGTAAAGGCTGTAAATGACAGCTGCAGCTGATGTC			900
QY 342 ArgValAspValAlaLysSerValIleThrSerGlyLeuGlyTyrMetHisCysCysLeuAsn			361
Db 901 TATCTCTCTGTGGCCATTCCTGTGTGATTCCTGTGGCGTGGACACGTGCTTCAT			960
QY 362 ProLeuLeuTrrAlaPheValGlyValLysPheArgGlyArgMetTrrPheLeuLeuLeu			381
Db 961 CCCATGCTTTACACTTCCTGCTGGCGTAAAGTTCCGACATGACCTCTCTGCTTGTGACC			1020
QY 382 ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArgArg			401
Db 1021 AAGCTGGGCTGTGCTGGCCCGGCTCCCTT---TGCCAACTTTTCCCAACTGGGCGAAG			1077

OY	402	serSertrpserGluThrSerGluAlaSer	411	
Db	1078	AGTACTCTCTGAGTCAGAAATGCTACT	1107	
	RESULT 12			
	US-10-035-832-1410			
	; Sequence 1410, Application US/10035832			
	; GENERAL INFORMATION:			
	; APPLICANT: Morris, David			
	; APPLICANT: Engelhard, Eric			
	; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER			
	; FILE REFERENCE: A-71249/RMS/DCF			
	; CURRENT APPLICATION NUMBER: US/10/035,832			
	; CURRENT FILING DATE: 2002-07-22			
	; PRIOR APPLICATION NUMBER: US 09/7747,377			
	; PRIOR FILING DATE: 2000-12-22			
	; PRIOR APPLICATION NUMBER: US 09/7798,586			
	; PRIOR FILING DATE: 2001-03-02			
	; NUMBER OF SEQ ID NOS: 1613			
	; SOFTWARE: PatentIn version 3.1			
	; SEQ ID NO 1410			
	; LENGTH: 2517			
	; TYPE: DNA			
	; ORGANISM: Mus musculus			
	US-10-035-832-1410			
	Alignment Scores:			
	Pred. No.:	1,32e-49	Length:	2517
	Score:	640.00	Matches:	143
	Percent Similarity:	56.29%	Conservative:	54
	Best Local Similarity:	40.86%	Mismatches:	139
	Query Match:	29.75%	Indels:	14
	DB:	13	Gaps:	6
	US-09-101-518A-2 (1-415) x US-10-035-832-1410 (1-2517)			
OY	70	PhesrSerSerTrpYrAspTrpGlyGluAsnGluSerAspSerCysTrpSerProPro	89	
Db	76	TACACTACACACGACGAGATTCCTCCCTACAGGACGATCACTCTGCTCTACA-----	126	
OY	90	CysProGlnAspPheSerLeuAsnPheAspTrpGlnPheLeuProAlaLeuTrpSerLeu	109	
Db	127	GTCGAGGACCTTAAGTACTGACGCTCTTAAGCGGCTATTCAATGCTGGGCTTACAGCCTC	186	
OY	110	LeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArg	129	
Db	187	ATCTTCCTCTGGGATGATGATGGAAACATCTCTGGTGGCTGTAATCTCGAGAGAGCACCGG	246	
OY	130	ThrAlaLeuSerSerThrAspTrpPheLeuLeuHisLeuAlaValAlaAspThrLeuLeu	149	
Db	247	CACACTCGGACCTCAACCGAAGACCTTCTCTTCCACCTCGCAGTAGCGGACCTTCTCTTA	306	
OY	150	ValLeuThrLeuProLeuTrpAlaValAlaAlaValAlaGlnTrpValPheGlySerGly	169	
Db	307	GCTTCATCTGCGCTTTTGGACGTGGCTGAGGGCTCTGGGGTGGGCTTAGGAGCCTTC	366	
OY	170	LeuCysLysValAlaGlyAlaLeuPheAsnLeuAsnPheTrpAlaGlyAlaLeuLeuLeu	189	
Db	367	CTCTGCAAAACTGTCATGCGCTCTGACAGAATCAATTTCTACTGACAGCCTGCTGCTG	428	
OY	190	AlaCysLysSerPheAspArgTrpLeuAsnLysLeuAlaHisAlaThrGlnLeuTrpArgArg	209	
Db	427	GCGCTATAGCTGTAAGACGGGTACTGACCATGCTCCATGCTGTTCACGCGCTTACCGCGC	486	
OY	210	GlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuPhe	229	
Db	487	CGTGCACCTCTCTCCATCCACATCACTGCGACGGCATTTGGCGCGCGCTTCTGCTTC	546	
OY	230	AlaLeuProAspPheLysPheLeuSerAla-----HisHisAspGlnArgLeuAsn	246	
Db	547	GCGTTACCGGAACTCTCTTTTGGCCAAAGGTTGGCCAACTCTCAATCAACAGACTCCTTA---	603	
OY	247	AlaThrHisCysGlnTrpAsnPheProGlnValGlyValTrp-----AlaLeu	262	

Db 604 ---CCACAGTGCACCTTCTCCAGGAAAGCAAGCCGAAACCTAGAGCTGTTCACCTCC 660
Oy 263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrGlyTyr 282
Db 661 CGTTTCCTTACCACACATGGGGCTTCCTACATGCATGCTGTGTGGAGTGGTTTAC 720
Oy 283 AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgPheLeuAlaMet 301
Db 721 GTGGGGGTGTCCACAGCTACTAGCGAGCCCAAGCCGCCCTCAGCGGCAAGAGGGGTC 780
Oy 302 ArgLeuValValValValValAlaPheAlaLeuCysTrpTrpProTyrHisLeuVal 321
Db 781 AGGGTGCCATTATTAGACAAAGCATTTCTCTCTGCTGCTGCGCCCTACACATTTGTC 840
Oy 322 ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnGlyArgGlySer 341
Db 841 ATCTTCCTAGATACACTGAGAGAGCTGAAGGCTGTAATAGCAGTGAAGCTGAGTGC 900
Oy 342 ArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsn 361
Db 901 TATCTCTGTGTGGCCATCACTGTGTGAATTCCTGGCCCTGGCACACTGCTGTCAAT 960
Oy 362 ProLeuLeuTyrAlaPheValGlyValLysPheArgGlyArgMetTrpMetLeuLeu 381
Db 961 CCCATGCTTTACACCTTCGCTGGCGTAAGTTCCGACATGACCTCTCGGCTTGTGACC 1020
Oy 382 ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArgAsp 401
Db 1021 AAGCTGGGCTGTGGTGGCCGCCGCCCTCCCTT---TGCCAACTTTTCCCAAGTGGCGCAAG 1077
Oy 402 SerSerTrpSerGlnThrSerGlnAlaSer 411
Db 1078 AGTAGTCTCTGTGAGTCACAGAAATGCTACT 1107
RESULT 13
US-10-252-157-227
; Sequence 227, Application US/10252157
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: PA-0027-1 US
; CURRENT APPLICATION NUMBER: US/10/252,157
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,048
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: PERL Program
; SEQ ID NO 227
; LENGTH: 1777
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 218524.4
US-10-252-157-227
Alignment Scores:
Pred. No.: 1,46e-49 Length: 1777
Score: 637.50 Matches: 154
Percent Similarity: 51.09% Conservative: 57
Best Local Similarity: 37.29% Mismatches: 145
Query Match: 29.64% Indels: 57
DB: 13 Gaps: 10
US-09-101-518a-2 (1-415) x US-10-252-157-227 (1-1777)
Oy 17 GlnGlyAlaAlaGlnSerLysSerGlnThrLysSerAspSerIleThrLysGlnPheLeu 36
Db 353 GGAAGGCTCTTACAGGTGAAGC----- 376
Oy 37 ProGlyLeuTyrThrAlaProSerSerProPhePro---ProSerGlnValSerAspHis 55

Db 377 -----CCAGCAGCCAGCTCAGATTTAAGTTAACTTACCTCAAAATGAAGATTTT 424
Oy 56 GlnValLeuAsnAspAlaGlnValAlaAlaLeuGlnGlnAsnPhe----- 70
Db 425 AACATGAGAGATCAGC-----TTTGAAGATTTCGGAAGGTGAAGAT 469
Oy 71 SerSerSerTyrAspArgGlyGlnAsnGlnSerAspSerCysThrSerProProCys 90
Db 470 CTTAGTAATTTACAGTTACAGCTTACCCTGCCCCCTTTTCTACTAATATGCCGCCCATGT 529
Oy 91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
Db 530 GAACAGAA---TCCCTGGAAATCAACAAGATATTGTGGTCAATTATATGACCTGGTA 586
Oy 111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerAlaGlyThr 130
Db 587 TTCTCTCTAGCCCTGTGGGAAATCTCCGTGATGCTGTGATCTTAAACACAGAGGTC 646
Oy 131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
Db 647 GGGCGCTCCGTCACTATGTCTACTGTGAACTTACCTTGGCCACACTTCTTGGC 706
Oy 151 LeuThrLeuProLeuTyrAlaValAspAlaAlaValGlnTyrValPheGlySerGlyLeu 170
Db 707 CTGACCTTGGCCCATCTGTGGCGCCCTCCAGAGTGAATGGCTGATTTTGGACATTCCTG 766
Oy 171 CysGlyValAlaAlaValAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuAla 190
Db 767 TGCAGAGGTGTCCTCACTCTCTGAAGGAAGTCACTTAAATGAGTCCGTCTACTGAGCC 826
Oy 191 CysIleSerPheAspArgTyrLeuAsnIleValAlaThrGlnLeuTyrArgArgGly 210
Db 827 TGCATAGTGTGAGCGCTTACCTGCGCATTTGTTCATGCCACAGC----- 871
Oy 211 ProProAlaArgValThrLeuThr-----CysLeuAla 221
Db 872 -----ACACTGACCCAGAAAGCGCTACTGTGTCAAATTCATATGTCTCAG 916
Oy 222 ValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 241
Db 917 ATCTGGGGCTGTGCTCTGCTGCGCCCTGCGCCGTCTACTTTTCGGAAGACCGTCTAC 976
Oy 242 AspArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGly----- 258
Db 977 TCATCCAAATGTTAGCCAGC---TGC-----TATGAGACATGGCCAAATTA 1024
Oy 259 -----ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuProLeu 275
Db 1025 GCAAACTGGCGGATGCTGTAGAGATCTGCCCCCACTCTTGGCTTGCATCTGCGCACATG 1084
Oy 276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln 295
Db 1085 CTGATCATGCTGTCTGTCAACGAGATTCAACCTGCTGATCTGTTTAAAGCCCATAGGGG 1144
Oy 296 ArgArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrp 315
Db 1145 CAGAAACACCGGCGCATGGGGGTCACTTTGCTGTGCTCTACTTCTCCGCTTGTCTGG 1204
Oy 316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335
Db 1205 CTGCGCTTACAACTGTGCTCGTGGGCAACACCTCATAGAGCAACGAGATCCAGAGG 1264
Oy 336 AsnGlyGlyArgGlnSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355
Db 1265 ACCTGTGAGCGCGCATACATCGACCGGGCTCTGATGCCACGAGATTCTGGGCGATC 1324
Oy 356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGlyVal 375
Db 1325 CTTCACAGCTGCTCAACCCCTCACTAGCGCTTATTTGGCCAGAAATTTGCGCATGGA 1384
Oy 376 MetTrpMetLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
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Db 1385 CTCCTCAAGATTCTACCTATACATGGCTGTGATCAGACGAACTCCCTGCCCAAGACACC 1444
QY 396 SerSerSerArgArgAspSerSerTrpSerGluThrSer 408
Db 1445 AGGCGTTCCTTTGTGTGGCTCTCTCTTCACAGGACACTTCC 1483

RESULT 14
US-10-251-385-65
; Sequence 65, Application US/10251385
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-251-385-65

Alignment Scores:
Pred. No.: 1,39e-49 Length: 1119
Score: 635.00 Matches: 147
Percent Similarity: 54.72% Conservative: 50
Best Local Similarity: 40.83% Mismatches: 145
Query Match: 29.52% Indels: 18
DB: Gaps: 8

US-09-101-518A-2 (1-415) x US-10-251-385-65 (1-1119)
QY 67 LeuGluAspPheSerSerSerSerTyr-----AspTyrGlyGluAsnGluSerAsp--- 82
Db 31 CTGGAACCTGGAGAGACCTGTTCTGGGAAGTGGACAGATTGACACACTTAACGACACC 90
QY 83 SerCysCysThrSerProProCysProGln-----AspPheSerLeuAsnPheAsp 99
Db 91 TCCCTGTGGAAATCATCTCTGCTGCCACAGAGGTCCTCATGGCTGATCGGCAACGTC 150
QY 100 ArgAlaPheLeuProAlaLeuTyrSerLeuPheLeuLeuGlyLeuGlyLeuGly 119
Db 151 GCCGTGTGGTGGCCGTGGCTACAGCTCATCTCTGCTGGCGGTGATCGGCAACGTC 210
QY 120 AlaValAlaValAlaLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
Db 211 CTGGTCTGTGTGATCTCTGGAGCGGACCGGACAGACAGCATTCACAGGACCTTCTCTG 270
QY 140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuThrAlaValAsp 159
Db 271 TTCACCTGGCGCGCTGGCCGACCTCTGCTGCTCATCTGCTTGGCCGTGGCGGAG 330
QY 160 AlaAlaValGlnThrValPheGlySerGlyLeuCysGlyValAlaGlyAlaLeuPheAsn 179
Db 331 GGCTGTGTGGTGGCTGGCTGGGACCTTCTGCAAAACCTGTGATGGCCGACCAAA 390
QY 180 IleAspPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
Db 391 GTCAACTTCTACGACGACGACCTGCTGCGCTGATCGCCCTGGACCGCTTACCTGGCC 450
QY 200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
Db 451 ATTGTCTACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 510
QY 220 LeuAlaValThrGlnLeuCysLeuLeuPheAlaLeuProAspPheLeu----- 237
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Db 511 GGGACCATCTGGCTGGTGGCTTCTCTGCTGCCAGAGATTCCTTGGCCAAAGTC 570
QY 238 ---SerAlaHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
Db 571 AGCCAAAGGCCATACAACTACCTCTG-----CAAGCTTGACCTTCTTCCCAAGGAAC 624
QY 257 ValGlyArgThr-----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
Db 625 CAGCAGAAAGCCATGCTGTTGACCTCCGATTCCTCTTACCATGTGGGGGATTCCTG 684
QY 273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
Db 685 CTCGCCATGCTGGTGTGATGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
QY 292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValAlaPhe 311
Db 745 CAGCGGCGCCCTGACGGCGGAGAGGAGTCAAGGTGATGCTGCTGCTGCTGCTGCTGCTG 804
QY 312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
Db 805 TTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
QY 332 AlaLeuAlaArgAsnGlySerGlyArgGluSerArgValAlaValAlaLysSerValThrSer 351
Db 865 GCCGTGACAAATACCTGCAAGCTGAATGGCTCTCCCGCTGCATCCATCCATGTGTGAG 924
QY 352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValys 371
Db 925 TTCCTGCGCTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 984
QY 372 PheArgGluArgMetTrpMetLeuLeuLeuGlyCysProAsnGlnArgGlyLeu 391
Db 985 TTCGCGAGTACCTGTCGGGCTCTGACCAAGCTGGGCTGACCGGCTGCTGCTGCTGCTG 1044
QY 392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
Db 1045 TGGCAGCTCTTCCCTGAGCTGGCGCAGG---AGCAGTCTCTGAGTCAAGAAATGGCACCC 1101

RESULT 15
US-10-035-832-1414
; Sequence 1414, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1414
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-832-1414

Alignment Scores:
Pred. No.: 1,39e-49 Length: 1119
Score: 635.00 Matches: 147
Percent Similarity: 54.72% Conservative: 50
Best Local Similarity: 40.83% Mismatches: 145
Query Match: 29.52% Indels: 18
DB: Gaps: 8

US-09-101-518A-2 (1-415) x US-10-035-832-1414 (1-1119)
QY 67 LeuGluAsnPheSerSerSerTyr-----AspTyrGlyGluAsnGluSerAsp--- 82
Db 31 CTGGAACCTGGAGAGACCTGTTCTGGGAAGTGGACAGATTGACACACTTAACGACACC 90
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Oy	83	serGcySnrhSreProPrcyProglN-----AspBseSerLeuSnhpeAs	99
Db	91	TCCTGGTGGAAATCATCTCTGCTCCCTGCCACAGAGGGCCCTCATGGCTCTTCAAG	150
Oy	100	ArgAlaIbheLeuProAlaLeuTyTserLeuLeuPheLeuGlyLeuLeuGlysnGly	119
Db	151	GCCGTGTTCCGACCCCGGGCCCTACAGCTCATCTTCTCTCGGGGGGTACGGCAACGTC	210
Oy	120	AlaValAlaAlaValLeuLeuSerAlaGlyGlyAlaLeuSerSerThiAspThiPheLeu	139
Db	211	CTGGGTGGTGGATCCCTGGAGCGGCACCGGCACACGCAAGTTCACGAGACTTCTCTG	270
Oy	140	LeuHisLeuAlaValAlaAspThiLeuLeuValLeuThiLeuProLeuThrAlaValAsp	159
Db	271	TTCACCTGGCCCGCGCCGACCTCTGCTGCTGCTTATGCTTGGCTTTGCCGCGCCAG	330
Oy	160	AlaAlaValGlnThrValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn	179
Db	331	GGCTCTGGTGGCTGGGCTCGGGGACCTTCCTCGAAACGTGATGGCTCGCAAA	390
Oy	180	IleAsnIbheTyAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyIleAsn	199
Db	391	GTCACATTCTACTGACACACCTGCTCTCGGCTCGATGCGCGTGGACGACATCTGGCC	450
Oy	200	IleValHisAlaThrGlnLeuTyTArgArgGlyProProAlaArgValThrIleuThrcys	219
Db	451	ATTGTCACACCGCCGTCATGCTTACCGGCACCGCGCGCTCTCTCATGCATCACTACCTGT	510
Oy	220	LeuAlaValThrPheGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu-----	237
Db	511	GGGACCATCTGGCGTGGGGCTTCTCTCGGCTTCGCGAGATTTCTTCTGCCCAAGTC	570
Oy	238	---SerIleHisAspGlyAlaGlyLeuAsnAlaThiHisCysGlnItyrAsnIbheProGln	256
Db	571	AGCCAAAGGCATCAACAACCTCCG-----CCAGTTGGACCTTCTCCACAGAGAC	624
Oy	257	ValGlyArgThr-----AlaLeuArgValIleGlnIleuValAlaGlyPheLeu	272
Db	625	CAAGCAAGAAACGCGATGCGCTGCTCACCTCCGATCTCTACCAATGTGGCGGATTTCTG	684
Oy	273	LeuProLeuLeuValMetAlaTyTyrTyTAlaHisIleLeuAlaValLeu---LeuVal	291
Db	685	CTGGCCATCTGGTGAAAGGGCTGCTGCTCACTGTCGGGGGTAGTCACAGTTGGCGCCAGCC	744
Oy	292	SerArgGlyGlnArgGlyAlaMetArgLeuValValValValAlaIbhe	311
Db	745	CAGCGGCGCCCTACGGCGCAAGAGGACAGTGAGGTGGCCATCTGGTGACAACATCTTC	804
Oy	312	AlaLeuCysThrProTyTHisLeuValValLeuValAspIleLeuMetAspLeuGly	331
Db	805	TTCCTCTGCTGTCACCGCTACACATCGTCATCTTCTGGACACCTGGCGAGGCTTAAG	864
Oy	332	AlaLeuAlaArgsnCysGlyArgGlyIserArgValAspValAlaLysSerValThiSer	351
Db	865	GGCTGGGACATACCTGCGACAGTGAATGGCTCTCTCCCTGGCCATCACTATGTGTAG	924
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Db	925	TTCCTGGGCTGGCCGACGATCTGCTCTCAACCCCATGCTTACACTTTTGCGCGGCTTAAG	984
Oy	372	PheArgGlyAlaArgMetThrPheLeuLeuLeuGlyLeuGlyCysProAsnGlnArgGlyLeu	391
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Job time : 431 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 03:19:18 ; Search time 57 Seconds
(without alignments)
8084.359 Million cell updates/sec

Title: US-09-101-518a-1

Perfect score: 1876

Sequence: 1 cctgaaggagagagcagcagga.....atcgctcagagaaaaaaa 1876

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued_Patents_NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1541.6	82.2	1670	3 US-08-709-838-1	Sequence 1, Appl
2	1541.6	82.2	1670	4 US-08-829-839-1	Sequence 1, Appl
3	240	12.8	1679	1 US-08-202-056-6	Sequence 6, Appl
4	240	12.8	1679	1 US-08-076-093A-5	Sequence 5, Appl
5	240	12.8	1679	1 US-08-701-265-5	Sequence 5, Appl
6	240	12.8	1679	2 US-08-284-586-5	Sequence 5, Appl
7	240	12.8	1679	2 US-08-805-478-5	Sequence 5, Appl
8	240	12.8	1679	2 US-08-802-627A-5	Sequence 5, Appl
9	240	12.8	1679	2 US-08-801-238-5	Sequence 5, Appl
10	240	12.8	1679	2 US-08-801-228-5	Sequence 5, Appl
11	240	12.8	1679	3 US-09-104-296-5	Sequence 5, Appl
12	240	12.8	1679	3 PCT-US94-06380-3	Sequence 5, Appl
13	238.4	12.7	2818	3 US-08-982-493-7	Sequence 7, Appl
14	238.4	12.7	2818	4 US-08-628-655-1	Sequence 7, Appl
15	231	12.3	1200	4 PCT-US95-03032-1	Sequence 1, Appl
16	226.2	12.1	1200	5 PCT-US92-02977-1	Sequence 1, Appl
17	217.8	11.6	1373	5 PCT-US92-02977-6	Sequence 6, Appl
18	217.8	11.6	1373	5 PCT-US95-03032-3	Sequence 6, Appl
19	216.6	11.5	1900	1 US-08-153-848-18	Sequence 3, Appl
20	216.6	11.5	1900	3 US-09-299-843A-18	Sequence 18, Appl
21	216.6	11.5	1900	4 US-09-088-337B-18	Sequence 18, Appl
22	216.6	11.5	1900	5 PCT-US93-11153-18	Sequence 18, Appl
23	216.6	11.5	2058	1 US-08-153-848-6	Sequence 6, Appl
24	216.6	11.5	2058	3 US-09-299-843A-6	Sequence 6, Appl
25	216.6	11.5	2058	4 US-09-088-337B-6	Sequence 6, Appl
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36	203.2	10.8	1748	1 US-08-202-056-8	Sequence 8, Appl
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38	198.8	10.6	2085	4 US-09-088-337B-65	Sequence 65, Appl
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44	193.6	10.3	2751	4 US-09-088-337B-23	Sequence 23, Appl
45	193.6	10.3	2751	5 PCT-US93-11153-23	Sequence 23, Appl

ALIGNMENTS

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RESULT 1
US-08-709-838-1
; Sequence 1, Application US/08709838
; Patent No. 6140064
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Marcel
; ATTORNEY/AGENT INFORMATION:
; NAME: Moser, Bernhard
; TITLE OF INVENTION: IP-10/MG RECEPTOR DESIGNATED CXCR3,
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08709,838
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: TK196-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1670 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 69..1172
; US-08-709-838-1

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Best Local Similarity 99.1%:   Pred. No. 0:
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Db 1618 AGGA 1621

RESULT 2
US-08-829-839-1
; Sequence 1, Application US/08829839
; Patent No. 6184358
;
GENERAL INFORMATION:
;
APPLICANT: Loetscher, Marcel
APPLICANT: Moser, Bernhard
APPLICANT: Qin, Shixin
APPLICANT: Mackay, Charles R.
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
TITLE OF INVENTION: ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,839
FILING DATE: 31-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,838
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TK196-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
;
INFORMATION FOR SEQ ID NO: 1:

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SEQUENCE CHARACTERISTICS:
LENGTH: 1670 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
FEATURE:
NAME/KEY: CDS
LOCATION: 69..1172
US-08-829-839-1

Query Match      82.2%; Score 1541.6; DB 4; Length 1670;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 303 CCACCCCGTTCGCCCTCAGAGTAGTGACACCAAGTGAATATGACGGCGAGGTTG 362
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QY 1263 TCTATGCTTTTGTAGGGGTCAAGTTTCGGGAGCGGATGTGATGCTCTTGGGCTGG 1322
Db 1018 TCTATGCTTTTGTAGGGGTCAAGTTTCGGGAGCGGATGTGATGCTCTTGGGCTGG 1077
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QY 1383 GGTCTGAGACTTCAGAGCGCTCTACCTGCGGCTGTGAGGCGGGAATCCGGGCTCCCTT 1442
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QY 1443 TCGCCCAAGTCTGACTTCCCGCATTCAGAGGCTCTCCCTCCCTCTGCGGGCTGTGGCT 1502
Db 1198 TCGCCCAAGTCTGACTTCCCGCATTCAGAGGCTCTCTCCCTCTGCGGGCTGTGGCT 1257
QY 1503 CTCCCAATATCTCTGCTCCCGGACTCATGCGAGCCCAAGCAACAGAGTCTCCCG 1562
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QY 1563 GAAGCCACCCCTCCAGCTGTGAGAGCTGCAACATTTGCTGCTTCTAGCTGCAAGCCCA 1622
Db 1318 GAAGCCACCCCTCCAGCTGTGAGAGCTGCAACATTTGCTGCTTCTAGCTGCAAGCCCA 1377
QY 1623 TCTGCGCGCCGAGGTGCTGCTGAGAGCCCACTGCTTCTATTTGGAATAAACA 1682
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QY 1683 TTATCTTTCCCAAGTGGGAGTACAGAGCATGGCTGAGAGGCTCTGCCATTAAG 1742
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QY 1743 CCAGAGCCGAGGCTCCAGCTCAGAGTGAAGTGGGCTGAGGCTCCCAAGCCCTATAT 1802
Db 1498 CCAGAGCCGAGGCTCCAGCTCAGAGTGAAGTGGGCTGAGGCTCCCAAGCCCTATAT 1557
QY 1803 TTGCTTTTATTTTATGCTAATAATCTGCTTAAACTTTTCAATTAACAGAGATGTC 1862
Db 1558 TTGCTTTTATTTTATGCTAATAATCTGCTTAAACTTTTCAATTAACAGAGATGTC 1617
QY 1863 AGGA 1866
Db 1618 AGGA 1621

RESULT 3
US-08-202-056-6
; Sequence 6, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IS-08-202-056-6

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Query Match	12.8%;	Score 240;	DB 1;	Length 1679;
Best Local Similarity	57.0%;	Pred. No. 2.5e-42;		
Matches 507; Conservative	0;	Mismatches 365;	Indels 18;	Gaps 3;

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Db	932	CAAAAGTCAGCAGGCGCAATACAAACATCTCTGCACAGTTCACATCTTCCACAAGAA	991
QY	931	CTTCCCAACA---GGTGGGCGCAGACGGCTCTGGGGGTGTGCAAGCTGTGTGGCTTCT	987
Db	992	CCAAAGCAAGAACGATGCCGTGTACCTCCGATTTCTCTAACCAATGTGGCGGATTTCT	1051
QY	988	GCTGCCCCCTGCTGATGAGCTAGGCTACTGCTATGCCACATCTGGGCGGTGCTG---CTGGT	1044
Db	1052	GCTGCCATGCTGTGTATGGCGTGTGTACTAGCTGGGGGTAGTGCACAGTTCGCCGACGG	1111
QY	1045	TTCCAGAGGGCCAGCGCGCTCTGGCGCCATATGCGGCTGTGTGTGTGCTGTGTGGCCCTT	1104
Db	1112	CCAGCGGCGCCCTCAGCGGCAAGAGCACTGACGGGTGCCATCTGTGTACAAAGCATCTT	1171
QY	1105	TGCGCTCTGTGGACCCCTATCACTGGTGTGCTGTGTGACATCTCTATGAGACTTGG	1164

Db 1172 CTCTCTGTGCGGTGACACCTTACACACATTCGTCTCGAGAACCTTGGCAGGGCTGA 1231

Qy 1165 CGCTTTGGCCCGCACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCACAGTGGTCACTC 1224

Db 1232 GGCCTGTGACAAATACCTGCAAGCTGATGGCTCTCTCCCGGGCCATCACATGTGTA 1291

Qy 1225 AGGCCTGGGCTACATGCACGTGCTGCTCAACCCGCTGCTCTATGCTTTGTAGGGGTCAA 1284

Db 1292 GTTCTCGGGGCTGGCCACAGTGTGCTCAACCCCAAGCTCTACACTTTCGCGGGGTAA 1351

Qy 1285 GTTCTCGGGAGGATGTGATGTGCTCTTGGCGCTGGGCTGCCCCAAC 1334

Db 1352 GTTCCGAGTGACCTGTGCGGGCTCTGTACGAAGCTGGGCTGTACCGGCC 1401

RESULT 4
US-08-076-093A-5
; Sequence 5, Application US/08076093A

GENERAL INFORMATION:
APPLICANT: Chuntcharapal, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PFA4 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

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;
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  WinPatIn (Genentech)
;

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APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993

; PRIOR APPLICATION DATA: 07/810782
 ; APPLICATION NUMBER: 07/810782
 ; FILING DATE: 19-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/677211
 ; PRIORITY DATE: 08-11-1989

ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 766P2
TELECOMMUNICATION INFORMATION:
415 435 5530

```

; TELEFAX: 415/952-9881
;
; TELEEX: 910/371-7168
;
; INFORMATION FOR SEQ ID NO: 5
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 1679 nucleotides
;
; type: nucleotide

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TOPLOGY:
US-08-076-093A-5

Query Match	12.8%	Score 240	DB 1	Length 1679
Best Local Similarity	57.0%	Pred. No. 2.5e-42		
Matches 507	Conservative 0	Mismatches 365	Indels 18	Gaps 3

Y	523	CMACGGCGCGGTGGCAGCCGCTGCTGTGAGCCGCGCAGACGCCCTTGAGCAGCACCGACAC	5825
QY	463	CTTGACACCGGGCCCTTCTTCTGGCAGGCGCTCTTCACAGCTCTCTTTCTGTGTGGGCGCTGTGGG	5222
Db	512	CTTCAGAGCGCGTGTTCGTGGCCCGTGGCGCTACAGAGCTATCTTTCCTCTCGTGGGCGTATCGG	5711


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: GENERAL INFORMATION:
: APPLICANT: Chuntharapal, Anan
: APPLICANT: Lee, James
: APPLICANT: Hebert, Caroline
: APPLICANT: Jin Kim, K.
: TITLE OF INVENTION: ANTIBODIES TO PPA RECEPTOR
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatlin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/805.478
: FILING DATE: 25-Feb-1997
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/284586
: FILING DATE: 10-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/076093
: FILING DATE: 11-JUN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/810782
: FILING DATE: 19-DEC-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P0706P2PIC1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-5530
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
:
: US-08-805-478-5
:
: Query Match 12.8%; Score 240; DB 2; Length 1679;
: Best Local Similarity 57.0%; Fred. No. 2.5e-42;
: Matches 507; Conservative 0; Mismatches 365; Indels 18; Gaps 3
:
: QY 463 CTTCGACCGGGCCCTTCCTCCGACGCGCCCTACAGCCTCTTCTGCTGGGGCGTGGG 522
:   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
: Db 512 CTTCAGAGCCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 571
:   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
: QY 523 CAACGCGCGGTGGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
:   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
: Db 572 CAACGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 631
:   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
: QY 583 CTTCCTGCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642
:   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
: Db 632 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 691
:   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
: QY 643 AGTGGACCTGCGCGTCACAGTGGGCTTTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG 702
:   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
: Db 692 GCGCGAGGGGCTCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCT 751
:   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
: QY 703 CTTCACATCAACTTCTTACGACGAGAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCT 762
:   ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
: Db 752 GCACAAAGTCAACTTCTTACGACGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
:   ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
: QY 763 CTGACACTAGTTCATGCCACCCAGCTCTACCGCGGGGGGCCCGCGCGGTGACCT 822

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Db	812	CTTGCCATTGTCCAGCCGCTCCATGCTACCGCCACCGCCGCTCTCTTCATCCACAT	871
Qy	823	CACCTGCTGTGCTGTGTGGGGGGCTTGGCTCTCTTTTGCCCTCCAGACTTCATCTTCT	882
Db	872	CACCTGTGGGACCATCTGTGGCTGGGCTTCTCTCTCTTGTGCTCCAGAGATTCTTCTGC	931
Qy	883	GTCGGCCACCACGACGAGCGCTCAAGC-----CACCACCTGCCAATACAA	930
Db	932	CAAAGTACGCGCAAGCCATCAACAACTCTCCACAGTTCACCTTCTCCCAAGACA	991
Qy	931	CTTCCCAACA---GGTGGGCGCAAGGCTGTGGGGGGCTGACACTGTGTGGGCTTCT	987
Db	992	CCAAAGCAGAAACGATCCTGTGTTCACCTTCCGATTCTCTTACCATGTGTGGGATTCT	1051
Qy	988	GCTGCCCCCTGTGTGTTCATGTGCTACTGTCTATGCCACATCTGGCCGCTGTG--CTGGT	1044
Db	1052	GCTGCCATGTGTGTATGTGGCTGTGTCTACGTGGGGGATGTACAAAGTTGTGCCAGGC	1111
Qy	1045	TTCCAGAGGCGCAGCGGCTCTGGGGCCATGTGGCTGTGTGTGTGTGTGTGTGTGT	1104
Db	1112	CCAGCGGGGCTCTAGCGGCGCAAGAGGCAATCAAGGTCATCTGTATCAAAAGCAT	1177
Qy	1105	TGCCCCGT	1166
Db	1172	CTTCTCTGT	1231
Qy	1165	CGCTTTGTGCGCCGCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1224
Db	1232	GCGCGGT	1291
Qy	1225	AGGCTGT	1284
Db	1292	GTTCTGT	1351
Qy	1285	GTTCTGT	1334
Db	1352	GTTCTGT	1401
RESULT 8			
US-08-802-627A-5			
Sequence 5, Application US/08802627A			
Patent No. 5892017			
GENERAL INFORMATION:			
APPLICANT: Lee, James			
TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR			
NUMBER OF SEQUENCES: 6			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Genentech, Inc.			
STREET: 460 Point San Bruno Blvd			
CITY: South San Francisco			
STATE: California			
COUNTRY: USA			
ZIP: 94080			
COMPUTER READABLE FORM:			
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: WinPatIn (Genentech)			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/802, 627A			
FILING DATE: 19-Feb-1997			
CLASSIFICATION: 514			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 08/284586			
FILING DATE: 10-AUG-1994			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 08/076093			
FILING DATE: 11-JUN-1993			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 07/810782			


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Db 632 CTTCCTGTTCCACATGCGCCGTCGACCTCTGCTGCTTCATCTTGCCCTTTGCCGT 691
Qy 643 AGTGCACGCTGCCCTGCATCGGCTCTTTGGCTCTGACCTCTGCAAGTGGACGTCCTT 702
Db 692 GCGCCGAGGGCTGTGTGGCTGCTGCGGAGACCTTCCTCTGTGAAAATGTTGCTCCCT 751
Qy 703 CTTCACATCAACTTCTGACGAGAGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762
Db 752 GCACAAAGTCAACTTCTGACGAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
Qy 763 CCTGAACATAGTTTCATGCCACCCAGCTTCACGCGCGGGGGCCCGCGCGCTGACCT 822
Db 812 CCTGGCATTTGTTCACAGCGCTGCTACCTACCGCCACCGCGCTGCTGCTGCTGCTGCT 871
Qy 823 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
Db 872 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
Qy 883 GTGCGCCACACAGACGAGCGCTTCACGC-----CAGCCACTGCCATACAA 930
Db 932 CAAAGTCACCCAAAGGCGATCACACACACCTCCGACGCTGCTGCTGCTGCTGCTGCT 991
Qy 931 CTTCACACA---GTTGGCGCGACAGGCTCTGCGGGTGTGACAGCTGCTGCTGCTGCT 987
Db 992 CCAAGAGAAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
Qy 988 GCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1044
Db 1052 GCTGCGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1111
Qy 1045 TTCCAGGCGCGACGCGGCTGCGGCGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1104
Db 1112 CCAGGGCGCGCTGCGGCGCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1171
Qy 1105 TTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
Db 1172 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
Qy 1165 GCTTGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1224
Db 1232 GCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1291
Qy 1225 AGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1284
Db 1292 GTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1351
Qy 1285 GTTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1334
Db 1352 GTTCCGCGAGTGCATGCTGCGGCTGCTGACGAAAGTGGGCTGTACCGGCG 1401

RESULT 10
US-08-801-228-5
; Sequence 5, Application US/08801228
; Patent No. 5922541
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
; TITLE OF INVENTION: PFAA RECEPTOR NUCLEIC ACID
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,228
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P07062P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/952-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1679 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
US-08-801-228-5
Query Match 12.8% Score 240; DB 2; Length 1679;
Best local similarity 57.0%; Pred No. 2.5e-42;
Matches 507; Conservative 0; Mismatches 365; Indels 18; Gaps 3;

Qy 463 CTTCGACGCGGCGCTTCCTGCGACGCGCTTCACAGCTCTCTTCTGCTGCGGCTGCGG 522
Db 512 CTTCGAGCGCGTGTGCTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 571
Qy 523 CAAAGCGCGGCTGCGGCGCGCTGCTGCTGCGGCGCGGAGGAGGAGGAGGAGGAGGAG 582
Db 572 CAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 631
Qy 583 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642
Db 632 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 691
Qy 643 AGTGCACGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
Db 692 GCGCGAGGCGCTGCTGCGGCGGCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 751
Qy 703 CTTCACATCAACTTCTGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 762
Db 752 GCACAAAGTCAACTTCTGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 811
Qy 763 CTGAACATAGTTTCATGCCACCCAGCTTCACGCGCGGGGGCCCGCGCGCTGACCTT 822
Db 812 CTGCGCATTTGTTCACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871
Qy 823 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
Db 872 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
Qy 883 GTGCGCCACACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 930
Db 932 CAAAGTCACCCAAAGGCGATCACACACACCTCCGACGCTGCTGCTGCTGCTGCTGCT 991
Qy 931 CTTCACACA---GTTGGCGCGACAGGCTCTGCGGGTGTGACAGCTGCTGCTGCTGCT 987
Db 992 CCAAGAGAAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
Qy 988 GCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1044
Db 1052 GCTGCGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1111
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: APPLICANT: K. Jin Kim
: APPLICANT: Genentech, Inc.
: TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY DISORDERS
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: palin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/06380
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/076093
: FILING DATE: 11-JUN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: 706P2P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-5530
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1679 bases
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: PCT-US94-06380-3
:
: Query Match 12.8%; Score 240; DB 5; Length 1679;
: Best Local Similarity 57.0%; Pred. No. 2,5e-42;
: Matches 507; Conservative 0; Mismatches 365; Indels 18; Gaps 3

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Db 992 CAAGTGCAGCAAGCCGATCAACAACAACACTCCCGCAGCTTGACACTTCTCCCAAGAGAA 991
OY 931 CTTCOCACA---GGTGGGCGCCAGACGGCTCTGGGGGTCTGCAGCTGAGCTGGCTTTCT 987
Db 992 CCAAGACAGAAACCCATCCCTGTTTCACTCCCGATTCTCTACATGTTGGCGGATTCCT 1051
OY 988 GCTGCGCCCTGTGTGTCATATGGCCCTACAGTGCATATGCCCAATCCGGGCGGTGCTG---CTGGT 1044
Db 1052 GCTGCGCCATGCTGTGTATGGGCTGTGTGCTACAGTGGGGGTAAGTGCACAGGATTCGCCAAGC 1111
OY 1045 TTCCAGGGGAGCCAGGCGGCGCTCGGGGCGCATGCGGGCTGTGGTGTGGTGTGGCTT 1104
Db 1112 CCAGCGGGCGCCCTTACGGGGGAGAAAGGACAGTCAAGGTGGCCATCTGTGTACAAAGCATCTT 1171
OY 1105 TGCCCTGTCTGTGAACCCCTATACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1164
Db 1172 CTTCCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1111
OY 1155 CGCTTTGGCCCGGCACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1224
Db 1232 GGCCTGTGACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1291
OY 1225 AGGCGTGGGACATGTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1284
Db 1232 GTTCTGTGGGCTGTGGCCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1331
OY 1285 GTTCCGGAGGAGCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1334
Db 1352 GTTCCGAGTGTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1401

RESULT 13
; Sequence 7, Application us/08982493
; Patent No. 6110695
GENERAL INFORMATION:
APPLICANT: Gunn, Michael D
APPLICANT: Williams, Lewis T
APPLICANT: Cyster, Jason G
TITLE OF INVENTION: Modulating B lymphocyte Chemokine /
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,493
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCSF98-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2818 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

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; NAME/KEY: CDS
; LOCATION: 85..1200
; US-08-982-493-7

Query Match      12.7%; Score 238.4; DB 3; Length 2818;
Best Local Similarity 56.9%; Pred. No. 6.2e-42;
Matches 506; Conservative 0; Mismatches 366; Indels 18; Gaps 3;

OY 463 CTTGACGCGGCGCTTCCTGACAGCCCTTACAGCCTCTCTCTGCTGGGCTGGG 522
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DB 228 CTTCAAGGCGGTGTGTGTCGCGCTGACACCTCATCTTCTCTGCGGCTGATCGG 287
OY 523 CAACGGCGGGGTGGACCGCTGCTGAGCCGCGGACAGCCCTGACAGCAGCAGAC 582
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 288 CAACGCTCTGTGTCTGTGTGATCTGAGCGGCGACCGGACAGCAGATTCACGAGAC 347
OY 583 CTTCTGCTGCTGACCTAGCTGTATGACAGACGCTGCTGCTGCTGCTGCTGCTG 642
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 348 CTTCTGCTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 407
OY 643 AGTGAAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 408 GCGCGAGGGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 467
OY 703 CTTCAACATCACTTCTAGCAGAGAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTA 762
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 468 GCACAAAGTCACCTTCTACTGACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 527
OY 763 CCGAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 822
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 528 CCGGCGCATTTGCTGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 587
OY 823 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
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DB 588 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647
OY 883 GTGCGCCCAACAGCAGAGCGCTCAACG-----CACCCACTGCCAATPACAA 930
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 648 CAAAGTCAGCAGAGGCTATCACAACAACCTCCGACCTGCTGCTGCTGCTGCTGCTG 707
OY 931 CTTCCACACA---GTGCGCGCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 987
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 708 CCAAGCAGAAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 767
OY 988 GCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1044
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 768 GCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 827
OY 1045 TTTCAGGCGCCAGCGGCGCTGCGGCGCATGCGGCTGTGTGTGTGTGTGTGTGTGT 1104
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 828 CCAGCGCGCGCGCTGACGCGCAGAGAGGAGTCAAGGCTGCTGCTGCTGCTGCTGCT 887
OY 1105 TGGCGCTCTGTGAGCGCGCTGATACCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 1164
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 888 CTTTCTCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 947
OY 1165 CGCTTGTGCGCGCACTGTGCGGAGAGAGGAGTGTGAGAGGCGCAAGCGCTGCTGCT 1224
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 948 GCGCGGTGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1007
OY 1225 AGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1284
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1008 GTTCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1067
OY 1285 GTTCTGCGGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1334
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1068 GTTCTGCGAGTACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1117
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RESULT 14
US-08-628-655-1
; Sequence 1, Application US/08628655
; Patent No. 623123
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; GENERAL INFORMATION:
; APPLICANT: Lipi, Martin
; APPLICANT: Forster, Reinhold
; APPLICANT: Emrich, Thomas
; APPLICANT: Wolf, Ingrid
; APPLICANT: Kriemer, Elisabeth
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST
; TITLE OF INVENTION: LEUCOCYTE-SPECIFIC G PROTEIN-COUPLED RECEPTORS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,655
; FILING DATE: 13-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8484-0011-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2818 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 85..1200
; OTHER INFORMATION:
; US-08-628-655-1

Query Match      12.7%; Score 238.4; DB 4; Length 2818;
Best Local Similarity 56.9%; Pred. No. 6.2e-42;
Matches 506; Conservative 0; Mismatches 366; Indels 18; Gaps 3;

OY 463 CTTGACGCGGCGCTTCCTGACAGCCCTTACAGCCTCTCTCTGCTGGGCTGGG 522
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DB 228 CTTCAAGGCGGTGTGTGTCGCGCTGACACCTCATCTTCTCTGCGGCTGATCGG 287
OY 523 CAACGGCGGGGTGGACCGCTGCTGAGCCGCGGACAGCCCTGACAGCAGCAGAC 582
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 288 CAACGCTCTGTGTCTGTGTGATCTGAGCGGCGACCGGACAGCAGATTCACGAGAC 347
OY 583 CTTCTGCTGCTGACCTAGCTGTATGACAGACGCTGCTGCTGCTGCTGCTGCTGCTG 642
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DB 348 CTTCTGCTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 407
OY 643 AGTGAAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 408 GCGCGAGGGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 467
OY 703 CTTCAACATCACTTCTAGCAGAGAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTA 762
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 468 GCACAAAGTCACCTTCTACTGACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 527
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QY 763 CCGAATAGTATGATCCAGCCAGCTTACCGCCGGGGCCCGCCGCGGAGACCT 822
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Db 528 CCGGGCATTTGTCAGCCCTCCATGCTACCGCCAGCCGCTCTCTCCATCCAT 587
QY 823 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
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Db 588 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647
QY 883 GTGGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
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Db 648 CAAAGTCAGCAAGGCAATACCAACAACTCCCTCCACAGTTGCACTTCCCAAGGAA 707
QY 931 CTGCCACACA---GGTGGGCGCGCACGGCTCTGGGGTCTGCTGCTGCTGCTGCT 987
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Db 708 CCAAGCAAGAAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 767
QY 988 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1044
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Db 768 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 827
QY 1045 TTCCAGAGGGGCGAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1104
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Db 828 CCAAGCGGGCGCTCAAGCGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 887
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QY 1165 CGCTTTGGCCCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1224
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Db 948 GGGCGGTGCAATATCTGCAAGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTG 1007
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Db 1068 GTTCCGCAATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1117

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RESULT 15 PCT-US95-03032-1

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; Sequence 1, Application PC/TUS9503032
; GENERAL INFORMATION:
; APPLICANT: Repligen Corporation
; APPLICANT: The Trustees of Boston University
; TITLE OF INVENTION: ANTIBODIES TO INTERLEUKIN-8 RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 555x
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03032
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/237,937
; FILING DATE: 02-MAY-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/210,250
; FILING DATE: 15-MAR-94
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/803,842
; FILING DATE: 09-DEC-91
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/726,606
; FILING DATE: 09-JUL-91
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/685,101
; FILING DATE: 10-APR-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04766/015M01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1200
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-03032-1

Query Match      12.3%  Score 231, DB 5; Length 1200;
Best Local Similarity 55.5%  Pred. No. 1,9e-40;
Matches 491; Conservative 0; Mismatches 385; Indels 9; Gaps 2;

QY 446 CAGGACTTACAGCTGAACTTGACCGGGGCTTCTGCGACCCCTTACAGCTTCTTT 505
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QY 506 CTGTGGGGCTGCTGCGCAACGGCGGGTGGAGCCCTGCTGCTGACCGCGGACACC 565
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Db 273 CTGTGAGGCTGCTGCGGCACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 332
QY 566 CTGAGCAGCAACCGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 625
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Db 333 GCTTGGGTACACCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 392
QY 626 ACATGCGCGCTTGGGAGTGGAGCTGCGCTCCAGTGGGTCTTGGCTGCGCTGCG 685
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Db 393 ACATGCGCTATGCGGCGCGCTGCTCCCAAGAAAGGCTGGAATTTTGGGACGCGCT 452
QY 686 AAATGGCAGAGTCCCTTCTTCAACATCACTTACCGAGAGCCCTGCTGCTGCTG 745
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 453 AAGGTGCTGCTGCTTGAAGGAAGTCACTTCACTGAGTGAATCTGCTGCTGCTG 512
QY 746 ATCAGCTTGAACGCTACGAACTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 805
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Db 513 ATCAGTGTGAACGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 572
QY 806 CCGGCGCGGTGACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 865
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Db 573 C---ACTTGTCAAGTCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 629
QY 866 CCAAGCTTCACTTTC-----TGTGCGCCACACGACGAGAGGCGCTCAAGCCACC 919
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Db 630 CCGTCTTCTTCTTCCCAAGTCTTCTTCTCAAACTTCAACCCGCGCTGCTATAG 689
QY 920 TGGCAATACAACTTCCACAGAGTGGCGGACGCGCTGCGGGGCTGCGAGCTGTG 979
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Db 690 GACCTGGGTACACACAGGAAATGGCGATGCTGCTGCGGATCTGCGACACACTTTC 749
QY 980 GCGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039
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Db 750 GCGTTATCTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 809
QY 1040 CTGCTTTCAGGGGCGAGCGCGCTGCGGCGCTGCGGCTGCTGCTGCTGCTGCTG 1099
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Db 810 TTCCAGGCGCAATGAGGCGAAGCACCGGCGCTGCGGCTGCTGCTGCTGCTGCT 869
QY 1100 GCGTTTCCCTGCTGCTGAGCCCTTATCACTGCTGCTGCTGCTGCTGCTGCTGCT 1159

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D _b	870	ATCTTCTCTCTCTCTCTGCTGGCTTCACAACTGTGTCTCTCTGCGAGACACCCTCATTTAGG	929
O _y	1160	CTGGGCGCTTTTGCCGCCCACTGTGGCCGAGAAGCAGGGTAGAGTGCCCAAGTCGGTC	1219
D _b	930	ACCCACCGATCCAGGAGAGACTGCAGCGCTCGCAATGACATTGACCGGGCCCTGGACGCC	989
O _y	1220	ACCTCAGGCGCTGGGCTCATGACACTCTGCTCTCAACCCGCTGCTCTATAGCCTTTGTAGGG	1279
D _b	990	ACCGAAGTCTGGGCTTCTCGCACACTGCTCTCAACCCCATATCTTAGGCTTCAITGGC	1049
O _y	1280	GTCAGTTCGGGGAAGCGGATGTGGATGCTCTTGGCGGCTTGGC	1324
D _b	1050	CAAACTTTGCGCAATGATCTTCCTCAAGATGCTTTGGCGCCCGGGC	1094

Search completed: November 2, 2002, 04:19:48
Job time : 75 secs

QY	1801	ATTGSGCTTTTATTTATGCTAAATCCGCTTAAACCTTTCAATAAACGAGATCG	1860
Db	157560	ATTTCCTCTTTATTTATTTATGCTAAATCCGCTTAAACCTTTCAATAAACGAGATCG	157501
QY	1861	TCACGA	1866
Db	157500	TCACGA	157495

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HSGPCRIN8	
LOCUS	1670 bp mRNA linear
DEFINITION	H.sadpns mRNA for G-protein coupled receptor.
ACCESSION	X59876
VERSION	X59876.1 GI:1552845
KEYWORDS	G protein-coupled receptor; interleukin-8 receptor.
	PRI 16-MAY-1997

CDS

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RLCCPFGQIRQPSRSSRDSWSVSEYASGCI"

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QY	423	GCTGTACCTCCCCGCCCTTCCACAGACATTCAGCTTAACCTTGACCGGGCTTTCCTGC	482
Db	178	GCTGTACCTCCCCGCCCTTCCACAGAGACTTCAGCTTAACCTTGACCGGGCTTTCCTGC	237
QY	483	CAGCCCTCAGACGCCCTTTCGATGCGGGCTCTGGGCAAGCGCGGGGAGAGCG	542
Db	238	CAGCCCTCAGACGCCCTTTCGATGCGGGCTCTGGGCAAGCGCGGGGAGAGCG	297
QY	543	TGCTCTGAGCGGGGGAGAGAGCTTGAGACAGACCGAGACCTTCTGGTCCACCTAGCTG	602
Db	298	TGCTCTGAGCGGGGGAGAGAGCTTGAGAGAGACCGAGACACCTTCTGGTCCACCTAGCTG	357
QY	603	TAGCAGACAGCTGCTGTGCTGACATGCGGCTCTGGGAGCACTGAGAGCTGCCCTCAGT	662
Db	358	TAGCAGACAGCTGCTGTGCTGACATGCGGCTCTGGGAGCACTGAGAGCTGCCCTCAGT	417
QY	663	GGGCTCTTGGGCTCTGGGCTCTGGCAAGTGGAGGGCTCTCTCAACATCAACTTCTACG	722
Db	418	GGGCTCTTGGGCTCTGGGCTCTGGCAAGTGGAGGGCTCTCTCAACATCAACTTCTACG	477
QY	723	CAGGAGCCCTCTGCTGGGCTGACATCACTTTCAGCCGTACCTGAACTAGTTCATGGCA	782
Db	478	CAGGAGCCCTCTGCTGGGCTGACATCACTTTCAGCCGTACCTGAACTAGTTCATGGCA	537
QY	783	CCCACTCTACCGCGGGGGGCCCGCGCGGCTGACCTCACTGCTGTGCTG	842
Db	538	CCCACTCTACCGCGGGGGGCCCGCGCGGCTGACCTCACTGCTGTGCTG	597
QY	843	GGCTCTGCTGCTTTCGCCCCCAGACTTCATCTTCTGTGCGGCCACACAGACAGAC	902
Db	598	GGCTCTGCTGCTTTCGCCCCCAGACTTCATCTTCTGTGCGGCCACACAGACAGAC	657
QY	903	GCCCTAACGCGCACCCACTATGCAATACAACTTCCACAGAGTGGAGCGGCAAGGCTGCGGG	962
Db	658	GCCCTAACGCGCACCCACTATGCAATACAACTTCCACAGAGTGGAGCGGCAAGGCTGCGGG	717
QY	963	TGCTGACAGTGGTGGCTGAGCTTTCGTCTGCCCCCTGCTGTCATGGCTACTGATGCCC	1022
Db	718	TGCTGACAGTGGTGGCTGAGCTTTCGTCTGCCCCCTGCTGTCATGGCTACTGATGCCC	777
QY	1023	ACATCTGAGCGCTGCTGCTGCTTTCAGAGGGGCGAGCGGCGCTGCGGGCATGGGAGCTGG	1082
Db	778	ACATCTGAGCGCTGCTGCTGCTTTCAGAGGGGCGAGCGGCGCTGCGGGCATGGGAGCTGG	837
QY	1083	TGGTGGTGGTGGTGGCTTTCGCTCTGCTGGAGACCCCTATACCTGGGAGGCTGG	1142
Db	838	TGGTGGTGGTGGTGGCTTTCGCTCTGCTGGAGACCCCTATATACCTGGTGGTGGCTGG	897
QY	1143	TGGACATCTCATGAGACCTGGGCGGCTTTCGCCCCGCACTGTGGCCGAGAAAGCAGGGTAG	1202
Db	898	TGGACATCTCATGAGACCTGGGCGGCTTTCGCCCCGCACTGTGGCCGAGAAAGCAGGGTAG	957
QY	1203	ACGTGGCCAAAGTCGCTACCTCAGGCTCTGGGCTATCATCTGCTGCTCAACCGCTGC	1262
Db	958	ACGTGGCCAAAGTCGCTACCTCAGGCTCTGGGCTATCATCTGCTGCTCAACCGCTGC	1017
QY	1263	TCTATGCTTTGTAGGGGTCAAGTTCGGGGAGCGGAGTGGATGCTGCTTGGGCGCTGG	1322
Db	1018	TCTATGCTTTGTAGGGGTCAAGTTCGGGGAGCGGAGTGGATGCTGCTTGGGCGCTGG	1077
QY	1323	GCTGCCCAACAGAGAGGGCTCCAGAGAGCAGCATCTTTCGCCGGGAGTTCATCTCT	1382
Db	1078	GCTGCCCAACAGAGAGGGCTCCAGAGAGCAGCATCTTTCGCCGGGAGTTCATCTCT	1137
QY	1383	GGTCTGAGACCTCAGAGCGCTCTACTCTGGGCTTGTGAGCGCGGAATCCGGGCTCCCTT	1442
Db	1138	GGTCTGAGACCTCAGAGCGCTCTACTCTGGGCTTGTGAGCGCGGAATCCGGGCTCCCTT	1197
QY	1443	TGCGCCCAAGTCTGACTTCCCGGATTCAGAGGCTTCCTCCCTGCGCGGCTCTGGCT	1502
Db	1198	TGCGCCCAAGTCTGACTTCCCGGATTCAGAGGCTTCCTCCCTGCGCGGCTCTGGCT	1257
QY	1503	CTGCCAATATCTGCTGCCGGGAGCTACATGAGAGGCCCGAGCAACAGAGTCTCCGG	1562

Dd	1258	CTCCCAATATTCCTGCTCCGGAGCTACTGACGCCACCACACAGGTCTCCGG	1317
Oy	1563	GAAgCACCCTCCCGcTCTGAGAcTGCACCATTTGCTCTTAAGCTGGCCAAGCCCCA	1622
Dd	1318	GAAGCACACCTCCAGCTGTGAGGAcTGCACACATTGCTGCTTAGTGCCAACCCCA	1377
Oy	1623	TCTTCGCGCGGAgGTGGCTGCTTGAGGCCCACTGccCTTCTCATTTTGAAACTAAAC	1682
Dd	1378	TCTTCGCCCCGAgGTGGCTGCTTGAGCCCCCACTGccCTTCTCATTTTGAAACTAAAC	1437
Oy	1683	TTCACTCTCCCAATGGGGGAgTACAAGGCATGGCGTAGAGGTGCTGGCCCCAGAAG	1742
Dd	1438	TTCACTCTCCCAATGGGGGAgTACAAGGCATGGCGTAGAGGTGCTGGCCCCAGTAG	1497
Oy	1743	CCAGAGCCCAGGcCTCCAGCTCAGCAgTGACTGTGGcCATGGTCCCAAGAcCTCTATAT	1802
Dd	1498	CCAGAGCCCAGGcCTCCAGCTCAGCAgTGACTGTGGcCATGGTCCCAAGAcCTCTATAT	1557
Oy	1803	TTGCTCTTTTATTTTAAngTCTAAAATCCTGCTTAAAACTTTCAATAAACAGATGCTC	1862
Dd	1558	TTGCTCTTTTATTTTAAngTCTAAAATCCTGCTTAAAACTTTCAATAAACAGATGCTC	1617
Oy	1863	AGGAAAAAaaaaaa 1876 	
Dd	1618	AGGACCAAAAAaaa 1631	
RESULT 3			
LOCUS	ARL17009	1670 bp	DNA linear PAT 16-MAY-2001
DEFINITION	Sequence 1 from patent US 6140064.		
ACCESSION	ARL17009		
VERSION	ARL17009.1 GI:14097915		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1670)		
TITLE	Loetscher,M. and Moser,B.		
JOURNAL	Method of detecting or identifying ligands, inhibitors or promoters		
FEATURES	of CXc chemokine receptor 3		
source	Patent: US 6140064-A 1 31-Oct-2000;		
	Location/Qualifiers		
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BASE COUNT	272 a 574 c 436 g 388 t		
ORIGIN			

Query Match	82.2%	Score 1541.6;	DB 6;	Length 1670;
Best Local Similarity	99.1%;	Pred. No. 5.8e-267;		
Matches 1550; Conservative	0;	Mismatches 14;	Indels 0;	Gaps 0;

OY	303	CCCTGCGTTC	CCCGCCCT	CACAGGGATG	ATGACACCAAGTGTCT	AAATATACCCCGAGTTG	362
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OY	363	CCGCGCTCTCTG	GAGAACTTCA	GTCTTCTCTATG	ATGAGAAACAGAGATG	ACTGT	422
Db	118	CCGCGCTCTCTG	GAGAACTTCA	GTCTTCTCTATG	ATGAGAAACAGAGATG	ACTGT	177
OY	423	GCTGTACTCTCC	CGCGCTTG	CCCAACAGACTT	CAGCTGTAACTT	TGGACCGGCGCTTCTGC	482
Db	178	GCTGTACTCTCC	CGCGCTTG	CCCAACAGACTT	CAGCTGTAACTT	TGGACCGGCGCTTCTGC	237
OY	483	CAGCCCTTAC	AGCTCTCTTTC	TGCTGGGGGCTGTGGG	AACGGCGCGGTGGAGCGG		542
Db	238	CAGCCCTTAC	AGCTCTCTTTC	TGCTGGGGGCTGTGGG	AACGGCGCGGTGGAGCGG		297
OY	543	TGCTGTAGCG	CGGCGAGCGCTT	GAGACAGACCGACCTT	CTGTGCTCCACCTAGCTG		602
Db	298	TGCTGTAGCG	CGGCGAGCGCTT	GAGACAGACCGACCTT	CTGTGCTCCACCTAGCTG		357

QY	603	TAGCAGACAGCTCTCTGGTGTCTGACACTGCGCGCTCTGGGCAGTGGAGCGTGGCCCTCCAGT	662
Db	358	TAGAGAGACAGCTCTCTGGTGTCTGACACTGCGCGCTCTGGGCAGTGGAGCGTGGCCCTCCAGT	417
QY	663	GGGCTTTGGGCTGGGCGCTGGCAAGATGGACAGTCCCGCTTCAACATCAACTCTACG	722
Db	418	GGGCTTTGGGCTCTGGGCTCTGGCAAGATGGAGTGCCTCTTCAACATCAACTCTACG	477
QY	723	CAGGAGCCCTCTGCTGGCGCTGCATGACTGTTGACCGCTACCTGAACTAGTTCAATGCGCA	782
Db	478	CAGGAGCCCTCTGCTGGCGCTGCATGACTGTTGACCGCTACCTGAACTAGTTCAATGCGCA	537
QY	783	CCCAAGCTTACCGCGCGGGGGCCCCCGCGCGCTGACCTCAACCTGCTGGCTGTCTGG	842
Db	538	CCCAAGCTTACCGCGCGGGGGCCCCCGCGCGCTGACCTCAACCTGCTGGCTGTCTGG	597
QY	843	GGCTGTGCTCTTTTGGGCTCCGAGCTCACTCTCTGTCGGGGCCACACGACGAGCG	902
Db	598	GGCTGTGCTCTTTTGGGCTCCGAGCTCACTCTCTGTCGGGGCCACACGACGAGCG	657
QY	903	GGCTTCAAGCGCACCCACTGCGCAATACAACTTCCACAGGTGGGGCGCACAGGCTCTGGCGG	962
Db	658	GGCTTCAAGCGCACCCACTGCGCAATACAACTTCCACAGGTGGGGCGCACAGGCTCTGGCGG	717
QY	963	TGCTGTCAAGTGTGGCTGGCTTTCTGTGCGCCCTGCTGTGATGAGGCTACTGTATGCC	1022
Db	718	TGCTGTCAAGTGTGGCTGGCTTTCTGTGCGCCCTGCTGTGATGAGGCTACTGTATGCC	777
QY	1023	ACATCTCGGCGGCTGCTCTGTTTCCAGGGGGGACGAGGGGGCGCTGGGGGGCATGGGGCTGG	1082
Db	778	ACATCTCGGCGGCTGCTCTGTTTCCAGGGGGGACGAGGGGGCGCTGGGGGGCATGGGGCTGG	837
QY	1083	TGGTGTGTGTGTGTGTGGCTTTTGCCCTCTGCTGTGAGACCCCTATCACTGATGTGTGTGG	1142
Db	838	TGGTGTGTGTGTGTGTGGCTTTTGCCCTCTGCTGTGAGACCCCTATCACTGATGTGTGTGG	897
QY	1143	TGGACATCTCTATGAGACCTGGGGGCTTTGGCCCGCAACTGTGTGGCGAGAAAGCAGGATAG	1202
Db	898	TGGACATCTCTATGAGACCTGGGGGCTTTGGCCCGCAACTGTGTGGCGAGAAAGCAGGATAG	957
QY	1203	ACGTTGGGCAAGTCTGCTGACCTCAAGGCGCTGGGGCTACATGTGACATGTGCGCCAAACCGGCTGC	1262
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QY	1263	TCTATGCTTTGTAGGGGTCAAGTTCGCGAGCGGATGTGTGATGTGCTCTTTCGCGCTCGG	1322
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DEFINITION 279783
ACCESSION 279783.1 GI:2281709
VERSION 1
KEYWORDS G Protein-coupled Receptor CKR-L2.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo:
REFERENCE 1 (bases 1 to 1563)
AUTHORS Gutierrez,J., Varona,R., Zaballós,A., Lind,P. and Marquez,G.
JOURNAL unpublished
REFERENCE 2 (bases 1 to 1563)
AUTHORS Zaballós,A.
JOURNAL Direct Submission
SUBMITTED (03-SEP-1996) Angel Zaballós, Research, Pharmacia &
Upjohn, Antonio Lopez 109, Madrid, 28026, Spain
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DEFINITION Human orphan receptor GPR9 (GPR9) gene, partial cds.
ACCESSION U32674
VERSION U32674.1 GI:1002740
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1293)
Marchese, A., Helber, M., Nguyen, T., Heng, H.H.Q., Saldivia, V.R.,
Cheng, R., Murphy, P.M., Tsui, L.-C., Shi, X., George, S.R., O'Dowd, B.F.
and Docherty, J.M.
Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
and GPR14, encoding receptors related to interleukin 8,
neuropeptide Y, and somatostatin receptors
Genomics 29 (2), 335-344 (1995)
96115583

TITLE
JOURNAL 2 (bases 1 to 1293)
MEDLINE Marchese, A., Helber, M., Nguyen, T., Heng, H.H.Q., Saldivia, V.R.,
AUTHORS Cheng, R., Murphy, P.M., Tsui, L.-C., Shi, X., George, S.R., O'Dowd, B.F.
and Docherty, J.M.
Direct Submission
JOURNAL Submitted (31-JUL-1995) B.F. O'Dowd, Department of Pharmacology,
University of Toronto, 8 Raddle Creek Rd., Toronto, Ontario M5S
1A8, Canada

FEATURES
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BASE COUNT 201 a 458 c 357 g 277 t
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ACCESSION		AF223642				complete cds.
VERSION		AF223642.1	GI:8572056			
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SOURCE		Norway rat.				
ORGANISM		Rattus norvegicus				

REFERENCE	1 (bases 1 to 1678)
AUTHORS	Wang,X., Li,X., Schmidt,D.B., Foley,J.J., Barone,F.C., Ames,R.S. and Sarau,H.M.
TITLE	Identification and molecular characterization of rat CXCR3: receptor expression and interferon-inducible protein-10 binding are increased in focal stroke
JOURNAL	Mol. Pharmacol. 57 (6), 1190-1198 (2000)
MEDLINE	20286573
PUBMED	10825390
REFERENCE	2 (bases 1 to 1678)
AUTHORS	Wang,X., Li,X., Schmidt,D.B., Foley,J.J., Barone,F.C., Ames,R.S. and Sarau,H.M.
TITLE	Direct Submission
JOURNAL	Submitted (11-JAN-2000) Cardiovascular Sciences, DuPont Pharmaceuticals, Experimental Station E400/3420B, Wilmington, DE 19880/0400, USA

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RESULT 7
AB003174 1608 bp mRNA linear ROD 28-OCT-1998
LOCUS AB003174
DEFINITION Mus musculus mRNA for interferon-inducible protein 10 receptor,
complete cds.
ACCESSION AB003174.1 GI:3798731
VERSION 1
KEYWORDS interferon-inducible protein 10 receptor.
SOURCE Mus musculus blood cytotoxic T cells cell_line:CTL-2 cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 1608)
AUTHORS Tamaru, M.
TITLE Direct Submission
JOURNAL Submitted (17-APR-1997) Masahiro Tamaru, Japan Tobacco Inc. Central
Pharmaceutical Research Institute, Pharmaceutical Frontier Research
Laboratory; 13-2, Fukuura 1-chome, Kanazawa-ku, Yokohama,
Kanagawa 236, Japan (E-mail: tamaru@ikl.jti.co.jp,
Tel:81-45-786-7694, Fax:81-45-786-7692)
2 (sites)
REFERENCE Tamaru, M., Tomioka, Y., Yatsunami, K. and Narumi, S.
TITLE Cloning of the murine interferon-inducible protein 10 (IP-10)
JOURNAL receptor and its specific expression in lymphoid organs
MEDLINE Biochem. Res. Commun. 251 (1), 41-48 (1998)
FEATURES
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RDRPRVALCTIVWGLCTFLPALPDFITVLSANDOLNTHOYNPOVGRPALRVLQ
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Best Local Similarity 76.2%; Pred. No. 3.9e-142;
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384 GCTTCTTATGACTATGAGAAAGAGAGTGAAGTGTGCTGCTGACCTCCCGCCCTGCC 443
Db 160 CTTCTCTCAGATATATGAGGAAAAAGAGAGCAGC---TTCTCTGACTCCCGCCCTGCC 216
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Db 217 CACAGATTTACAGCTGAACTTTGACAGAACCTTCTGCCAGCCCTTACAGCCTCTCT 276
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Db 277 TCTTGCTGGGGCTGTAGGAAATGGGGGTGGTGTGCTGTGCTAGTACGACGCACTG 336
564 CCTGAGCAGCAGCAGCAGCTTCTGCTCCAGCTGATGAGAGACAGCAGTGTGCTG 623
Db 337 CCTGAGCAGCAGCAGCAGCAGCTTCTGCTCCAGCTGATGAGCAGATTTCTGCTGT 396
624 TGAACCTGCGCTGTGGGAGTGAAGAGCTGCCGTGAGTGGTCTTGGCTGAGCCT 683
Db 397 TAACTTTCATTTGTGGAGTGAAGTGAATGCTGTGCTGCTGAGTGGGTTCGGCCCTG 456
684 GCAAGTGGAGGTGGCTTCAACATCAACTTTCAGTGAAGAGAGCCCTCTGCTGCT 743
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744 GCATCAGCTTTGACCGCTTACATCAACTTTCAGTGAAGAGAGCCCTTACCGCGGAG 803
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804 CCCCGGCGCGGTGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 863
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1104 TTGCGCTGCTGAGCCCTTATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1163
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1164 GCGCTTTGGCGCCCACTGTGTGCGCGAAGAGAGGATGAGAGTGGCCAACTGCTCACT 1223

OY	1224	CAGCGCTGGGCGTACATGCATGCTGCCCAACCCGCTCCTATACCCTTTGAAGGGCA	1283
Db	908	CGGGCATGGGCTACTGTACCTGCTCTCCTAAACCGCTCTCTATGCCCTTTGGGGAAGA	967
OY	1284	AGTTCCGGGAGCGGATGTGCATGCTGCTCTTCGCGCTGGCTGCCCAACAGAGAGGGC	1343
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OY	1344	TCCAGAGCAGACCATGCTCTTCGCCGGGATTCATCTGCTGTGAGACTTCAGAGGCTT	1403
Db	1038	CCCACGGGACGGCCGATCTTCACGGAGAGAAATCATCCGTGGTGTGAGACAACTAGGGCTT	1087
OY	1404	CCTACTCGGGCTTTGAGAGCGCGAATTCGGGGCTGCCCTTTGGC--CCAGAGCTGACTTC	1461
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DEFINITION	Homo sapiens gene for chemokine receptor CXCR3, partial cds.		
ACCESSION	AB032735		
VERSION	AB032735.1 GI:7209692		
KEYWORDS	Chemokine receptor CXCR3.		
SOURCE	Homo sapiens DNA.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (sites)		
JOURNAL	Kato,H., Tsuchiya,N. and Tokunaga,K.		
MEDLINE	Single nucleotide polymorphisms in the coding regions of human		
PUBMED	CXK-chemokine receptors CXCR1, CXCR2 and CXCR3		
REFERENCE	Genes and immunity. 1 (5), 330-337 (2000)		
AUTHORS	2 (bases 1 to 319)		
TITLE	Kato,H., Tsuchiya,N. and Tokunaga,K.		
JOURNAL	Direct Submission		
MEDLINE	Submitted (24-SEP-1999) Hitoshi Kato, University of Tokyo,		
PUBMED	Department of Human Genetics, Graduate School of Medicine; 7-3-1		
REFERENCE	Hongo, Bunkyo-ku, Tokyo 113-0033, Japan		
AUTHORS	(E-mail:kato@em.u-tokyo.ac.jp, Tel:81-3-5841-3693,		
TITLE	Fax:81-3-5802-8619)		
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OY 1203	ACGTGCCAAGTCGCTACCTCAGGCCTGCGGTACATGCTGCTGCTCAACCCGCTGC 1262
Db 61	ACGTGCCAAGTCGCTACCTCAGGCCTGCGGTACATGCTGCTGCTCAACCCGCTGC 120
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Db 121	TCTATGCTTTGTAGGGTTCAGTTCGGGGAGCGGATGTGATGCTGTCTTGCGGCTCG 180
OY 1323	GCTGCCCAACACAGAGAGGGCTCCAGAGGCAAGCATCTCTCCGCGGGATTATCTCT 1382
Db 181	GCTGCCCAACACAGAGAGGGCTCCAGAGGCAAGCATCTCTCTCCGCGGGATTATCTCT 240
OY 1383	GGTCTGAGACCTCAGAGGCTCTTACTCGGGGCTGTGTGAGGCGGAATCGGGCTCCCTT 1442
Db 241	GGTCTGAGACCTCAGAGGCTCTTACTCGGGGCTGTGTGAGGCGGAATCGGGCTCCCTT 300
OY 1443	TGCCCCACAGTCTGACTTC 1461
Db 301	TGCCCCACAGTCTGACTTC 319
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DEFINITION	Homo sapiens gene for chemokine receptor CXCR3, partial cds.
ACCESSION	AB032736
VERSION	AB032736.1 GI:7209694
KEYWORDS	Chemokine receptor CXCR3.
SOURCE	Homo sapiens DNA.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (stiles)
TITLE	Kato,H., Tsuchiya,N. and Tokunaga,K. Single nucleotide polymorphisms in the coding regions of human CXc-chemokine receptors CXCR1, CXCR2 and CXCR3
JOURNAL	Genes and immunity. 1 (5), 330-337 (2000)
MEDLINE	21040285
PUBMED	11196695
REFERENCE	2 (bases 1 to 319) Kato,H., Tsuchiya,N. and Tokunaga,K. Direct Submmission Submitted (24-SEP-1999) Hitoshi Kato, University of Tokyo, Department of Human Genetics, Graduate School of Medicine; 7-3-1 Honjo, Bunkyo-ku, Tokyo 113-0033, Japan (E-mail:katon@em.u-tokyo.ac.jp, Tel:81-3-5641-3693, Fax:81-3-5802-8619)
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BASE COUNT      52 a      103 c      96 g      68 t
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Best Local Similarity 99.7%; Pred. No. 3.7e-47;
Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 AGGTGGCCAAAGTCGATCAGCTCAGGCGCTGAGCTACATGCACTGCTCCTCAACCCGCTGC 120
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DB 121 TCTATGCCCTTTTATGAGGGTCAAGTTCGGGAGCGGATGTGGATGCTGCTTTCGCGCTGG 180
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DB 181 GGTGCCCAACAGAGAGAGGCGCTTCAGAGGAGGCAATGCTTCCGCGGAGATTCAATCCT 240
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DB 241 GGTCTGAGACCTCAGAGGCGCTCCTACTCGGCTTGTGAGCGCGGAATCCGGGCTCCCTT 300
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DB 301 TGGCCCAACAGTGTGACTTC 319

RESULT 11
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DEFINITION Sequence 5 from patent US 5776457.
ACCESSION AR015971
VERSION AR015971.1 GI:3972248
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1679)
AUTHORS Lee,J. and Wood,W.I.
TITLE Antibodies to human PFAA receptor and compositions thereof
JOURNAL Patent: US 5776457-A 5 07-JUL-1996;
FEATURES
source Location/Qualifiers
BASE COUNT      327 a      532 c      457 g      363 t
ORIGIN
Query Match      12.8%; Score 240; DB 6; Length 1679;
Best Local Similarity 57.0%; Pred. No. 2.6e-33;
Matches 507; Conservative 0; Mismatches 365; Indels 18; Gaps 3;

OY 463 CTTCACAGCGGCTTCCTCCAGCCCTCAGAGCTCCTCTTCTGCTGGGCTGCTGGG 522
DB 512 CTTCACAGCGGCTTCCTCCAGCCCTCAGAGCTCCTCTTCTGCTGGGCTGCTGGG 571
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OY 583 CTTCCTGCTCCACCTAGCTGTAGCAGACAGCTGTGTGCTGACACATCGCGCTGTGGC 642
DB 632 CTTCCTGCTCCACCTAGCTGTGCGCGGCGACGCTGTGTGCTGATCTGTGCTTGGCGG 691
OY 643 AGTGAAGCGTGGCGTCCAGAGGCTCTTTGGCTGTGGCTTGTGCAAGATGCAAGTGCCT 702
DB 692 GAGCGAGGCTGTGTGGGCTGTGGGCTGTGGGACCTTCTGTGAAAACGTGTGATTCCT 751
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DB 872 CACTGCTGCTGTGTGTGGGCTGTGCTGCTGCTTTCGCTCCAGACTTCATTTCT 931
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OY 1165 CGCTTTGGCGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1224
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OY 1285 GTTCCGGAGCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1334
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DEFINITION Sequence 5 from patent US 5840856.
ACCESSION AR060749
VERSION AR060749.1 GI:5987199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1679)
AUTHORS Chuntcharapai,A., Lee,J., Hebert,C. and Kim,K.Jin.
TITLE Antibodies to a human PFAA superfamily receptor
JOURNAL Patent: US 5840856-A 5 24-NOV-1998;
FEATURES
source Location/Qualifiers
1. 1679
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BASE COUNT      327 a      532 c      457 g      363 t
ORIGIN
Query Match      12.8%; Score 240; DB 6; Length 1679;
Best Local Similarity 57.0%; Pred. No. 2.6e-33;
Matches 507; Conservative 0; Mismatches 365; Indels 18; Gaps 3;

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Db 512 CTTCAAGGGCGTGTGTGTCGCCGTGACAGCCCTCATCTTCTCTGCGGGCTGATCG 571

OY 523 CAAGCGCGGGTGGACGCGCTGCTGAGCGCGGACAGCCCTGAGCAGCAGCAGAC 582
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Db 572 CAACGTCGTGTGCTGTGATCTGGAGCGGACCGCAGACAGCATGTTCCAGGAGAC 631

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Db 632 CTTCTGTTCCACTGTGCGGTGCGACCTCTGCTGTGTATCTTGTGCGCTTGCCGT 691

OY 643 AGTGAAGCTGCGCTCAGTGGGCTTTTGGCTCTGAGCTTGCAGAGTGCAGGTCGCT 702
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Db 692 GCGCGAGGGCTGTGTGGGTGGGTCTCTGGGAGACTTCTCTGAAAAGTGTGATTCCT 751

OY 703 CTTCAACATCACTTCTACGACAGAGCCCTCTGCTGACCTGTGACATGCTTTGACCG 762
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OY 823 CACTGCTGCTGTGAGGGGCTGTGCTGCTTTTCGCGCTCCAGACTTATCTTCT 882
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OY 883 GTGCGCCACACGACGAGCGCTCAAGC-----CACCACCTGCCAATACAA 930
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LOCUS
DEFINITION Sequence 5 from patent US 5892017.
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VERSION
KEYWORDS
SOURCE
ORGANISM      Unknown.
REFERENCE      Unclassified.
AUTHORS      1 (bases 1 to 1679)
TITLE      Lee,J. and Wood,W.I.
JOURNAL      Nucleic acid encoding PF4A receptor
FEATURES      Patent: us 5892017-A 5 06-APR-1999;
              Location/Qualifiers
              source
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BASE COUNT      327 a      532 c      457 g      363 t
ORIGIN
Query Match      12.8%; Score 240; DB 6; Length 1679;
Best Local Similarity 57.0%; Pred. No. 2.6e-33;
Matches 507; Conservative 0; Mismatches 365; Indels 18; Gaps 3;

OY 463 CTTGACCGGGCCCTTCCTGACAGCCCTTACAGCCCTCTCTTCTGCGGGCTGCGG 522
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Db 512 CTTCAAGGGCGTGTGTGTCGCCGTGACAGCCCTCATCTTCTCTGCGGGCTGATCG 571

OY 523 CAAGCGCGGGTGGACGCGCTGCTGAGCGCGGACAGCCCTGAGCAGCAGCAGAC 582
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Db 572 CAACGTCGTGTGCTGTGATCTGGAGCGGACCGCAGACAGCATGTTCCAGGAGAC 631

OY 583 CTTCTGCTTCACCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 642
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Db 632 CTTCTGTTCCACTGTGCGGTGCGACCTCTGCTGTGTATCTTGTGCGCTTGCCGT 691

OY 643 AGTGAAGCTGCGCTCAGTGGGCTTTTGGCTCTGAGCTTGCAGAGTGCAGGTCGCT 702
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Db 692 GCGCGAGGGCTGTGTGGGTGGGTCTCTGGGAGACTTCTCTGAAAAGTGTGATTCCT 751

OY 703 CTTCAACATCACTTCTACGACAGAGCCCTCTGCTGACCTGTGACATGCTTTGACCG 762
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Db 752 GCACAAAGTCACTTCTACTGACAGAGCTGTGCTGCGCTGATGCGGTGAGACGCTA 811

OY 763 CCGAAGCATAGTTCATGACACCAAGCTTACGCGCGGGGGGGCGCGCGCTGACCT 822
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OY 823 CACTGCTGCTGTGAGGGGCTGTGCTGCTTTTCGCGCTCCAGACTTATCTTCT 882
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OY 883 GTGCGCCACACGACGAGCGCTCAAGC-----CACCACCTGCCAATACAA 930
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OY 1045 TTCCAGGGGCGACGCGGCTGTGCGGCTATGCGGCTGTGTGTGTGTGTGTGTGTGTGT 1104
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RESULT 14
ARI03431
LOCUS AR103431 1679 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6087475.
ACCESSION AR103431
VERSION AR103431.1 GI:12815019
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1679)
AUTHORS Lee, J. and Wood, W. I.
TITLE PF4A receptor
JOURNAL Patent: US 6087475-A 5 11-JUL-2000;
FEATURES
source 1.1679
location/Qualifiers
BASE COUNT 327 a 532 c 457 g 363 t
ORIGIN
Query Match 12.8%; Score 240; DB 6; Length 1679;
Best Local Similarity 57.0%; Pred. No. 2.6e-33;
Matches 507; Conservative 0; Mismatches 365; Indels 18; Gaps 3;

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OY 523 CAAGCGCGGCTGGAGCGCTGCTGAGCGCGGAGACCCCTGAGCAGCAGCAGC 582
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Db 692 GGGCGAGGGCTGTGTGGGCTGCTGGGAGCTTCTCTGCAAAAGTGTGATGCTGCT 751
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OY 703 CTTCACATCACTTCTACGAGAGCCCTCTGCTGGGCTGTGATGAGCTTTGACCGCTA 762
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Db 752 GCACAAAGTCACTTCTACTGACAGCAGCTGCTGCGCTGTGATGCGCTGAGACGCTA 811
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OY 763 CCGAATCATAGTTCAATGACCGACCGCTTACCGCGGGGGGGGGGGGGGGGGGGGGGGGG 822
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Db 812 CCGGCGCATTTGTCAGCGCGCTTCACTGACCGCACCGCGGCTCTCTCTCCATCCACAT 871
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OY 823 CACCTGCTGCTGTCTGTGCGGCTGCTGCTGCTTTCGCGCTTCCAGACTTCACTTCTCT 882
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OY 883 GTTCGGCCCAACGAGAGCGGCTCAAGC-----CAGCCACTGCCAATACAA 930
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OY 931 CTTCACACA-----GTGGGCGGACAGGCTCTGGGCGGTGCGAGCTGGTGGCTTTCT 987
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RESULT 15
113754
LOCUS 113754 1679 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 6 from patent US 5440021.
ACCESSION 113754
VERSION 113754.1 GI:996820
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1679)
AUTHORS Chundharapal, A., Herbert, C., Kim, K. J. and Lee, J.
TITLE Antibodies to human IL-8 type B receptor
JOURNAL Patent: US 5440021-A 6 08-AUG-1995;
FEATURES
source 1.1679
location/Qualifiers
BASE COUNT 327 a 532 c 457 g 363 t
ORIGIN
Query Match 12.8%; Score 240; DB 6; Length 1679;
Best Local Similarity 57.0%; Pred. No. 2.6e-33;
Matches 507; Conservative 0; Mismatches 365; Indels 18; Gaps 3;

OY 463 CTTCGACCGGCGCTTCTGCTGACAGCCCTCTACAGCTCTCTTCTGCTGGGCTGCTGGG 522
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Db 512 CTTCAGAGCGGCTGTGTGCTGCGCTGACCTATCTTCTCTGCGGCTGATCGG 571
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OY 523 CAAGCGCGGCTGGAGCGCTGCTGAGCGCGGAGACCGCTGAGCAGCAGCAGCAGCAGCAGC 582
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OY 583 CTTCCTGCTTCACTTACCTGTACAGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 642
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OY 643 AGTGAAGCTGCGCTCAGTGGGCTTTTGGCTCTGAGCTCTGCAAAAGTGAGAGTGCCT 702
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OY 763 CCGAATCATAGTTCAATGACCGACCGCTTACCGCGGGGGGGGGGGGGGGGGGGGGGGGG 822
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OY 883 GTTCGGCCCAACGAGAGCGGCTCAAGC-----CAGCCACTGCCAATACAA 930
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Run on: November 2, 2002, 04:07:46 ; Search time 229 seconds
(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1874.4	99.9	1876	18	AAAT72800
2	1873.2	99.9	1877	22	AAH35033
3	1541.6	82.2	1670	19	AAV26557
4	1097	58.5	1107	21	AAA30593
5	1095.4	58.4	1107	21	AAA30714
6	1094.6	58.3	1159	20	AA232713
7	844.4	45.0	1620	19	AAV34793
8	240	12.8	1679	13	AAO37107
9	240	12.8	1679	16	AAO99009

10	240	12.8	1679	16	AAO80522	Human lymphocyte P
11	238.4	12.7	1119	21	AAA30626	Human G protein-co
12	238.4	12.7	1119	21	AAA30727	DNA encoding human
13	238.4	12.7	2818	20	AAK87710	Human Burkitt's ly
14	238.4	12.7	3620	22	ABA09117	Human Burkitt lymph
15	231	12.3	1200	13	AAO30011	Sequence encoding
16	231	12.3	1200	16	AAO99949	Recombinant high a
17	229	12.2	3011	24	AAV34899	Human DNA sequence
18	229	12.2	4017	23	AAK83768	DNA encoding novel
19	217.8	11.6	1373	16	AAO99951	Recombinant high a
20	216.6	11.5	1137	21	AAA30632	Human G protein-co
21	216.6	11.5	1710	23	AAK76560	DNA encoding novel
22	216.6	11.5	1900	15	AAO66162	Partial coding seq
23	216.6	11.5	1900	19	AAV18349	Human V31 seven tr
24	216.6	11.5	1900	21	AAV1709	Human V31 seven tr
25	216.6	11.5	2058	15	AAO66153	Putative seven tra
26	216.6	11.5	2058	19	AAV18345	Human V31 seven tr
27	216.6	11.5	2058	21	AAV18345	Genomic clone of 7
28	216.6	11.5	2160	15	AAO66160	Putative seven tra
29	216.6	11.5	2160	19	AAV18347	Human V31 seven tr
30	216.6	11.5	2160	21	AAV1707	Human V31 seven tr
31	216.6	11.5	6923	22	AAK69852	Human 77M receptor
32	216	11.5	1068	24	AAK16599	Human immune/haema
33	215	11.5	1137	21	AAA30729	DNA encoding baboo
34	213.4	11.4	2087	22	AAK69854	Human immune/haema
35	211.8	11.3	2154	15	AAO64125	Human immune/haema
36	211.8	11.3	2154	19	AAV22684	Epstein Barr virus
37	211.8	11.3	2154	19	AAV25490	DNA encoding G-pro
38	209.8	11.2	1373	13	AAO30013	CDNA for Epstein B
39	209.6	11.2	1068	24	AAK16596	Sequence encoding
40	204.8	10.9	2785	23	AAK7796	DNA encoding rhesu
41	204.8	10.9	12789	24	AAK16876	DNA encoding novel
42	204	10.9	1609	24	ABL32812	Human interleukin
43	203.2	10.8	1068	17	AAK40128	Human immune syste
44	203.2	10.8	1068	17	AAK16589	Human IL-8 recepto
45	203.2	10.8	1068	24	ABK16594	DNA encoding human

ALIGNMENTS

RESULT 1	
AA772800	
ID	AA772800 standard; CDNA; 1876 BP.
AC	AA772800;
XX	
DT	28-SEP-1997 (first entry)
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DE	Human G-protein chemokine receptor HSATU68 cDNA.
XX	
KW	HSATU68: G-protein chemokine receptor; 7-transmembrane receptor
KW	signal transduction; gene therapy; diagnosis; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
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FT	complement (173..190)
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FT	1402..1420
FT	primer_bind
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PN	WO9725340-A1.
XX	
PD	17-JUL-1997.
XX	
PF	11-JAN-1996; 96WO-US00499.
XX	
PR	11-JAN-1996; 96WO-US00499.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.

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Db	1141	GGTGAGCATCCTCATGGACCTGGGGCCGCTTTGGCCGCGCAACTGTGGCCGAGAAAGCAGGGT	1200	
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Db	1201	AGAGGTGGCCAAAGTCGGTCACTTCAGGCGCTGGGCTTACATGCACTGTCCCTCAACCCGCT	1260	
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Db	1861	TCAGAGAAAAAATAAATA 1876		

RESULT 3

AAV26557

ID AAV26557 standard; DNA; 1670 BP.

XX AAV26557;

AC 14-AUG-1998 (first entry)

XX 14-AUG-1998 (first entry)

DE Human IP-10/Mig receptor CXCR3 gene.

KW ds; chemokine receptor; cellular signal; treatment; T cell;

KM inflammatory disease; antitumour; antiviral.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 69..1175

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FT		/*tag= b
FT	polyA_site	1624..1670
FT		/*tag= c
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PN	WO9811218-A1.	
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PD	19-MAR-1998.	
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PF	10-SEP-1997;	97WO-US15915.
XX		
PR	31-MAR-1997;	97US-0829839.
PR	10-SEP-1996;	96US-0709838.
XX		
PA	(KOCH-) KOCHER INST THEODOR.	
XX	(LEUKOSITE INC.	
PI		
XX	Loetscher M, Mackay CR, Moser B, Qin S;	
DR	WPI; 1998-207381/18.	
DR	P-PsDB; AAM54371.	
XX		
PT	DNA encoding CXC chemokine receptor 3 - inhibitors and promoters of	
PT	which, are useful for treatment of inflammation or in anti-tumour or	
PT	anti-viral therapy	
XX		
PS	Claim 6; Fig 1; 137pp; English.	
XX		
CC	The mammalian CXC chemokine receptor 3 (CXCR3) gene encodes a protein	
CC	which can selectively bind one or more chemokines and can mediate	
CC	cellular signaling and/or a cellular response in response. Inhibitors	
CC	and promoters of mammalian CXCR3 can be detected and identified using	
CC	host cells expressing CXCR3. CXCR3 inhibitors can be used for treatment	
CC	of inflammatory diseases which are T cell mediated. CXCR3 promoters are	
CC	useful for antitumour or antiviral therapy.	
SQ	Sequence 1670 BP; 272 A; 574 C; 436 G; 388 T; 0 other:	
Query Match	82.2%; Score 1541.6; DB 19; Length 1670;	
Best Local Similarity	99.1%; Pred. NO. 0;	
Matches 1550; Conservative	0; Mismatches 14; Indels 0; Gaps 0;	
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OY	363 CGGCCCTCTGGAGAATTACACTCTTCTATGACTATGAGAAAAAGAGTGAATCGT	422
Db	118 CGGCCCTCTGGAGAATTACACTCTTCTATGACTATGAGAAAAAGAGTGAATCGT	177
OY	423 GCTGTACTCCCCCGCCCTGCACAGAGACTTACGCTGAATTCGACGGGCTTCTGTC	482
Db	178 GCTGTACTCCCCCGCCCTGCACAGAGACTTACGCTGAATTCGACGGGCTTCTGTC	237
OY	483 CAGCCCTCTAGAGCCCTCCCTTTCGTGCTGGGGCTGCTGGGCAACGGCGGGTGGACCGG	542
Db	238 CAGCCCTCTAGAGCCCTCCCTTTCGTGCTGGGGCTGCTGGGCAACGGCGGGTGGACCGG	297
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Db	298 TCCTCTGAGCGCGGAGACAGCCCTGAGAGACGACGACCTTCCGTGCACACTAGTGTG	357
OY	603 TAGCAGACAGCTGTGTGTGTGACACTGCGCTCTGGCAGTGAAGCGTGCCTCCAGT	662
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OY	663 GGCTCTTGGCTCTGTGGCTCTGCAAAAGTGGAGGTGCCCTCTTCAACATCAACTTCTAGC	722
Db	418 GGCTCTTGGCTCTGTGGCTCTGCAAAAGTGGAGGTGCCCTCTTCAACATCAACTTCTAGC	477
OY	723 CAGGAGCCCTCTGTGGCTGATCAGCTTGAACGCTGAACAATGATTCATGGCA	782

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Db 538 CCCACTCTACCGCGGGGGGGGGGGGGGGGGGGGGGATACCTTACCTGCGCTGTCTGGG 597
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Oy 1023 ACATCTGGCGCTGCTGCTGCTTCCAGGGGCGCAGCGGGGCGCATGCGGCTGG 1082
Db 778 ACATCTGGCGCTGCTGCTGCTTCCAGGGGCGCAGCGGGGCGCATGCGGCTGG 837
Oy 1083 TGGTGGTGGTGGTGGCTGCTTGGCTGCTGCTGAGACCCCTATCAGCTGCTGCTGG 1142
Db 838 TGGTGGTGGTGGTGGCTGCTTGGCTGCTGCTGAGACCCCTATCAGCTGCTGCTGG 897
Oy 1143 TGGACATCTCATGACCTTGGGGCGCTTTGGCGCCGCACTGTGGCGGAGAAACAGAGTAG 1202
Db 898 TGGACATCTCATGACCTTGGGGCGCTTTGGCGCCGCACTGTGGCGGAGAAACAGAGTAG 957
Oy 1203 ACGTGGCAAGTCGGTCACTACCTGAGGCTGGGCTATCATGCTAGCTGCTGCTCAACCGCGTGC 1262
Db 958 ACGTGGCAAGTCGGTCACTACCTGAGGCTGGGCTATCATGCTAGCTGCTGCTCAACCGCGTGC 1017
Oy 1263 TCTATGCTTTGTAGGGGTCAAGTTCGGGAGCGGAGTGTGATGCTGCTTTGGCGCTGG 1322
Db 1018 TCTATGCTTTGTAGGGGTCAAGTTCGGGAGCGGAGTGTGATGCTGCTTTGGCGCTGG 1077
Oy 1323 GCTGCGCCCAACAGAGAGGGCTCCAGAGGACGCCATGCTTTCCCGCGGGGATTTATCT 1382
Db 1078 GCTGCGCCCAACAGAGAGGGCTCCAGAGGACGCCATGCTTTCCCGCGGGGATTTATCT 1137
Oy 1383 GGTGTGAGACCTCAGAGAGGCTCTTACTGCGGCTTGTGAGGCGGGAATCCGGGCTCCCTT 1442
Db 1138 GGTGTGAGACCTCAGAGAGGCTCTTACTGCGGCTTGTGAGGCGGGAATCCGGGCTCCCTT 1197
Oy 1443 TCGCCCAAGTCTGACTTCCCGGCAATTCAGGCTCTCTCCCTCTGTCGCGGCTGTGCT 1502
Db 1198 TCGCCCAAGTCTGACTTCCCGGCAATTCAGGCTCTCTCCCTCTGTCGCGGCTGTGCT 1257
Oy 1503 CTCCCAATATCTCTGCTCCCGGGGACTCAGTGGCAAGCGCCAGACACCAAGGTCTCCGG 1562
Db 1258 CTCCCAATATCTCTGCTCCCGGGGACTCAGTGGCAAGCGCCAGACACCAAGGTCTCCGG 1317
Oy 1563 GAAGGCACTCTCCAGCTCTGAGAGCTGACCATTTGCTGCTTAGCTGAGCAACCCCA 1622
Db 1318 GAAGGCACTCTCCAGCTCTGAGAGCTGACCATTTGCTGCTTAGCTGAGCAACCCCA 1377
Oy 1623 TCTGTCGCGCGGAGGTGGCTCTCTGAGACCCCACTGCCCTTCTCATTTTGAACACTAAAC 1682
Db 1378 TCTGTCGCGCGGAGGTGGCTCTCTGAGACCCCACTGCCCTTCTCATTTTGAACACTAAAC 1437
Oy 1683 TTTCAATTTCCCAAGTGGGGGAGTACAAAGCATGGGCTAGAGGCTGCTGCCCATGAAG 1742
Db 1438 TTTCAATTTCCCAAGTGGGGGAGTACAAAGCATGGGCTAGAGGCTGCTGCCCATGAAG 1497
Oy 1743 CCAGAGCCAGGCTCCAGCTCAGAGTGTGAGTGTGGCCATGGTCCCAAGACCTTATAT 1802
Db 1498 CCAGAGCCAGGCTCCAGCTCAGAGTGTGAGTGTGGCCATGGTCCCAAGACCTTATAT 1557
Oy 1803 TTTGCTCTTTTATTTTATGTCTAAATCTGCTTAAACTTTTCAATAAACAAGATGCTC 1862
Db 1558 TTTGCTCTTTTATTTTATGTCTAAATCTGCTTAAACTTTTCAATAAACAAGATGCTC 1617
```

```
Oy 1863 AGGA 1866
Db 1618 AGGA 1621

RESULT 4
AAA30593
ID AAA30593 standard; cDNA, 1107 bp.
XX
XX AAA30593;
AC 21-AUG-2000 (first entry)
XX
XX
DE Human G protein-coupled receptor GPR9 cDNA.
XX
XX G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200022129-A1.
PN
XX
XX 20-APR-2000.
PD
XX
XX 12-OCT-1999; 99WO-0523938.
PF
XX
XX 13-OCT-1998; 98US-0170496.
PR
XX
XX (AREN-) ARENA PHARM INC.
PA
XX
XX Behan DP, Chalmers DT, Liaw CW;
PI
XX
XX WPI: 2000-329165/28.
DR
XX
XX P-PSDB; AAY90614.
PT
XX
XX Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents.
PS
XX
XX Example 1: Page 115; 341pp; English.
CC
XX
XX The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC and AAA30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(A)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC or Ala, and is preferably Lys. When the endogenous residue at this
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC The 15 amino acid stretch between the substituted amino acid and the pro
CC may be endogenous, non-endogenous, or a mixture of endogenous and
CC non-endogenous residues. The constitutively active GPCRs are useful for
CC identifying antagonists, agonists and partial agonists for use as
CC pharmaceutical agents. The mutant proteins are also useful in research
CC settings for elucidating the roles of the receptors in normal and
CC diseased conditions. Antagonists for a particular GPCR are useful for
CC treating diseases and disorders associated with that receptor. Because
CC the novel mutant GPCRs are constitutively active, they can be used
CC directly for screening of compounds without the need for endogenous
CC ligands. The present sequence represents cDNA encoding a human wild-type
CC GPCR used in an exemplification of the invention. This was cloned and
CC subjected to site-directed mutagenesis (SDM) to generate DNA encoding
CC the corresponding mutant of the invention.
XX
XX Sequence 1107 bp; 163 A; 380 C; 324 G; 240 T; 0 other;
SO
XX
XX Query Match 58.5%; Score 1097; DB 21; Length 1107;
XX Best Local Similarity 100.0%; Pred. NO. 4,1e-234;
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Matches 1097:  Conservative  0:  Mismatches  0:  Indels  0:  Gaps  0:
OY 324 AGGTGAGTGCACCAAGTGTAAATGACGCCGAGGTTCCGCCCTCTGTGAGAACTTCA 383
    |||||||
Db 11 AGGTGAGTGCACCAAGTGTAAATGAGCGCGAGGTTCCGCCCTCTGTGAGAACTTCA 70
OY 384 GCTCTTCTATATGATGAGAAAAAGAGAGTACTGTGTGTACTCTCCGCCCTGCG 443
    |||||||
Db 71 GCTCTTCTATATGATGAGAAAAAGAGAGTACTGTGTGTACTCTCCGCCCTGCG 130
OY 444 CACAGAGACTTACCGTGAACCTTGACCGCGGCGCTTCCGTCACGCCCTTACAGCTCTCT 503
    |||||||
Db 131 CACAGAGACTTACCGTGAACCTTGACCGCGGCGCTTCCGTCACGCCCTTACAGCTCTCT 190
OY 504 TTCTGCTGGGGCTGTGTGGCAACGGCGGCGGTGGCAAGCCGTGTGTGAGCCGCGAG 563
    |||||||
Db 191 TTCTGTGGGGCTGTGTGGCAACGGCGGCGGTGGCAAGCCGTGTGTGAGCCGCGAG 250
OY 564 CCCTGAGCAGCACCGACACCTTCTGTCTCCACCTAGCTGTAGACAGACAGCTGTGTGC 623
    |||||||
Db 251 CCCTGAGCAGCACCGACACCTTCTGTCTCCACCTAGCTGTAGACAGACAGCTGTGTGC 310
OY 624 TGACACTGCGGCTGTGGGAGTGGAGCGGCGGCTGCAGTGGGTCTTTGGCTGTGCGCTCT 683
    |||||||
Db 311 TGACACTGCGGCTGTGGGAGTGGAGCGGCTGCAGTGGGTCTTTGGCTGTGCGCTCT 370
OY 684 GCAGAGTGGCAGGTGCGCTCTTCAACATCACTTCTACGAGAGCCCTCTCTGTGGCT 743
    |||||||
Db 371 GCAGAGTGGCAGGTGCGCTCTTCAACATCACTTCTACGAGAGCCCTCTCTGTGGCT 430
OY 744 GCATCAGCTTTTACCGGCTTACCTGAACATAGTTTCATGCCCACCCAGCTTACCGCGGGGCG 803
    |||||||
Db 431 GCATCAGCTTTTACCGGCTTACCTGAACATAGTTTCATGCCCACCCAGCTTACCGCGGGGCG 490
OY 804 CCGCGGCGCGGCTGACCCCTCACTGCTGGGCTGTGTGGGGGCTGTGGCGCTTTTTCGCC 863
    |||||||
Db 491 CCGCGGCGCGGCTGACCCCTCACTGCTGGGCTGTGTGGGGGCTGTGGCGCTTTTTCGCC 550
OY 864 TCCAGAGACTTCACTTCTGCTGTGCGCCACACAGAGAGCGGCTTCAAGCGCACCACTGCG 923
    |||||||
Db 551 TCCAGAGACTTCACTTCTGCTGTGCGCCACACAGAGAGCGGCTTCAAGCGCACCACTGCG 610
OY 924 AATTAACACTTCCCAAGGTGGGCGCGACGCGCTGTGCGGGTGTGCAAGCTGTGCGTGCCT 983
    |||||||
Db 611 AATTAACACTTCCCAAGGTGGGCGCGACGCGCTGTGCGGGTGTGCAAGCTGTGCGTGCCT 670
OY 984 TTCTGTGCGCGCTGTGCTATGAGGCTTATGCTATGCGCCACATCCGAGGCGCTGCTCG 1043
    |||||||
Db 671 TTCTGTGCGCGCTGTGCTATGAGGCTTATGCTATGCGCCACATCCGAGGCGCTGCTCG 730
OY 1044 TTTTCAGAGGCGCAGCGCGCTGTGCGGGCCATCGCGCTGTGTGTGTGCTGTGTGCGCT 1103
    |||||||
Db 731 TTTTCAGAGGCGCAGCGCGCTGTGCGGGCCATCGCGCTGTGTGTGTGCTGTGTGCGCT 790
OY 1104 TTGCGCTGTGCGGAGCCCGCTATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1163
    |||||||
Db 791 TTGCGCTGTGCGGAGCCCGCTATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 850
OY 1164 GCGCTTTTGGCCGCAACTGTGTGCGCAGAAAAGCAGGAGTACGTGGCAGTGGTCACTT 1223
    |||||||
Db 851 GCGCTTTTGGCCGCAACTGTGTGCGCAGAAAAGCAGGAGTACGTGGCAGTGGTCACTT 910
OY 1224 CAGGCGCTGGGCTACATGCACTGCTGCTCAACCCGCTGCTATAGCTTTTGTAGGGGTCA 1283
    |||||||
Db 911 CAGGCGCTGGGCTACATGCACTGCTGCTCAACCCGCTGCTATAGCTTTTGTAGGGGTCA 970
OY 1284 ACTTCCGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1343
    |||||||
Db 971 ACTTCCGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1030
OY 1344 TCCAGAGGAGCAGCATGCTTCCCGCGGGAGTTCATCCTGTGTGTGAGCTTACAGAGGCT 1403
    |||||||
Db 1031 TCCAGAGGAGCAGCATGCTTCCCGCGGGAGTTCATCCTGTGTGTGAGCTTACAGAGGCT 1090
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OY 1404 CCTACTCGGGCTGTGA 1420
    |||||||
Db 1091 CCTACTCGGGCTGTGA 1107

RESULT 5
AAA30714
ID AAA30714 standard; DNA; 1107 BP.
XX
XX AAA30714;
XX
XX 21-AUG-2000 (first entry)
XX
XX DNA encoding human mutant G protein-coupled receptor GPR9 (M254K).
DE
XX
XX G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist; mutant; ss.
XX
XX Homo sapiens.
OS Synthetic.
PN WO200022129-A1.
XX
XX 20-APR-2000.
PD
XX
XX 12-OCT-1999; 99WO-US23938.
PF
XX 13-OCT-1998; 98US-0170496.
PR
XX (AREN-) ARENA PHARM INC.
PA Behan DP, Chalmers DT, Liaw CW;
PI WPI; 2000-329165/28.
XX
XX DR P-PSDB; AAY90648.
XX
XX Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents _
XX
XX Example 2; Page 223; 341pp; English.
PS
XX The invention relates to constitutively active, non-endogenous versions
XX of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
XX AAY90677 and AAY90683-Y90687), and to DNA encoding them (AA30709-A30743
XX and AA30775-A30779). The mutant proteins of the invention contain a
XX mutation in a portion of the protein comprising intracellular loop 3
XX (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
XX is substituted for an endogenous residue in IC3 at a position 16 amino
XX acids N-terminal of an endogenous proline in TM6 to form a sequence
XX X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
XX or Ala, and is preferably Lys. When the endogenous residue at this
XX position is Lys, this residue is replaced by His, Arg or preferably Ala.
XX The 15 amino acid stretch between the substituted amino acid and the Pro
XX may be endogenous, non-endogenous, or a mixture of endogenous and
XX non-endogenous residues. The constitutively active GPCRs are useful for
XX identifying antagonists, agonists and partial agonists for use as
XX pharmaceutical agents. The mutant proteins are also useful in research
XX settings for elucidating the roles of the receptors in normal and
XX diseased conditions. Antagonists for a particular GPCR are useful for
XX treating diseases and disorders associated with that receptor. Because
XX the novel mutant GPCRs are constitutively active, they can be used
XX directly for screening of compounds without the need for endogenous
XX ligands. Sequences AAA30709-AA30743 and AAA30775-A30779 represent DNAs
XX encoding the mutant human GPCRs of the invention.
XX
XX Sequence 1107 BP; 164 A; 380 C; 324 G; 239 T; 0 other;

Query Match 58.4%; Score 1095.4; DB 21; Length 1107;
Best Local Similarity 99.9%; Pred. No. 9.3e-234;
Matches 1096: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
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OY 324 AGGTAGTACCAACCAAGTCTAAATGAGCCGAGGTGCCGCTCTGAGAACTTCA 383
 DB 11 AGGTAGTACCAACCAAGTCTAAATGAGCCGAGGTGCCGCTCTGAGAACTTCA 70
 OY 384 GCTCTCTCTATGATATGAGAGAAAAGAGAGTACTGCTGTACTCCGCCCTGCC 443
 DB 71 GCTCTCTCTATGATATGAGAGAAAAGAGAGTACTGCTGTACTCCGCCCTGCC 130
 OY 444 CACAGGACTTCAGCCCTGAACTTCGACCGGGCTTCTGCGACCCCTCTACAGCTCTCT 503
 DB 131 CACAGGACTTCAGCCCTGAACTTCGACCGGGCTTCTGCGACCCCTCTACAGCTCTCT 190
 OY 504 TTCTGCTGGGGCTGCTGGGCAACGGGCGGTGACCGCTGCTGCTGAGCCGGGAGAG 563
 DB 191 TTCTGCTGGGGCTGCTGGGCAACGGGCGGTGAGCCCTGCTGCTGAGCCGGGAGAG 250
 OY 564 CCCTGAGCAGCAGCAGCACTTCTGCTCCACCTAGCTTAGAGAGACGCTGCTGTGC 623
 DB 251 CCCTGAGCAGCAGCAGCACTTCTGCTCCACCTAGCTTAGAGAGACGCTGCTGTGC 310
 OY 624 TGCACACTGCGCTCTGGGAGTGGAGCGTCCGCTCAGTGGGTCTTGGCTCTGCGCTCT 683
 DB 311 TGCACACTGCGCTCTGGGAGTGGAGCGTCCGCTCAGTGGGTCTTGGCTCTGCGCTCT 370
 OY 684 GCAAGTGGCAGGTGCGCTCTTCAACATCACTTCTACGAGAGCGCTCTGCTGGCGCT 743
 DB 371 GCAAGTGGCAGGTGCGCTCTTCAACATCACTTCTACGAGAGCGCTCTGCTGGCGCT 430
 OY 744 GCATGAGCTTTGACCGGCTACGTGAACATAGTTCAGCCAGCTCTACCGCGGGGGG 803
 DB 431 GCATGAGCTTTGACCGGCTACGTGAACATAGTTCAGCCAGCTCTACCGCGGGGGG 490
 OY 804 CCGCGGCGCGGCTGAGCCCTGACCTGCTGGGCTCTGCTGGGCGCTCTGCTTTTGGCC 863
 DB 491 CCGCGGCGCGGCTGAGCCCTGACCTGCTGGGCTCTGCTGGGCGCTCTGCTTTTGGCC 550
 OY 864 TCCGAGACTTCATCTTCTGCTGCGCCACACAGAGAGCGGCTCAACAGCAGCCACTGCC 923
 DB 551 TCCGAGACTTCATCTTCTGCTGCGCCACACAGAGAGCGGCTCAACAGCAGCCACTGCC 610
 OY 924 AATPACAATCTCCACAGAGTGGCGCGCAGCGCTCTGCGGGTGTGAGTGGTGGCT 983
 DB 611 AATPACAATCTCCACAGAGTGGCGCGCAGCGCTCTGCGGGTGTGAGTGGTGGCT 670
 OY 984 TTCTGCTGCGCTGCTGCTGATGAGCTTACTGCTATGCTCCACATCTGCGCGCTCTCTG 1043
 DB 671 TTCTGCTGCGCTGCTGCTGATGAGCTTACTGCTATGCTCCACATCTGCGCGCTCTG 730
 OY 1044 TTTCCAGGGGCCAGGGCGGCTGCGGGCCATGCGGCTGGTGGTGGTGGTGGGCT 1103
 DB 731 TTTCCAGGGGCCAGGGCGGCTGCGGGCCATGCGGCTGGTGGTGGTGGTGGGCT 790
 OY 1104 TTGCGCTCTGCTGGAAGCCCTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1163
 DB 791 TTGCGCTCTGCTGGAAGCCCTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850
 OY 1164 GGGCTTTGGCCCGCAACTGTGGCCGAGAAAGAGAGGTAAACGTGGCCAAAGTGGTACCT 1223
 DB 851 GGGCTTTGGCCCGCAACTGTGGCCGAGAAAGAGAGGTAAACGTGGCCAAAGTGGTACCT 910
 OY 1224 CAGGCTGGGCTACATGACACTGCTGCTCAACCCGCTGCTATGCTTGTAGAGGGTCA 1283
 DB 911 CAGGCTGGGCTACATGACACTGCTGCTCAACCCGCTGCTATGCTTGTAGAGGGTCA 970
 OY 1284 AGTTCGGGAGCGGATGTGGATGCTGCTTTCGCGCTGGGCTGCCCAACGAGAGGGC 1343
 DB 971 AGTTCGGGAGCGGATGTGGATGCTGCTTTCGCGCTGGGCTGCCCAACGAGAGGGC 1030
 OY 1344 TCCAGAGGAGGCAATGCTTTCGCGCGGGGATTCATCTGCTGTGAGACCTAGAGGCT 1403
 DB 1031 TCCAGAGGAGGCAATGCTTTCGCGCGGGGATTCATCTGCTGTGAGACCTAGAGGCT 1090

OY 1404 CCTACTCGGGCTTGTGA 1420
 DB 1091 CCTACTCGGGCTTGTGA 1107
 RESULT 6
 AA32713
 ID AA32713 standard; cDNA; 1159 BP.
 XX
 AC AA32713;
 XX
 DT 31-JAN-2000 (first entry)
 XX
 DE Human chemokine receptor CXCR3b cDNA.
 XX
 KW Chemokine receptor; CXCR3b; splice variant; N-terminus; CXCR3a;
 KW seven transmembrane; G-protein coupled; CXC; IP10; Mlg; T-lymphocyte;
 KW recruitment; selective; activated; T-cell; neutrophil; inflammation;
 KW tissue distribution; therapy; rheumatoid arthritis; psoriasis;
 KW multiple sclerosis; transplantation; atherosclerosis; restenosis;
 KW cytokine; delayed type hypersensitivity reaction; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..52
 FT exon
 FT /tag= a
 FT /note="Novel exon found in CXCR3b transcripts"
 FT CDS 23..1159
 FT /tag= b
 FT /product= "N-terminal fragment of CXCR3b"
 PN MO9350299-A1.
 XX
 PD 07-OCT-1999.
 PF 26-MAR-1999; 99WO-SE00501.
 XX
 PR 30-MAR-1998; 98SE-0001098.
 XX
 PA (ASTR) ASTRA PHARM LTD.
 PA (ASTR) ASTRA AB.
 PI Delaney S;
 XX
 DR WPI: 1999-633638/54.
 DR P-PSDB: AAY50129.
 XX
 PT New polynucleotide encoding a variant chemokine receptor -
 XX
 PS Claim 1: Fig 2: 18bp: English.
 XX
 CC This sequence represents cDNA encoding human chemokine receptor CXCR3b,
 CC a splice variant of chemokine receptor CXCR3 (also referred to as
 CC CXCR3a). Chemokines are a family of small cytokines which bring about the
 CC recruitment of leukocytes during inflammation. The CXC chemokines
 CC mostly attract neutrophils, while the CC chemokines are less selective.
 CC All chemokine receptors are seven transmembrane G-protein coupled
 CC receptors and most are receptors for a number of chemokines, CXCR3a
 CC being a receptor for the CXC chemokines IP10 and Mlg. CXCR3a is
 CC expressed in activated, but not in resting T-lymphocytes, and may
 CC therefore play an important role in the selective recruitment of
 CC T-cells which occurs in T-cell mediated inflammatory conditions.
 CC CXCR3b may have an altered pattern of tissue distribution and
 CC function in the inflammatory process. Cells expressing the active
 CC CXCR3b are useful for identifying ligands, especially agonists and
 CC antagonists, of a chemokine receptor. In addition, the receptor
 CC facilitates identification of chemokines responsible for mediating
 CC inflammation reactions via interaction with CXCR3b. The modulation
 CC of inflammatory responses is of therapeutic benefit in many conditions
 CC such as rheumatoid arthritis, psoriasis, multiple sclerosis,
 CC transplantation, delayed type hypersensitivity reactions, atherosclerosis
 CC and restenosis.

CC also involve chemical antagonists which block complex production or
 CC utilize competitive binding. Binding compounds identified (agonists or
 CC antagonists) can be used to modulate the physiological responses in cells
 CC (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal
 CC proliferation, regeneration, generation and atrophy. The polypeptides
 CC are also used to produce antibodies useful diagnostically, for drug
 CC screening or for polypeptide purification. The polynucleotides are useful
 CC to produce probes for detecting the polypeptides, and to isolate the
 CC polypeptides or related sequences, especially from other species. They
 CC also allow transformation of cells for polypeptide production.

SO Sequence 1620 BP; 366 A; 457 C; 405 G; 392 T; 0 other;

Query Match 45.0%; Score 844.4; DB 19; Length 1620;

Best Local Similarity 76.6%; Pred. No. 5.7e-178; Matches 1101; Conservative 0; Mismatches 326; Indels 11; Gaps 5;

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OY 324 AGGTAGTGTACCCAGCAAGTGTAAATGACGCCAGGTTGCCGCCCTCTGAGAACTTCA 383
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 76 AGGTTAGTGAAGCTCAAGTGTAGATGCTCGAGCTTCTCTTCTTGGAAGAAAGCA 135
OY 384 GCTCTTCTATACTATGAGAAAGAGAGTACTGCTGCTGACTCTCCGCCCTGCC 443
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 136 CCTCTCCCTACATATATGGGAAACGAGAGCGAC---TTCTCTGACTCCCGCCCTGCC 192
OY 444 CACAGGACTTACGCTGAACTTCGACCCGGGCTCTCTGCGCAGCCCTTACAGCTCTCT 503
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 193 CACAGGATTTTACGCTGAACTTTGACAGAACTTCTGCGAGGCCCTTACAGCTCTCT 252
OY 504 TTCTGCTGGGCTGCTGGGCAAGCGCGCGTGCGACGCCGTGCTGAGCCGCGAGAC 563
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 253 TCTTGCTGGGCTGCTGAGCAGATGGGGCGTGCTGCTGCTAGTACAGATCAGCGAC 312
OY 564 CCCTGAGCAGCAGCAACACTTCTGCTGCTACCTGCTGAGCAACAGCTGCTGCTG 623
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 313 CCTTACGAGCAGCAGCAACCTTCTGCTGCTACCTGCTGAGCGATGTTCTGCTG 372
OY 624 TGACATGCGGCTGCGGAGTGTAGAGCGCGCTGCGTCAAGGGGCTTGGCTGGGCT 683
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 373 TAACTCTTTCATTTGCGGAGTGTAGTGTCTGCTGCTGAGTGGGTTTGGCCCTG 432
OY 684 GCAAGTGTGAGGTGCGCTCTTTCACATCACTTCTACGAGAGCCCTCTGCTGCT 743
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 433 GCAAGTGTGAGCGCGCTTTCACATCACTTCTATGCAAGGGGCTTCTGCTGCT 492
OY 744 GCATAGCTTTGACCGCTTACCTGAAATAGTTCATGCAACCACTTACCGCGGGGC 803
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 493 GTATAGCTTTCACAGATATCTGAGCATGTGACGCCACCAAGATCTACCGAGGAC 552
OY 804 CCGCGCGCGGCTGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 863
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 553 CCGGGTGTGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
OY 864 TCCGAGACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 923
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 613 TCCGAGATTTTCACTTACCTATCAGCCAACTAGATCAGCGCTCAATGCAACCT 672
OY 924 AATTAACACTTCCACAGGTGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 983
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 673 AGTACAACCTTCCACAGGTGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
OY 984 TTCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1043
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 733 TCTCTGCTGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
OY 1044 TTTCCAGGGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 793 TCTCCAGAGGCGGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 852
OY 1104 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1163
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 853 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 912

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OY 1164 GCGCTTGGCCCGCACTGTGGCCGAGAAAGCAGGAGTGTAGACGTGGCCAACTGCTACCT 1223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 913 GAGTTTGGCCCGCACTGTGGTGTGAAAAAGCCAGCTGTGATGTGGCCAACTGCTACCT 972
OY 1224 CAGGCTGGGCTTACATGACACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1283
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 973 CGGCGATGGGGTACATGACACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1032
OY 1284 AGTTCGGGAGCGGATGTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1033 AGTTAGAGAGAAATGTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
OY 1344 TCCAGAGGAGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1093 CCGAGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1152
OY 1404 CCTACTGCGGCTTGTGAGGCGCGGATCCGCGGCTCCCTTTCCG--CCACAGTGTGACTTC 1461
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1153 CCTACTGCGGCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1212
OY 1462 CCGGCAATTCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1213 ACTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
OY 1522 CCGGAGCTACTGTGAGAG--CCGAGCAGCAGAGTGTGCGGAGGAGCCAGCCCTCCAGCT 1580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1273 CCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1329
OY 1581 CTGAGGAGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1638
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1330 ACAGAGCAACACATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1389
OY 1639 GCGTCTGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1698
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1390 AGTGTCTGAGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1449
OY 1699 GCGGAGAGTACAAGCATGGCATGGCGTGTGAGGCGTCCGCAATGAAGCCAGCGGCGC 1756
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1450 GAGAGAGGAGAGGAGCAATAGCAGAGAGGCGGCGGCTTGTGAGCAGCTGAATGTGCC 1507

```

```

RESULT 8
AA037107
ID AA037107 strand: DNA; 1679 BP.
XX
XX AA037107;
AC
XX
XX
XX 12-MAR-1993 (first entry)
DT
XX
DE New platelet factor 4 receptor superfamily member PF4AR11.
XX
XX IL-6R; G-protein coupled receptor family; rhodopsin superfamily;
KW pro-inflammatory cytokine; 8tr.9; ss.
XX
XX Homo sapiens.
FH
FT
FT CDS
FT Location/Qualifiers
FT /tag= a
FT /product= PF4AR11
XX
PN W09217497-A.
XX
XX 15-OCT-1992.
PD
XX
XX 23-MAR-1992; 92WO-US02317.
PF
XX
XX 29-MAR-1991; 91US-0677211.
PR
XX 19-DEC-1991; 91US-0810782.
PA
XX (GETH ) GENENTECH INC.
XX
XX Holmes WE, Lee J, Wood WI.
PI

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```
XX WPI: 1992-366191/44.
DR P-PSDB; AAR27793.
XX Isolated human platelet factor 4 super-family receptor
XX polypeptide and corresp. antibodies and DNA - useful as
PT diagnostic and screening agents, and for treating inflammation or
PT PF4R-mediated disorders
XX
XX Claim 7; Fig 5; 78pp; English.
CC The IL-8 receptor cDNA sequence was isolated (see AA029505) and a
CC 874bp sub-fragment of the coding sequence was used as a probe to
CC screen human cell line HL60 and human peripheral blood lymphocyte
CC cDNA libraries. Two new gene sequences were found that are clearly
CC related to the IL-8 receptor. One of these was contained in clone
CC 8tr.9 and is predicted to encode an amino acid sequence which is
CC 36% and 38% identical with the high and low affinity IL-8 receptor
CC sequences, respectively. See also AA037107.
XX
XX Sequence 1679 BP; 327 A; 532 C; 457 G; 363 T; 0 other;
SQ
Query Match 12.8%; Score 240; DB 13; Length 1679;
Best Local Similarity 57.0%; Pred. No. 9.8e-44;
Matches 507; Conservative 0; Mismatches 365; Indels 18; Gaps 3;
OY 463 CTTTGACCGGGCCCTTCTGCTCCAGCCCTCTACAGCCCTCTTCTGCTGGGCTGGG 522
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 512 CTTTCAAGGGCGGTGCTGCTGCGCGTGGCTACAGCCCTCATCTCTGCGCTGATCGG 571
OY 523 CAACGGCGGGTGGGACCGCTGCTGTGAGCCGGCGACAGCCCTGAGCAGCAGCAGAC 582
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 572 CAACGTCCTGCTGCTGCTGATCTGAGGCGGACCGCAGACAGTGTTCCAGGAGAC 631
OY 583 CTTCTGCTGCTACGCTGATGAGCAGACAGCGCTGCTGCTGCTGCTGCTGCTGCTG 642
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 632 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 691
OY 643 AGTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 692 GGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 751
OY 703 CTTTCAACATCACTTCTACGAGAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 762
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 752 GCACAAAGTCACTTCTACGAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 811
OY 763 CCGTAACATAGTTTCAATGACACCGAGCTTACCGCGGGGGCCCGCGCGGTGACCGT 822
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 812 CCGTGGCATTTGTCACGCGCGTTCATGCTTACCGCGCGCGCGCTCTCTCCATCCACAT 871
OY 823 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 872 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
OY 883 GTGCGGCCACACGAGAGCGCTCAAGC-----CAGCCACTGCCAATACAA 930
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 932 CAAAGTCAACCAAGGCGATCACACAAATCCCTGACCTTGGACCTTCTCCCAAGAGAA 991
OY 931 CTTCCACACA---GTTGGCGCGACAGCGCTCTGCGGGTGGAGCTGCTGCTGCTTCT 987
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 992 CCAAGAGAAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
OY 988 GCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1044
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1052 GCTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1111
OY 1045 TTTCAGAGGCGCAGCGGCTGCTGCGGCGCATGCGGCTGCTGCTGCTGCTGCTGCTGCT 1104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1112 CCAGGCGGCGCCCTCAAGCGCAGAGGAGTCAAGGCTGCTGCTGCTGCTGCTGCTGCT 1171
OY 1105 TGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1172 CTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
```

```
OY 1165 CGCTTGGCCCGGCACTGTGGCCGAGAGACAGGATGAGAGTGGCCAGTGGTCACTTC 1224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1232 GGGCGTGGCAATATCACTGCAAGCTGATGCTCTCTCCCGTGGCATCACTATGCTGA 1291
OY 1225 AGGCTTGGCTTACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1292 GTTCTGCGGCGCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1351
OY 1285 GTTCCGGAGCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1334
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1352 GTTCCCGAGTACCTGTGCGGCTCTGACAGCAAGCTGGGCTGATCCGGCC 1401
RESULT 9
AA099009
ID AA099009 standard; cDNA; 1679 BP.
XX
XX AA099009;
XX
XX 26-MAR-1996 (first entry)
XX
XX Chemokine superfamily receptor coding sequence.
XX
XX Interleukin; IL-8; inflammation; psoriasis; dermatitis;
XX rheumatoid arthritis; inflammatory bowel disease;
XX chronic lung inflammation; treatment; antibody;
XX affinity purification; detection; ss.
XX
XX Homo sapiens.
XX
XX US5440021-A.
XX
XX 08-AUG-1995.
XX
XX 29-MAR-1991; 91US-0677211.
XX
XX 25-FEB-1994; 94US-0202056.
XX
XX 29-MAR-1991; 91US-0677211.
XX
XX (CHUN/) CHUNTHARAPAI A.
XX (HEBE/) HERBERT C.
XX (KIM/) KIM K J.
XX (LEE/) LEE J.
XX
XX Chuntharapai A, Hebert C, Kim KJ, Lee J;
XX
XX WPI: 1995-283151/37.
XX P-PSDB; AAR92239.
XX
XX New antibodies against interleukin 8 type B receptor - used to treat
XX or prevent inflammation, also for detecting receptor expression and
XX purify.
XX
XX Example 2; Columns 51-54; 62pp; English.
XX
XX Antibodies directed against the interleukin-8 receptor B can be used
XX to treat or prevent inflammation e.g. psoriasis, dermatitis,
XX rheumatoid arthritis and particularly inflammatory bowel disease and
XX chronic lung inflammation. When immobilised, these antibodies may
XX be used to detect interleukin-8 receptor B expression in cells and
XX tissues and for affinity purification of interleukin-8 receptor B
XX from cells. This sequence is an additional chemokine superfamily
XX receptor which was identified by probing lambda libraries of genomic
XX DNA from a human monocyte-like cell line (L-60) and human peripheral
XX blood lymphocytes using a large fragment of the interleukin-8 type
XX A receptor DNA (see AA099006).
XX
XX Sequence 1679 BP; 327 A; 532 C; 457 G; 363 T; 0 other;
SQ
Query Match 12.8%; Score 240; DB 16; Length 1679;
Best Local Similarity 57.0%; Pred. No. 9.8e-44;
Matches 507; Conservative 0; Mismatches 365; Indels 18; Gaps 3;
```

QY	463	CTTGGACGCGGCGCTTCCCTGCGACCCGCTAAAGCCCTCTTTGCGGGGCTCTGGG	522
Db	512	CTTAAAGGCCGTGTTGCTGCGCCGTGGCCTTACAGCCCTCATCTTCTCTCGGGGCTAATGG	571
QY	523	CAACGGGCGGTGGACAGCCGTGCTGTGAAGCCGGGCGAGAGCCCTGAGCAGCACCGACAC	582
Db	572	CAACGCTCGGTGTGTGTGATCTCGAGGGGCGACCGGACAGACGAGCATGTTCCACGGAGAC	631
QY	583	CTTCCCTCTCCACTTACGCTTACCAACAGCGTGCCTGGTGTGACACACTTCCGCTTGCGGC	642
Db	632	CTTCTCTTTCACCTTGCGCGCTGGCCCAACCTCTCGCTGAGCTTTCATCTTGGCCCTTTGCGCGT	691
QY	643	AGTGGAGCTGCGGTTCACATGGGTCTTTTGGCTCTGGGCTCTCAAGAGGAGCGGCCCT	702
Db	692	GGCGGAGGGCGCTGTGTGGCGCTGGGTCTCGGGGAGACCTCTCTGCAAAACGTGATTTGGCT	751
QY	703	CTTTCACATCAACTTCTACGAGGAGGCCCTCTGCTGCGCTGCATATCAGCTTTGACCGCTA	762
Db	752	GCACAAGATCAACTTCTTCTACGACGACGCGCTGCTCCGGGCTGCATAGCGCTGTGAGCGCTGA	811
QY	763	CGTCAACATATGTTTCATCCCAACCGATACACGGCGGGGGGGCCCGGGCCCGGTACGCT	822
Db	812	CGTGGCCATGTCTCAGCGCGCTCCATGCTTACGCGCACCGCGCGCTCTCTTCATCCACAT	871
QY	823	CACCTGCGCTGCTGTCTGGGGGCTGTGCGCTCTTTCGCGCTCCAGACTTCATCTTCT	882
Db	872	CACCTGTGGGACATCTGCGCTGTGGGCTTCCCTCTTTCGCTTGCAGAGATCTTCTTGC	931
QY	883	GTCGGGCCACAGACGAGCGGCTCAACGC-----CACCCACTGCCATTAACA	930
Db	932	CAAAAGTACGCCAAGGCCATCAACAACCTCCGACAGCTGACCTCTCTCCAGAGAA	991
QY	931	CTTCCACACA---GATGGGCGGCACCGGCTCTGCGGAGTGTGACAGTGTGGGCGCTTCT	987
Db	992	CCAAGCAGAAAGCGATGCCGTGTTTCAACCTCCGATTTCTCTTACATGTGGCGGATTTCT	1051
QY	988	GCTGCCCCCTGCTGTATGAGCTTACTGTCTATGCCCCATCTGGCCGTGCTG--CTGCT	1044
Db	1052	GCTGCCCATCTGTGTATGTGGCGTGTGCATAGTGGGGGATGACAGAGTTTCCGACAGC	1111
QY	1045	TTTCCAGGGGACAGCGGCGCTCTGCGGCGCAATGGCGGTGGTGGTGTGCTGGGCTT	1104
Db	1112	CCAGCGGCGGCGCTCAGAGGGGAGAAAGGAGTACAGGGTGGCATCTGTGTGACAGATCTT	1171
QY	1105	TGCGCTCTGTCGACCCCTATATCACTGTGTGTGCTGTGTGACATCTTCATGAGACTGGG	1164
Db	1172	CTTCTCTGTGTGTACCCCTACCCATCTGTCTATCTTCTCGGACACCTGGCGAGGCTGAA	1231
QY	1165	CGCTTTGGCCGACAGTGTGGCGGAGAAAGACAGGGTACAGCGGGCCAGTGGTCACTC	1224
Db	1232	GGCGGTGACAAATCTGCAAGCTGAATGGCTCTCTCCCGTGGCGCATATCATTGTGA	1291
QY	1225	AGGCGTGGGTACATGCATGCTGCTCAACCGCGCTCTATGTGCTTTGTATAGGGGTCAA	1284
Db	1292	GTTTCTGTGGCGCTGGCCACACTGCTGCTCAACCCCAATGCTCTACATTTTGGCGGGGTAA	1351
QY	1285	GTTCCGGGAGCGGATGTGATGTGTCTTTTGGCGCTGGGCGTCCGCCAAC	1334
Db	1352	GTTCCGAGTGAACCTGTCTGGGTCTCTTGAACGAAGTGGGCGCTTACCGGCG	1401

RESULT 10	
AAQ80522	
ID	AAQ80522 standard; cDNA; 1679 bp.
XX	
AC	AAQ80522;
XX	
DT	18-JUL-1995 (first entry)
XX	
DE	Human lymphocyte PFAAR cDNA.
XX	
KW	Interleukin-8 receptor; IL-8 receptor; PFAAR

KW	platelet factor superfamily receptor; lymphocyte; chemotactic;
KM	inflammation; inflammatory disease; arthritis; emphysema; cystic;
KM	fibrosis; colitis; bronchitis; meningitis; therapeutic; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 369..1487
FT	/tag= a
XX	
PN	MO9428931-A.
PD	22-DEC-1994.
XX	
PF	07-JUN-1994; 94WO-US06380.
XX	
PR	11-JUN-1993; 93US-0076093.
XX	
PA	(GETH) GENENTECH INC.
PI	Chuntharapai A, Hebert C, Kim KU, Lee J;
DR	WPI; 1995-036114/05.
XX	P-PSDB; AAR68813.
PT	Treatment of inflammatory disorders - by administering an
PR	antibody capable of binding a platelet factor 4 superfamily
PT	receptor polypeptide
XX	
PS	Disclosure: Page 56-58; 83pp; English.
XX	
CC	2 PF4R members were identified by probing lambda libraries from
CC	human monocyte-like cell line HL-60 and human peripheral blood
CC	lymphocytes using a large fragment of IL-8 receptor DNA (full
CC	sequence given in AA080520). The nucleotide sequences of the 2
CC	PF4Rs are given in AA080521 and AA080522, and their respective
CC	amino acid sequences in AAR68812 and AAR68813.
XX	
SQ	Sequence 1679 BP; 327 A; 532 G; 457 G; 363 T; 0 other;
Query Match	12.8%; Score 240; DB 16; Length 1679;
Best Local Similarity	57.0%; Pred No. 9.8e-44;
Matches 507; Conservative	0; Mismatches 365; Indels 18; Gaps
OY	463 CTTTCAGCGGGGCTTTCGTGCACGCCCTCTACAGCCTCTTTCTGCTGGGCTGCTGGG 522
Dd	
OY	512 CTTCGAAGGCCGCTGTGCTGCTGCTGCGGTGACAGCCTCATCTTCTGCTGGGCTGATCGG 571
OY	523 CAACGGCGCGGTGGACGCCCTGCTGTACAGCGCGGGGACAGCCCTTGAGACAGCACGACAC 582
Dd	
OY	572 GAACCTCTCCCTGGCTGCTGATCTCTGAGCGGACAGCGGACAGACGACGAGTTCACAGGAGAC 631
OY	583 CTTCCTGCTCCACCTAGCTGTAGACAGACAGCGGTGCTGGCTGACACTGCTGCTGGGCT 642
Dd	
OY	632 CTTCTGTTCACACTGAGCCGCTGACCCTCTGCTGGCTGCTTCACTTCTGCTGCTGGCT 691
OY	643 AGTGACGCTGCGCTGCAAGTGGTCTTTGGCTCTGAGCTCTGCAAAAGTGACAGTGGCT 702
Dd	
OY	692 GGCGAGGGGCTGTGGGCTGGGTCTGTGGGAGACCTTCTCTGCAAAACGTGATTGCTCCCT 751
OY	703 CTTCAACATCAACTTCTACGACAGAGACCTCTGCTGCTGAGCTGCTCATGAGCTTTGACGCGTA 762
Dd	
OY	752 GCACAAGAAGCACTTCTACTGTCAGACAGACCTGCTCCCTGAGCTCATGCGCGTGGACGCGTA 811
OY	763 CGTGAACATAGTTCANATGCAACGACAGCTTACAGCGCGGGGGCCCCGGCCCGGCTGACCT 822
Dd	
OY	812 CTTGCAATTTGTCCACGCGCTCATGCTTACCGCACGCGCGGCTCTCTTCATCCACAT 871
OY	823 CACCTGCTGCTGCTGTGAGGGCTGCTGCTGCTTTTTCGCGCTTCCAGACTTCATCTTCTCT 882
Dd	
OY	872 CACCTGTGGGACATCTGTGCTGTGGGCTTCTCTCTTGTGCTGACAGATATCTCTTGGC 931
OY	883 GTGGGCCACACGACGAGCGCTTCAAGC-----CACCACTGCCAATACAA 930

Db 932 CAAGTCGAGCAAGGCGCATACACAACTCCGTCACGTTGACCTTCTCCCAAGAGAA 991
QY 931 CTTCACACA---GGTGGGCGCGACGGCTCTGCGGGTCTGACGCTGGCTGGCTTTCT 987
Db 992 CCAAGAGAGAAAGCGCATGCTGTTTCACTCCGATTCCTCTTACCATGTGGCGGATTCCT 1051
QY 988 GCTGCCCCCTGCTGTCATGAGGCTACTGCTATATGCGCAATCTTGGCGGCTG---CTGGT 1044
Db 1052 GCTGCCATGCTGTGATGGGCTGTGCTACGTTGGGGGTAGTGCACAGGTTGGCGCAGGC 1111
QY 1045 TTCCAGGGGCGACGGGCGCTGGGGCCATGGCGCTGGTGTGTGTGTGTGTGTGTGTGTGT 1104
Db 1112 CCAAGCGGCGCGCTCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1171
QY 1105 TGGCCTCTGCTGAGCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
Db 1172 CTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
QY 1165 CGCTTTGGCGCGCACTGTGGCGGAGAAAGCAAGGAGAGAGGAGAGGAGAGGAGAGGAG 1224
Db 1232 GGGCGTGGCAATACCTGCAAGCTGATGAGTGTCTCTCCCGTGGCCATCAGCATGTGTA 1291
QY 1225 AGGCGTGGGCTATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1284
Db 1292 GTTCCTGGGCGCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1351
QY 1285 GTTCGCGGAGCGGATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1334
Db 1352 GTTCGCGGAGCGGATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1401

RESULT 11

AAA30626
ID AAA30626 standard; cDNA: 1119 BP.

AC AAA30626;

DT 21-AUG-2000 (first entry)

DE Human G protein-coupled receptor BLR1 cDNA.

KW G protein-coupled receptor; GPCR; constitutively active;

KW Intracellular loop 3; transmembrane domain 6; drug screening;

KW agonist; antagonist; ss.

OS Homo sapiens.

PN WO200022129-A1.

PD 20-APR-2000.

PF 12-OCT-1999; 99WO-US23938.

PR 13-OCT-1998; 98US-0170496.

PA (AREN-) ARENA PHARM INC.

PI Behan DP, Chalmers DT, Liaw CW;

DR WPI: 2000-329165/28.

XX P-PSDB; AAY90627.

XX Non-endogenous constitutively activated human G protein-coupled

XX PT receptors, useful for identifying agonists for use as pharmaceutical

XX agents -

XX Example 1: Page 151; 341p; English.

XX The invention relates to constitutively active, non-endogenous versions

XX of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
XX AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
XX and AAA30775-A30779). The mutant proteins of the invention contain a

CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC or Ala, and is preferably Lys. When the endogenous residue at this
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC The 15 amino acid stretch between the substituted amino acid and the pro
CC may be endogenous, non-endogenous, or a mixture of endogenous and
CC non-endogenous residues. The constitutively active GPCRs are useful for
CC identifying antagonists, agonists and partial agonists for use as
CC pharmaceutical agents. The mutant proteins are also useful in research
CC settings for elucidating the roles of the receptors in normal and
CC diseased conditions. Antagonists for a particular GPCR are useful for
CC treating diseases and disorders associated with that receptor. Because
CC the novel mutant GPCRs are constitutively active, they can be used
CC directly for screening of compounds without the need for endogenous
CC ligands. The present sequence represents cDNA encoding a human wild-type
CC GPCR used in an exemplification of the invention. This was cloned and
CC subjected to site-directed mutagenesis (SDM) to generate DNA encoding
CC the corresponding mutant of the invention.

SO Sequence 1119 BP; 191 A; 390 C; 290 G; 248 T; 0 other;

Query Match 12.7%; Score 238.4; DB 21; Length 1119;
Best Local Similarity 56.9%; Pred. No. 2e-43;
Matches 506; Conservative 0; Mismatches 366; Indels 18; Gaps 3;

QY 463 CTTCGACCGGGCTTCTCTGCGACCCCTTACAGCCCTCTTCTGCTGGGCTGCTGGG 522
Db 144 CTTCAGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 203
QY 523 CAAGCGGCGGCTGCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
Db 204 CAAGCGGCGGCTGCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 263
QY 583 CTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642
Db 264 CTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 323
QY 643 AGTGAAGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702
Db 324 GGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 383
QY 703 CTTCACATCAATCTTACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 762
Db 384 GCACAAAGTCATCTTACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 443
QY 763 CCTGAACATAGTTCATGACGACCGAGCTTACGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 822
Db 444 CCGGCGCATTTGTCCAGCGCGTCCATGCGTCCATGCGTCCATGCGTCCATGCGTCCATGCGTCC 503
QY 823 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
Db 504 CACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563
QY 883 GTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 930
Db 564 CAAGTCGAGCAAGGCGCATACACAACTCCGTCACGTTGACCTTCTCCCAAGAGAA 623
QY 931 CTTCACACA---GGTGGGCGCGACGGCTCTGCGGGTCTGACGCTGGCTGGCTTTCT 987
Db 624 CCAAGAGAGAAAGCGCATGCTGTTTCACTCCGATTCCTCTTACCATGTGGCGGATTCCT 683
QY 988 GCTGCCCCCTGCTGTCATGAGGCTACTGCTATATGCGCAATCTTGGCGGCTG---CTGGT 1044
Db 684 GCTGCCATGCTGTGATGGGCTGTGCTACGTTGGGGGTAGTGCACAGGTTGGCGCAGGC 743
QY 1045 TTCCAGGGGCGACGGGCGCTGGGGCCATGGGCGCTGGTGTGTGTGTGTGTGTGTGTGTGTGT 1104
Db 744 CCAAGCGGCGCGCTCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 803
QY 1105 TGGCCTCTGCTGAGCCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164

FT CDS 108..1172
 FT /*tag= a
 XX
 PN MO9218641-A.
 XX
 PD 29-OCT-1992.
 XX
 PF 10-APR-1992; 92MO-US02977.
 XX
 PR 10-APR-1991; 91US-0685101.
 PR 09-JUL-1991; 91US-0726606.
 PR 09-DEC-1991; 91US-0803842.
 XX
 PA (REP) REPLIGEN CORP.
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Navarro J, Thomas KM, Witt DP;
 XX
 DR WPI; 1992-382123/46.
 DR P-PSDB; AAR28272.
 XX
 PT Recombinant mammalian interleukin-8 receptor - used for screening
 PT interleukin-8 binding antagonists, used to treat inflammation
 XX
 PS Disclosure; Fig 1; 71pp; English.
 XX
 CC Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to
 CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (AAQ30015). This probe was designed based on the
 CC sequence deduced from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were
 CC isolated. The insert of one of these plaques, termed F3R was
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments.
 CC
 SQ Sequence 1200 BP; 234 A; 366 C; 294 G; 304 T; 2 other;

Query Match 12.3%; Score 231; DB 13; Length 1200;
 Best Local Similarity 55.5%; Pred. No. 8.9e-42;

Matches 491; Conservative 0; Mismatches 385; Indels 9; Gaps 2;

QY 446 CAGGACTTCAGCTCGAAGCTGACCGGCGCTCTGCGACGCGCTTACAGCTTCCTT 505
 DB 213 CTGGTAGTACCCAGACACTTAACAATATGTGTGCTCTCATATGCGCTGTGCTTC 272
 QY 506 CTGCTGGGGCTGTGGGCAACGGCGGGGTGGAGCGTGTGCTGAGCCGCGGAGACCC 565
 DB 273 CTGCTGAGCGCTGTGGGCAACCTCCGTGGTATGCTGTACTGTATGATGACCGGAGCAAC 332
 QY 566 CTGAGAGAGCAGCAGCACTCTCTGCTCCACCTGATGCTGTAGCAGACAGCGTGTGCTG 625
 DB 333 CGTTGGGTACACGACCTCTTACCTGTGAACCTGTGCGCATGGCCGACTTTTGTGCGCTG 392
 QY 626 ACATGCGCGCTGTGGGAGTGGAGCGCTGCGAGTGGGTCTTTGGAGCTGTGCGCTGCG 685
 DB 393 ACCATGCGCTATCTGGGCGCTGTCAAGGAAAGGCTGTGATTTTCGACGCGCGCTGTGCG 452
 QY 686 AAGTGGCAGAGTCCCTCTTCAACATCAACTTACGACGAGCGCTCTGTGCGCTGCG 745
 DB 453 AAGGTGGTCTCGTTGTGAAGAAAGTCAACTTGTACAGTGGATCCGCTGCGCGCTGCG 512
 QY 746 ATGAGCTTTGACCGCTACTGAAACATAGTTATGACCAACCGAGCTTACCGCGGGGGGCC 805
 DB 513 ATCAGTGTGAGCCGCTACCTGGCGCAATGTCTACTGTGACACTGACCAAGAAAGCGC 572
 QY 806 CCGGGCCCGGAGCCGCTACAGCTGCGGTGCTGGGGGCTGCGCTGTGCTTTGCGCGCTC 865
 DB 573 C---ACTGTGTAAGTTCAATATGTGTGGGCACTGTGGGCGCTGTCTGATTTTGTCCCTG 629

QY 866 CCAAGCTTCATCTTCC-----TGTGCGGCCACACGACGAGCGGCTCAACGCCACCCAC 919
 DB 630 CCCTTCTCTCTCCGCGCAAGTCTTTCTCCAAACATTCACGCCGGGTCTGTATGAG 689
 QY 920 TGCCAAATACAACTTCCCAAGGTGGCGGACGCGCTCTGCGGGTGTGCACTGTGGCT 979
 DB 690 GACCTGGGTACAAACACAGCGAATGCGCATGTGTGCGGATCCGACACACTTTC 749
 QY 980 GGCCTTCTGCGCCCGCTGCTGATGCGCTACCTATGCCCCAATCCGCGGCTGCTG 1039
 DB 750 GCGTTCACTCTGCGCGCTGTGATGCTGTGTGCTATGGGTTACCGCTGCGACGCTG 809
 QY 1040 CTGGTTTCAGGGGCGCAGCGCGCTGCGGCGCATGCGGCTGTGTGTGTGTGTG 1099
 DB 810 TTCCAGGCCCAACATGGGGCAGAAAGCAACGGGCGCATGCGGGTCACTCTGCGCTGCTC 869
 QY 1100 GCGTTTCCCTCTGTGTGACCCCTATACCTGTGTGTGTGTGTGTGTGTGTGTGTG 1159
 DB 870 ATCTTCTCTCTGT 929
 QY 1160 CTGGGCGCTTTGGCGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1219
 DB 930 ACCCAGCTGATCCAGGAGAGCTGTACAGCTGTGCAATGACATGACCGGCGCTGTGAGCC 989
 QY 1220 ACCTCAGGCGCTGTGCTATGCACTGTGCTGCTCAACCGCGCTGTGTGTGTGTGTGTG 1279
 DB 990 ACCGAGATTTCTGGGCTTCTGTGACAGCTGTGCTCAACCCCAATCATGCGCTCATTTGGC 1049
 QY 1280 GTCAAGTTCGGGAGCGGATGTGATGCTCTTGTGCGCTGTGGGC 1324
 DB 1050 CAAACATTTGCAATGATGATTCATGATGCTGTGCGCGCGC 1094

Search completed: November 2, 2002, 04:24:01
 Job time : 250 secs

[illegible]

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RESULT 3  
BI821147  
LOCUS       BI821147               749 bp    mRNA          linear   EST_04-OCT-2001  
DEFINITION  G630J35039F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176136 5' ,  
             mRNA sequence.  
ACCESSION   BI821147  
VERSION     BI821147.1      GI:15932697  
KEYWORDS    EST.  
SOURCE      human.  
ORGANISM    Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
  
REFERENCE   1 (bases 1 to 749)  
            NIH-MGC http://mgc.ncl.nih.gov/.  
            National Institutes of Health, Mammalian Gene Collection (MGC)  
            Unpublished (1999)  
CONTACT    Robert Strausberg, Ph.D.  
            Email: gcgabs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11438 row: n column: 09  
High quality sequence stop: /47.
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FEATURES	SOURCE
location/Qualifiers	1..749
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:5176136"	
/clone_11p="NIH MGC_115"	
/lab_host="DH10B"	
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C.	

BASE COUNT	ORIGIN	Gruber (Invitrogen). 021. Note: this is a NIH-MGC Library."	Research Genetics tracking	code
121 a	274 c	201 g	153 t	

Query Match	34.9%	Score 655;	DB 10;	Length 749;
Best Local Similarity	97.5%;	Pred. No. 1.7e-126;		
Matches 697;	Conservative 0;	Mismatches 15;	Indels 3;	Gaps 3.

QY	303	CGTCCGCGGTTCCGGCCCTCAGAGAGTAGACACCAACAGTGGTAAATGACGGCGAGTTTG	362
Db	28	CCAGGCCCAAGCCATGTCCTCTTGAGGTAGTAGACCAACCAAGTGCCTAAATGACGCCGAGTTTG	87
QY	363	CCGCCCCCTCCGAGAGAACTTCA - GCCTTCTCTATGACTATGAGAAAAACGAGAGTACTCG	421
Db	88	CCGCCCTCCTGGAGAACTTCAGGCTCTCTCTATGACTATGAGAAAAACGAGAGTACTCG	147
QY	422	TGCTGTACCTCCCCCGCCCTGGCCACAGGACTTCAGCTTAACCTTGACACCGGGGCTTCCCTG	481
Db	148	TGCTGTACCTCCCCCGCCCTGGCCACAGGACTTCAGCTTAACCTTGACACCGGGGCTTCCCTG	207
QY	482	CCAGCCCTTACAGACTCCTCTTTCGCTGGGGAGCTCTGGGCAACGGCGGGTGGCAGCC	541
Db	208	CCAGCCCTTACAGACTCCTCTTTCGCTGGGGAGCTCTGGGCAACGGCGGGTGGCAGCC	267
QY	542	TGTCGTCTGAGCGCGGCGAGAGCCCTGAGCAGACACCACCTTCTGCTCCACTTAAGT	601
Db	268	TGTCGTCTGAGCGCGGCGAGAGCCCTGAGCAGACACCACCTTCTGCTCCACTTAAGT	327
QY	602	GTAGCAGACAGCCTGCTGGTGGTGAACACTAGCGGCTCTGGGCAAGTGAAGCTGGCGGTCAG	661
Db	328	GTAGCAGACAGCCTGCTGGTGGTGAACACTAGCGGCTCTGGGCAAGTGAAGCTGGCGGTCAG	387
QY	662	TGGGCTTTTGGCTCTGGCCCTGCAAAAGTGGAGGTGGCCCTTCAACATCAACTTCTAC	721
Db	388	TGGGCTTTTGGCTCTGGCCCTTGGCAAAAGTGGAGGTGGCCCTTCAACATCAACTTCTAC	447
QY	722	GGAGGAGCCCTCTGCTGGCCCTGCAACACTTTCAGCCGTACTCTGAACAAATGATTCATGGC	781
Db	448	GCAAGAGCCCTCTGCTGGCCCTGCAACACTTTCAGCCGTACTCTGAACAAATGATTCATGGC	507
QY	782	ACCCAAGCTTACCGCGGGGGGCCGCCGGCGCGCGTGAACCTTCACCTGAGCTGTGTCGG	841
Db	508	ACCCAAGCTTACCGCGGGGGGCCGCCGGCGCGCGTGAACCTTCACCTGAGCTGTGTCGG	567
QY	842	GGGCTCTGCTCTGCTTTTGCCCTCCAGACTTCATCTTCTGTGGGCCACACAGACGAG	901
Db	568	GGGCTCTGCTCTGCTTTTGCCCTCCAGACTTCATCTTCTGTGGGCCACACAGACGAG	627
QY	902	CGCCTCAACGACCAACCACTGCAATGACAATCCCAAGAGTGGGGCGACAGGCTGTGC - G	960
Db	628	CGCCTCAACGACCAACCACTGCAATGACAATCCCAAGAGTGGGGCGACAGGCTGTGC - G	687
QY	961	GGTGTGCAAGCTGTGGGC - TGGCTTTTCTGCTGCCCTCTGCTGGTCAATGAGCTACTG	1014
Db	688	GGTGTGTGCAAGCTGTGGGCTTTGGCTTTCTGCTGCCCTCTGCTGGTCAATGAGCTACTG	742

RESULT	4
A1587350/c	
LOCUS	
DEFINITION	A1587350 617 bp mRNA linear EST 14-MAY-1995 tcttg1c12.x1 NCI_CGAP_PanI Homo sapiens cDNA clone IMAGE:2224726 3'
ACCESSION	
VERSION	A1587350.1 GI:4573791
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 617) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
AUTHORS	

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-tr@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 1908 Std Error: 0.00
Seq primer: 400P from Gibco
High quality sequence stop: 180
POLYA=NO.

FEATURES
source Location/Qualifiers
1. 617
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2224726"
/clone_lib="NCI-CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site.1: SalI;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

BASE COUNT 141 a 145 c 200 g 124 t 7 others
ORIGIN

Query Match 26.3%; Score 493.6; DB 9; Length 617;
Best Local Similarity 92.4%; Pred. No. 8.2e-93;
Matches 570; Conservative 0; Mismatches 41; Indels 6; Gaps 5;

OY 1265 TATGCTTTGTAGGGGTCAAGTTCCGGGAGCGG-ATGTGATGTCGCTC-TTGGCGCTGG 1322
|||||
DB 617 TATGCTTTGTAGGGGCAAGTTCCGGGAGCGGAATGTGATGTCGCTTTTGGCGCTGG 558
|||||

OY 1323 GCTGCCCCAACGAGAGA--GGGCTCCAGAGGAGGAGCATGCTTCCCGCGGGAGTTATC 1380
| |||
DB 557 GGCTGCCCCAGAGAAAGGGGCTCCAGAGGAGGAGCATGCTTCCCGCGGGAGTTATC 498
|||||

OY 1381 CTGGCTGTGAGACTCAGAGAGGCTCTACTCGGGCTTTGTAGGCGCGGAATCCGGGCTCCC 1440
||| |||
DB 497 TGGGTTTGAACTCAGAAAGGCTCTACTCGGGCTTTGTAGGCGCGGAATCCGGGCTCCC 438
|||||

OY 1441 TTTCGCCACAGTCTGACTTCCCGCATTTCCAGGCTCCTCCCTCGCCGGGCTGG 1500
|||||
DB 437 TTTCGCCACAGTTTNACTCCCGCATTTNCAAGCTCTCTCCCTTTGGCGGATNTGG 378
|||||

OY 1501 CTCTCCCCAATATCTCTCGCTCCGCGGACTCACTGGCAGGCCGAGACACACAGAGTCTGCC 1560
|||||
DB 377 CTCTCCCCAATATCTCTCGCTCCGCGGACTCACTGGCAGGCCGAGACAC-CCAGGTCCTCC 319
|||||

OY 1561 GGGAGGCCACCTCCAGCTGTGAGAGTGCACGACATGTGCTCTTACTGCCAAGCCC 1620
|||||
DB 318 GGGAGGCCACCTCCAGCTGTGAGAGTGCACGACATGTGCTCTTACTGCCAAGCCC 259
|||||

OY 1621 CATCTGCGCGCGGAGTGGCTGTGGAG--CCCACTGCTCTTCTCATTTGGAACCTTA 1679
|||||
DB 258 CATCTGCGCGCGGAGTGGCTGTGGAG--CCCACTGCTCTTCTCATTTGGAACCTTA 199
|||||

OY 1680 AACCTCATCTTCCCAAGTGGGAGTAGAAGGATGGCGGTAGAGGAGTGTGCCCATATG 1739
|||||
DB 198 AACCTCATCTTCCCAAGTGGGAGTAGAAGGATGGCGGTAGAGGAGTGTGCCCATATG 139
|||||

OY 1740 AAGCCACAGCCGAGGCTCTCAGACTCAGACGATGCTGGCCATGTGCCCAAGACCTCTA 1799
|||||
DB 138 AAGCCACAGCCGAGGCTCTCAGACTCAGACGATGCTGGCCATGTGCCCAAGACCTCTA 79
|||||

OY 1800 TATTTGCTTTTATTTTATGCTAAATCTGCTTAAATTTTAACTTAAATAAAGATC 1859
|||||
DB 78 TATTTGCTTTTATTTTATGCTTAAATCTGCTTAAATTTTAACTTAAATAAAGATC 19
|||||

OY 1860 GTCAGGAAAAAAAAAAAA 1876
|||||
DB 18 GTCAGGAAAAAAAAAAAA 2

RESULT 5
BI975807 578 bp mRNA linear EST 23-OCT-2001
LOCUS 484335 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BI975807
ACCESSION BI975807
VERSION BI975807.1 GI:16350212
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 578)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahnenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G.,
Pettea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGACG
Plate: 110 row: A column: 16
Seq primer: ATTGAGTGACATATAC.
Location/Qualifiers
1. 578
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

BASE COUNT 92 a 199 c 152 g 135 t
ORIGIN

Query Match 21.3%; Score 398.8; DB 10; Length 578;
Best Local Similarity 82.7%; Pred. No. 5e-73;
Matches 470; Conservative 0; Mismatches 92; Indels 6; Gaps 1;

OY 299 CCTTCTCTCCCGCTTCCCGCTCAGAGTGAAGTACACCAAGTGTAAATAGCCCGAG 358
| | | | |
DB 17 CTTACAGCCCGCATATGATGTTCCCTAGATGAAGCAAGCAAGATTTCCAACTTCGAT 76
| | | | |

OY 359 GTTGGCGGCTCTCGGAGAACTTCACTTCTTGTACTATGAGGAAACAGAGAGTGAC 418
| | | | |
DB 77 TTTTGCTTACTCTCTGAAAA-----CTTCTTCTATGACTACGAGAAAAATAGACTAC 130
| | | | |

OY 419 TGTGCTGTACTCTCCCGCGCTGCCACAGAGACTTACAGCTTAAGTTGACCGGCGCTTC 478
| | | | |
DB 131 TTTGCTGTACTCTCCCGCGCTGCCACAGAGACTTACAGCTTAAGTTGACCGGCGCTTC 190
| | | | |

OY 479 GTGCAGCCCTGTACAGCCTCTCTTGTGCGGAGTGTGGGAGAGCGCGGCTGGCA 538
| | | | |

Db 191 CTGCCGCTCTTACAGCCTCTCTTTGTGCTGGGGCTTCTGGTAATGATCGTGCA 250
QY 539 GCCGTGCTGTGAGCGCGGAGACGCCCTGAGACGACGACCTTCTGCTCCACTTA 598
Db 251 GTGTGCTGTGAGCCAGAGGGGCGCCCTGAGACGACGACCTTCTGCTGCACTTG 310
QY 599 GCTGTAGACACAGCAGCTGTGTGCTGTGACACTGCGGCTGTGGGAGTGCAGCTGCCGTC 658
Db 311 GCTGTGCGCATGACACTGTGTGCTGTGACACTGCTCTCTGGGAGTGTGATGCGCATC 370
QY 659 CAGTGGCTCTTTGGCTGTGCTGTGCAAGTGGCAGGTGCCCTCTTCAACATCACTTC 718
Db 371 CAGTGGCTCTTTGGCTGTGCTGTGCAAGTGGCAGGTGCCCTCTTCAACATCACTTC 430
QY 719 TAGCAGAGACCCCTCGTGGGCTGTGATCAGCTTTACCGCTTACCGTACATCACTTGCAT 778
Db 431 TAGCAGAGGAGCCCTCTGCTGTGCTGTATCAGCTTGCATGCTGATGACATTTGTGCAC 490
QY 779 GCCACCCAGCTTACGCGCGGGGCGCCCGCGGCTGACGCTCAGCTGCTGCTGTC 838
Db 491 GCCACCCAGCTTACGCGCGGGGCGCCCGCGGCTGACGCTGCTGCTGCTGCTGCTGCTG 550
QY 839 TGGGGCTCTGCTGCTCTTTTGGCCCTCC 866
Db 551 TGGGGCTCTGCTGCTCTTTTGGCCCTCC 578

RESULT 6
AM655246 471 bp mRNA linear EST 25-APR-2001
LOCUS 106015 MARC 180V Bos taurus CDNA 5', mRNA sequence.
DEFINITION AM655246
ACCESSION AM655246
VERSION AM655246.1 GI:7421144
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 471)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W., Rohrer,G.A., Chitko-McKown,C., Perle,G., Holt,I., Karamecheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACAGCTATGACCAT
BACKWARD: GTTTCACAGTACGACG
Plate: 86 row: D column: 24
Seq primer: ATTGAGTGACACTATAG.
Location/Qualifiers
1..471
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 180V"
/tissue_type="pooled"
/lab_host="PH10B"
/note="Vector: PCMV SPOB6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."

BASE COUNT 72 a 152 c 148 g 99 t
ORIGIN
Query Match 20.6%; Score 385.8; DB 9; Length 471;
Best Local Similarity 88.9%; Pred. No. 2,5e-70;
Matches 417; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 900 AGGCTTACAGCCAGCCACTGACCATATACACTTCCACAGAGTGGGCGGACGGCTGCG 959
Db 3 ACCGCTCATATGCCACCCACTGACCATATACACTTCCACAGAGGCGCACAGACTTGC 62
QY 960 GGGTGTGACAGCTGTGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1019
Db 63 GCATCTGACAGCTGTGAGGAGCTTCTGCTGCGCCCTGCTGCTGCTGCTGCTGCTGCTG 122
QY 1020 CCACATCTGCGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1079
Db 123 CCCGATCTGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 182
QY 1080 TGT 1139
Db 183 TGT 242
QY 1140 TGTGTGACATCTCATGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTG 1199
Db 243 TGTGTGACATCTCATGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTG 302
QY 1200 TAGACGTGCCCAGTGTGCTGCTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTG 1259
Db 303 TGTGTGACATCTCATGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTG 362
QY 1260 TGT 1319
Db 363 TGT 422
QY 1320 TGGGCTGCCCAACACAGAGAGGCTCCAGAGGCAAGCCATGCTTCCCG 1368
Db 423 TGGGCTGCCCAACACAGAGAGGCTCCAGAGGCAAGCCATGCTTCCCG 471

RESULT 7
AJ346279 348 bp mRNA linear EST 14-AUG-2001
LOCUS AJ346279
DEFINITION SHR-000016-0-E11 HM3/S3 Homo sapiens CDNA, mRNA sequence.
ACCESSION AJ346279
VERSION AJ346279.1 GI:15167462
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 348)
Laveder,P., De Pita,C., Toppo,S., Valle,G. and Lanfranchi,G.
Specific subtraction of abundant mRNAs in skeletal muscle
Unpublished (2001)
Contact: Laveder P
CIRI Biotechnology Centre
University of Padua
Via U. Bassi 58/B, 35121 Padua, Italy
sequencing centre identifier: HSPD50322
ABI Chromatograms and other information are available on WWW at
http://muscle.ciri.unipd.it
Seq primer: PCR.
Location/Qualifiers
1..348
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HM3/S3"
/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: p0PD (Custom); Site_1: EcoRI; Site_2: NotI; caucasian; Skeletal muscle cDNA was depleted of hundred most expressed mRNAs through an original two steps

subtractive procedure"

BASE COUNT 87 a 110 c 74 g 77 t

ORIGIN

Query Match 18.1%; Score 339.4; DB 9; Length 348;
Best Local Similarity 99.7%; Pred. No. 1.2e-60;
Matches 340; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1536 CACGCCAGACACACAGCTCCCGGAGACACCTCCAGCTGAGACTGACCA 1595
|||||
Db 7 CAGGCCAGACACACAGCTCCCGGAGACACCTCCAGCTGAGACTGACCA 66
1596 TTGCTGCTCTTACGTGCAAGCCCATCTGCGCCGAGAGTGTCTGAGCCCCA 1655
|||||
Db 67 TTGCTGCTCTTACGTGCAAGCCCATCTGCGCCGAGAGTGTCTGAGCCCCA 126
1656 CTGCGCTCTCATTTGGAACCTAAACTCATCTCCCAAGTGGGGAGTACAGGCA 1715
|||||
Db 127 CTGCGCTCTCATTTGGAACCTAAACTCATCTCCCAAGTGGGGAGTACAGGCA 186
1716 TGGCGTAGAGGGTGTGCGCCCAAGAACCCAGAGCCCTCCAGCTCAGAGTACTG 1775
|||||
Db 187 TGGCGTAGAGGGTGTGCGCCCAAGAACCCAGAGCCCTCCAGCTCAGAGTACTG 246
QY 1776 TGGCGTAGAGGGTGTGCGCCCAAGAACCCAGAGCCCTCCAGCTCAGAGTACTG 1835
|||||
Db 247 TGGCGTAGAGGGTGTGCGCCCAAGAACCCCTATATTTGCTCTTTATTTATGCTAAATCTGCT 306
QY 1836 TAAACCTTTCAATTAACAGATGTCAGGAAAAA 1876
Db 307 TAAACCTTTCAATTAACAGATGTCAGGAAAAA 347

RESULT 8
BF452722 468 bp mRNA linear EST 01-DEC-2000
LOCUS
DEFINITION ma5fa05.y1 Soares mouse 3bMS Mus musculus cDNA clone
CXCR3. [1] ; mRNA sequence.
ACCESSION BF452722
VERSION BF452722.1 GI:11518891
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 468)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:1457041
Seq primer: -40RP from Gibco
High quality sequence stop: 382.
Location/Qualifiers
1.468
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3820689"
/clone_lib="Soares mouse 3bMS"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer (5'
TGTTACCAATCTGAGTGGAGGCGCGCTGTTTTTTTTTTTTTTTTTTTTT

3]; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 90 a 143 c 119 g 116 t

ORIGIN

Query Match 14.6%; Score 273; DB 10; Length 468;
Best Local Similarity 80.9%; Pred. No. 8.8e-47;
Matches 331; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

QY 324 AGGTAGTACACACAGTCTTAATAGCCCGAGTTGCCCTCTGAGAACTTCA 383
|||||
Db 62 AGGTAGTACACACAGTCTTAATAGCCCGAGTTGCCCTCTGAGAACTTCA 121
QY 384 GCTCTTCTATGACTATGAGAAAACGAGAGTACTGCTGACTCCCCGCCCTGCC 443
|||||
Db 122 CTTCTCCCTACGATTAAGGGGAAAACGAGCCAGC--TTCTGACTCTCCGCCCTGCC 178
444 CACAGACTTCAGCCTGAACTTGACCGGCTCTGCTGCCAGCCCTTACAGCCTCTCT 503
|||||
Db 179 CACAGACTTCAGCCTGAACTTGACCGGCTCTGCTGCCAGCCCTTACAGCCTCTCT 238
QY 504 TTCTGCTGGGGCTGTGCGCAACGCGGTGCGACCGCTGTGCTGAGCCGCGACAG 563
|||||
Db 239 TTCTGCTGGGGCTGTGCGCAACGCGGTGCGACCGCTGTGCTGAGCCGCGACAG 298
QY 564 CCTGAGACACACGACACCTTCTGCTCACCAGCTGTAGACGACGACCTGTGCTGC 623
|||||
Db 299 CCTGAGACACACGACACCTTCTGCTCACCAGCTGTAGACGACGACCTGTGCTGT 358
624 TGACACTGCGCTGTGCGCAACGCGGTGCGACCGCTGTGCTGTGCTGTGCTGT 683
|||||
Db 359 TAACCTTTCATTTGTTGGGAGATGATGCTGTGCTGCTGCTGTGCTGTGCTGT 418
QY 684 GCAAGTGGAGAGTGTGCTTTCACATCACTTTCAGCAGAGACCT 732
|||||
Db 419 GCAAGTGGAGAGGCGCTTTCACATCACTTTCAGTATGATGAGGCGCTT 467

RESULT 9
BE589641 511 bp mRNA linear EST 28-AUG-2000
LOCUS
DEFINITION 195994 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE589641
VERSION BE589641.1 GI:9842680
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 511)
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and
Wells, K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
JOURNAL
COMMENT unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200, Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@lpsl.barc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGCAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 122 row: N column: 12

FEATURES	Seq primer: ATTTAGGTGACACTATAC.	Location/Qualifiers
SOURCE	1..511	/organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="BARC 5BOV" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pCMV SPORT6; site_1: XbaI; site_2: XhoI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."
BASE COUNT	97 a 167 c 135 g 112 t	
ORIGIN		
Query Match	14.4%; Score 269.8; DB 10; Length 511;	
Best Local Similarity	80.8%; Pred. No. 4.1e-46;	
Matches 329; Conservative	0; Mismatches 72; Indels 6; Gaps 1;	
OY	299 CCTTCCTCCCGCTTCCGCCCTCACAGGTGAGTACACCAAGCTTAATAGACGCCGAG	358
Db	111 GGTACACACCGCTATGATGCTCCCTGAGATGATGTAACCCCAAGACTTCCAAAGCTTCGAT	170
OY	359 GTTGGCGGCTCCCTGAGAACTTACAGCTCTCTCTATGACTATGAGAAACAGAGTAC	418
Db	171 TTGTGCTACTCTCTGAAAA-----CTCTTCTATGACTAGGAGAAATAGACCTAC	224
OY	419 TCGTCTGTACCTCCCGCCGCCACAGAGACTTACACCTGAACTTGCAGCCGCGCTTC	478
Db	225 TTGTGCTGACTGTCCCAACCGCCACAGAGACTTCAAGCTTCACTTGCAGCCGACCTTC	284
OY	479 CTGCCAGCCCTCTACAGCCTCTCTTCTGCTGGGGCTGTGGGACGCGCGGTGGCA	538
Db	285 CTGCCCTCTCTCTACAGCCTCTCTTGTGCTGGGGCTTGTGGTAATAGCATCGTGCA	344
OY	539 GCCGTGCTGAGCGGGCGGACAGCCCTGAGACACACCGACACTTCTGTCACCTA	598
Db	345 GCTGCTGCTGAGCAAGAGGGCGGCGCTGAGACACACCGACACCTTCTGTCGACTTG	404
OY	599 GCTGTAGCAGACACCTCTGCTGTGACACAGCGCGCTGTGGCAGTGACGCTCGTC	658
Db	405 GCTGTGGCGAGTACACTGCTGCTGTGACACTCCCTCTCTGTGGGAGTGGATGACGACATC	464
OY	659 CAGTGGGTCTTGTGCTGTGGCCTGTGCAAAAGTGGAGGCTGCCCTCTT	705
Db	465 CAGTGGGTCTTGTGCTGTGGCCTGTGCAAAAGTGGGAGTGGACCTCTT	511
RESULT 10		
BF453946/c		
LOCUS	708 bp	mRNA
DEFINITION	ma56605.x1 Soares mouse 3NBMs Mus musculus cDNA clone	
VERSION	IMAGE:3820689.3, similar to tr:088410 088410 CHEMOKINE RECEPTOR	
ACCESSION	BF453946	
KEYWORDS	BF453946.1 GI:11520115	
SOURCE	EST.	
ORGANISM	house mouse.	
	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 708)	
AUTHORS	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Other_ESTs: ma56a05.y1	
	Contact: Robert Strausberg, Ph.D.	
	Email: c9apbs-remail.nih.gov	
	This clone is available royalty-free through LNL; contact the	
	IMAGE Consortium (infoimage.lnl.gov) for further information.	
	MG1:1457041	
	High quality sequence stop: 444.	

FEATURES		Location/Qualifiers
source	1. 708	
	/organism="Mus musculus"	
	/strain="C57BL/6J"	
	/db_xref="taxon:10090"	
	/clone="IMAGE:3820689"	
	/clone_1lb="Soares mouse 3NDMS"	
	/sex="male"	
	/issue_type="Spleen"	
	/dev_stage="4 weeks"	
	/lab_host="DH10B"	
	/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCACTGTGAAGTGGAGCGCGCGCTGTGTTTATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Benco Soares and M.Falini Bonaldo."	
BASE COUNT	172 a 173 c 185 g 178 t	
ORIGIN		
Query Match	14.0%: Score 263; DB 10; Length 708;	
Best Local Similarity	68.6%: Pred. No.1,1e-44;	
Matches	422: Conservative 0; Mismatches 185; Indels 8; Gaps 4;	
QY	1139 CTGTGTGACATCTTCATGGACCTGGGCGCTTTGGCCCGCACTGTGGCCGAGAAACACAG	1198
DB	708 CTATGGATATCTTCATGGATGTGGAGATTTTGGCCCGCACTGTGTGTCGAGAAAGCCAC	649
QY	1199 GTAGAGCTGGGCCAATCTGGCTCACCTCAGGCGCGGCGTCTATGCACATCGTGGCTCAACCG	1258
DB	648 GTGGATGTGGCCAAATCACTCTTGCGGATGGGATGATCACTGTTGCTCAATTCG	589
QY	1259 CTGCTCTATGCTTTGTATAGGGGTCAAGTTCCCGGAGCGGATGTGATGCTGTCTTGTGCGC	1318
DB	588 CTGCTCTATGCTTTGTATAGGGGTCAAGTTCCCGGAGCGGATGTGATGCTGTCTTGTGCGC	529
QY	1319 CTGGGCTGCCCCAACCAAGAGAGGGCTCCAGAGAGGACCATGCTTCTTCCCGCGGATTTCA	1378
DB	528 CTGGGCGCGCTGTGACAGAGAGGGGCCACGCGGACGCTCTATGTCACAGGAGAAATCA	469
QY	1379 TCTCTGTGTGAGACCTCAGAGAGCGCTCTACTGTGGGCTTGTGAGGCGCGGAATCGGGGCTCC	1438
DB	468 TCTCTGTGTGAGAACACTGAGGCTCTCTATACCTGGGCTTGTATTTCTGGACTGGAACTGTA	409
QY	1439 CCTTTGCG--CCACAGCTGACTTCCCGCATTTCCAGGCTCTCTCCCTCCCTCTGCGCGCT	1496
DB	408 GCTGCGCGAGGCCAAGTCTTAACACACTTCAAGTCTTCTCTCCCTTGTAGTTGGGCTTAG	349
QY	1497 CTGGGCTTCCCAATATCTCTGCTCCCGGGAATCACTGGGCAC--CCAGACACACAGGT	1555
DB	348 CTGCAACTTACCCGTAATCTTCTGCTCCAGAGATGCATGACACTGACACTGATATATCCAGGT	289
QY	1556 CTTCGGGGAAGCACTCCACAGCTGTGAGACTGCACCATTTGCTGCTTTAGTGGCA	1615
DB	288 CTCTGAGTAATCA--TCTCATCAACAAGACACACACTTATCTGTGCTTAGTGGCA	232
QY	1616 AGCCCAATCTCTGGGCGCGGAGG--TGGGTGCTTGGAGGCCACATGCTCCCTTCATTTGGA	1673
DB	231 TGCCTATCTTCTGTCTTTTGAATAGCTGCTGAGGCCCGCCCGCTACTAATATTTAGC	172
QY	1674 AACTAAATCTTCATCTTCCCAAGTGGCGGAGTACAAGCATGTGCGTGAAGGCTGTGC	1733
DB	171 AAGTGAATCACTGACCTCTGTGTGAGAGAGGAGGCAAAATAGCAGAGAGGCGCAG	112
QY	1734 CCATGAAAGCCACAG 1748	
DB	111 GCGTGTGAGCACTG 97	

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RESULT 11
LOCUS      AM354767                      392 bp      mRNA      linear      EST 25-APR-2001
DEFINITION 36085 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  AM354767
VERSION     AM354767.1  GI:6853757
KEYWORDS   EST.
SOURCE      Bos taurus
            cow.
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 392)
            Smith,T.P.L., Grosse,M.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G.,
            Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keefe,U.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
TITLE       Contact: Smith TPL
JOURNAL     USDA, ARS, US Meat Animal Research Center
MEDLINE     PO Box 166, Clay Center, NE 68933-0166, USA
COMMENT     Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross-match with the -minscore 20
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTCACAGTACGACG
            Plate: 23 row: J column: 5
            Seq primer: ATTAGGTGACACTATAG.
FEATURES
            source
            1..392
            /organism="Bos taurus"
            /db_xref="taxon:9913"
            /clone_lib="MARC 1BOV"
            /tissue_type="pooled"
            /note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
            library made from pooled tissue from lymph node, ovary,
            fat, hypothalamus, and pituitary."
BASE COUNT  70 a 131 c 102 g 89 t
ORIGIN
Query Match 12.7%; Score 239; DB 9; Length 392;
Best Local Similarity 79.6%; Pred. No. 1.1e-39;
Matches 297; Conservative 0; Mismatches 70; Indels 6; Gaps 1;
299 CCTTCTCCCGCTCCCGCTCCAGTGAGTGAGCACCACCAAGTGTAAATGACGCCGAG 358
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
26 CGTACAGCCGACCTATGTGCTCTGAGATGAGTAAGGCGCAAGTTCACGCTCGAT 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
359 GTTGCAGCCCTCTGGAGAAGCTTCACTCTTCTATGACTATGAGAAACGAGAGTAC 418
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
86 TTTCCTACTCTCTGAAAA-----CTCTCTATGACTACGAGAAATGAGACTAC 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
419 TCGTGTGTAACCTCCCGCTCCGCCACAGAGACTTCAAGCTGAACCTGACCGGGCCTTC 478
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
140 TTCTGCTGTAATCCACCGCTCCACAGAGACTTCAAGCTCAACTCCGACCGACTTC 199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
479 CTGCGAGCCCTCTACAGCTCTCTTTCCTTTCCTGCTGGGCTGCTGGGCAACGCGGGTGCA 538
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
200 CTGCGCGCTCTACAGCTCTCTTTCCTTTCCTGCTGGGCTTCTGGGTATATGACATGTCGCA 259
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
539 GCGCTGCTGTGAGCGGCGAGACGCGCTGAGAGCAGCAGCAGCTTCTGCTCCACCTTA 598
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
260 GTCTGTCTGTGAGCGGCGGCGCTGAGAGCAGCAGCAGCAGCTTCTGCTGCACTTG 319

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Oy 599 GCTGTAGACAGACAGCTGCTGCTGTGACACTGCGCTCTGGGAGTGCAGCCTGCCCTC 658
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 320 GCTGTGCGCAGTCACTGCTGTGTGACACATCCCTCTCTGGGAGTGCAGTGCAGCTATC 379
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 659 CAGTGGCTTTG 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 380 CAGTGGCTTTG 392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
LOCUS      B1653693                      871 bp      mRNA      linear      EST 12-SEP-2001
DEFINITION 603300354F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5340828 5',
            mRNA sequence.
ACCESSION  B1653693
VERSION     B1653693.1  GI:15567929
KEYWORDS   EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 871)
            NIH-MGC http://mgc.ncl.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: c9abbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1M11865 row: 1 column: 13
            High quality sequence stop: 835.
FEATURES
            source
            1..871
            /organism="Mus musculus"
            /db_xref="taxon:10090"
            /clone="IMAGE:5340828"
            /clone_lib="NIH_CGAP_Mam3"
            /tissue_type="tumor, gross tissue"
            /note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: NotI;
            Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert 2 kb. Library constructed by Life
            Technologies, catalog #12017-018. Investigators providing
            samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference
            for transgenic model: Xu et al., Nature Genetics 22, 37-43
            (1999). Note: this is a NCI_CGAP Library."
BASE COUNT  164 a 274 c 221 g 212 t
ORIGIN
Query Match 8.7%; Score 162.8; DB 10; Length 871;
Best Local Similarity 53.2%; Pred. No. 9.2e-24;
Matches 417; Conservative 0; Mismatches 357; Indels 10; Gaps 3;
575 ACCGACACCTCTGCTGCAACCTAGCTGACGACAGCGTGTGCTGACACGCGG 634
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1  ACGGATACCTACTGCTCAACCTGCGCGGTGGCAGAAATCTTTCCTCTCGATTCTCC 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 635 CTCTGGCAGTGGAGCGCTGCGCTCAGTGGGCTTTCCTGCTGGCTTCGCAAGTGGCA 694
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TTCTGGGCTCTACAGCAGCAAGCTGCTGATTTTGGCTTACTCTGTATAGGGCATT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 695 GGTGCGCTCTTCAACATCACTTCTACGAGAGAGCCCTGCTGCTGCTGATACCTTT 754
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 TTGGCATCATTAAGTTAAGCTTCTTCAGGGGATGCTGCTGCTCATGACATCAGATT 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 755 GACCGCTACTGAACATAGTTCATGCC-----ACCAAGCTTACCGCGCGGGCCCGG 808
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GACCGCTACTGACCATTCGTCAGGCGGTGTGCGCATTCGCCACGCGCGCGGTGCTT 240

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QY	809	GC	CCCCGCGGACCCCTACACCTACCTGCGCTGTCGTGGGGGGCTGCTGCTCTTTTGGCCCTCCCA	868
Db	241	CTCATACAGCAAGCTCTCCTGTGTGTGGGCATCTTGATGCTGCTGCTCTTCTCTCTCCATCCCG	300	
QY	869	GACCTTCATCTTCTGCTGCGGCCACCACGACGAGGCCCTCAACGC--CAACCACCTGCCAA	925	
Db	301	GAGCTGCTCTACAGGGGCTCCAGAAAGAACAGGGCGAGGACAGCTGATGCTACAGT	360	
QY	926	TACAACTTCCACAGAGTGGCCGACAGGCTCTGCGGGTGTCTCAGCTGTGGTGGCTTT	985	
Db	361	GTCAGTGGCCCAAGTGGAGGCCCTTGATCACATCCAAAGTGGCCCAAGATGGTTTGGGTTC	420	
QY	986	CTGCGTGGCCCTGCTGCTATGGCTACAGCTATGCCCAATCCTGCGCGTGTGCTGTT	1045	
Db	421	CTAGTGCTCTATGCTGTGCTATGAGTTTCTGTCTACCTCATATTATCATCTTGTCTCCAG	480	
QY	1046	TCCAGGGGCGACAGGGCGCTGCGGCCCATAGCGGCTGTGTGTGTGCTGCTGCTGCTTT	1105	
Db	481	GCAGCAACTTTGACCGGGAAACAAAGGCCCATCAAGATGATATGCGGTGGTGTACTTTC	540	
QY	1106	GCCCTCTCTGTGACCCCTTATCCTGCTGTGCTGTGTGTGACATCTCTATGGACCTGGCC	1165	
Db	541	ATAGCTTTCACAGCTGCGCTTACATAGGGGTGTGCTGCGCTCAGACGCTGGCCAACTTCAAC	600	
QY	1166	GCTTTGGCCCGAATCTGTGGCGGAGAAAGCAAGGGTAGAGGTCGCCAAGCGGTCACTCA	1225	
Db	601	ATCACCAATAGCAGCTGGGAAACACGACAGCAAGCTCAATGCTTATGACCTCACTCAC	660	
QY	1226	GGCCTGGGCTACATGACATGCTGCTCTCAACCGCTGCTCTATGCTTTGTAAGGGTCAAG	1285	
Db	661	AGCGTGGCTCGTGCCTGCTGCTCAACCTTTCTTGATGCTTCAATGGGCTCAAG	720	
QY	1286	TTCGGGAGCGGATGTGATGCTCTCTTTTGGCGCT-GGGCTGCCCCAACAGAGGGCT	1344	
Db	721	TTCGCGACGACCTTCAAGCTCTTCAAGAGCAAGCTTGGGGCTGTCTCAGGCAGACGAGCT	780	
QY	1345	CCAG	1348	
Db	781	CCCC	784	
RESULT 13				
LOCUS	AL523112			
DEFINITION	AL523112 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC001B09 5			
ACCESSION	AL523112			
VERSION	AL523112.1			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eulalia; Primates; Catarrhini; Hominiidae; Homo.			
AUTHORS	Li, W.B., Gruber, C., Jessel, J. and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.			
FEATURES				
SOURCE	1..944			

enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : liangellifetech.com URL : <http://fulllength.invitrogen.com>

Query Match	8.6%;	Score 161.21;	DB 9;	Length 944;
Best Local Similarity	51.3%;	Pred. No. 2e-23;		
Matches 463;	Conservative	5;	Mismatches 424;	Indels 10;
				Gaps
QY	436	GCCTCGCCACAGGACTTTCAGCCTGAACCTTGCAGCGGGCCCTTCCTCCAGACCTCTACAG	495	
Db	24	GCTTTGTACAAAGCCGATGTCACAGGCTTCACCGGGCCCTTCCAAACCCAGTGTCCCT	83	
QY	496	CCCTCTCTTCTGTGTGGGGGTGCGGGCAACGGCGGGGTGGGACGGCTGTCTAGAGCG	555	
Db	84	GACCGTGGCTGCGGTGGGTCTGGCCGGCAATGGCCGTGTCTGGCCACCCAGCTGGACG	143	
QY	556	GCAGACAGCCCTGAGC-AAGCAGCAGACACTCTGCTCCACCTAGCTGTAGCAACAGC	614	
Db	144	CCGAGCGGCAAGCGCTCGCCACCGCTGCCACCTGGTCCAGCTGGCCGTGGCCAGACTCT	203	
QY	615	TGCTGTGTCTGACACTCGCCGCTGTGGGCAETGGACGCTGCCCTCCAGTGGGTCTTGGCT	674	
Db	204	TGCTGGCCCTGACACTCTCCCTTGGCGGCAAGAGGGCTCTTCAAGGGCTGAGTCTGGAA	263	
QY	675	CTGGACCTGTGCAAGTGGCAGAGTGCCTCTTTCAAATCAACTTCTACGAGAGGACCTCC	734	
Db	264	GTECCACTGTCCGACCATCTGTGCTCTACTGCGGCTTCCTTCCAGCGGCTTCTCT	323	
QY	735	TGCTGGCTTGACATGACTTTTGACCGCTACCTGAACATAGTTCATGCAACCCAGCTTAC-	793	
Db	324	TCTTGGCCTGATATCAGGCGGACCGGCTAGCTGGCCATCGGCGAGATCCAGCCGGGCG	383	
QY	794	CGCCGGGGGGCCCCGGCGCGCGGTAACCTTACTGCTGTCTGTCTGTGGGGCTCTGCTG	853	
Db	384	CGGCGCTTCACATCCCGGCGCGGACACTTGGTCTCGTATCGTGTGGCTGTGAACG	443	
QY	854	CTTTTGCACCTCCAGACTTATCTTCTCTGCGCCACAC-----GACAGAGGCTC	907	
Db	444	CTCTGGGCGCTGCTGCGGTGTCTTTCAGCAGAGATGGGCAAGGGGACCAAGACGC	503	
QY	908	AAGGCCACCCATGCCAAATACAACTTCCACAGGTGGCGCGCAAGGCTGTGGGTCTG	967	
Db	504	TGTGCTTCAACTTCCCGGAGGGGCTTCACGACAGCGTAAAGGGGCGAGCCCGTGGCS	563	
QY	968	CAGTGTGGGCTGTGCTTTCAGTGGCCCTGCTGTATAGGCTACATGCTATGCCACATC	1021	
Db	564	AGGGTGGCCCTGGGCTTTCGCGGTGCGGTGCGGTATGTATGTACCTGTGACCGCTTGC	623	
QY	1028	CTGGCGGTGCTGCTGTTTTCAGAGGGGCAAGCGGCGCTCGGGCCATGTGGGCTGTGGTG	1087	
Db	624	GGCGCAAGCGTGGCGGCGCGGCGGCGGCGGCGGCGGCGGTGGCGGTCTGTGGTG	683	
QY	1088	GTTGGTGTGTGGCTTGTGCGCTTGTGTGACCCCTTATACCTGTGTGTGTGTGAC	1147	
Db	684	GCTCTGTGTGGGCGCTTCTGTGTGTGTCAGCYGCCCTTACAGCCTCGCCCTGTGTGAT	743	
QY	1148	ATTCCTCAATGACACCGGCGCTTGTGGCCCGCAACTGTGTGGCGAAGAAAGAGGGTACAGTG	1207	
Db	744	ACTGCCATCTACTAGCTGTGGCGCGGAGGAGCTGCCCTTCCAGCAAGAGCAAGATGTC	803	
QY	1208	GCCAAATGCGTACACTTCAGGCGCTGGGCTACATGCACTGTGCTCTCAACCCGCTGCTAT	1267	
Db	804	GCACTGTGTGGTACACAGCGGCTTGTGGCCGTGGCGGCTGTGGCTCAATCCGTACTAC	863	
QY	1268	GCCTTTGTAGGGGTCAAGTTTCCGGGAGCGGATGTGATCTGTCTTGGGCTTGGGCTG	1327	

Db 864 GC-TTTCGGGCTGCGCTTCGCGAGAACCTGCGAGGCTGCTACGGGGGTGGAGCAGC 921

QY 1328 CC 1329

Db 922 CC 923

RESULT 14
BI395190/c
LOCUS BI395190
DEFINITION BI395190 573 bp mRNA linear EST 13-OCT-2001
TUEPEC185 5'RACE cDNA Equus caballus cDNA clone TUDPEC185, mRNA
sequence.
ACCESSION BI395190
VERSION BI395190.1 GI:16117704
KEYWORDS EST.
SOURCE horse.
ORGANISM Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
Pascual, I., Dhari, A.K., Fan, Y., Paradis, M.R., Arruga, M.V. and
Alcivar-Warren, A.
Alcivar-Warren, A.
Isolation of expressed sequence tags from a Thoroughbred horse
(Equus caballus) 5'RACE cDNA library
Unpublished (2001)
CONTACT: Alcivar-Warren, A.
Department of Environmental and Population Health
Tufts University School of Veterinary Medicine
200 Westboro Road, North Grafton, MA 01536, USA
Tel: (508) 839-7970
Fax: (508) 839-7091
Email: acacia.warren@tufts.edu
The cDNA was isolated from blood cells (buffy coat) of a
Thoroughbred septic foal
PCR Primers
FORWARD: 5'-(CUA)AGCCACGCGCTCGACTAGTAC-3'
BACKWARD: 5'-(CAU)4GCTTGGAGCGAGTGAAGTGA-3'
Insert Length: 573 Std Error: 0.00
Seq primer: M13 reverse.
Location/Qualifiers
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/db_xref="taxon:9796"
/clone="TUDPEC185"
/clone_lib="5'RACE cDNA"
/tissue_type="Blood cells (buffy coat) from a septic
female"
/dev_stage="Foal"
/lab_host="E. coli DH5"
/note="Vector: PAMPI (Gibco BRL). Obtained by 5'RACE
following the protocol of Gibco BRL. cDNA was synthesized
using a gene-specific (ILI-ra) primer (GSP1:
5'-CTGTTGAGCGCATGAGGT-3') from a genomic sequence. dCTP
was used to add a homopolymeric tail in the 3' end and the
gene-specific primer (GSP2:
5'-CAUCAUACAUCCTTGGAGCGAGTGAAGTGA-3') as the reverse
and a Universal Anchor Primer (Gibco BRL) as the forward
primer. cDNA was cloned through UDG cloning method."

BASE COUNT 138 a 135 c 200 g 100 t

ORIGIN

Query Match 8.4%; Score 158.4; DB 10; Length 573;
Best Local Similarity 60.4%; Pred. No. 7.4e+23;
Matches 261; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 463 CTTGACGCGGCTTCCTCCAGCCCTCTACAGCCTCTCTTCTGCTGGGCTGCTGGG 522

Db 464 CTTCAAGGCGCGTGTTCATCGCTATGCGCTCATCTCTCTGCGGTATGATGG 405

QY 523 CAAGCGCGGCGTGGACCGCTGCTGTGAGCGCGGACAGCCCTTACGACGACGAC 582

Db 404 CAACATCTGTGTGCTGTGATCTGTGAGCGGACCGCAACACGCAACTCCACGAGAC 345

QY 583 CTTCTGCTCCACCTAGCTGTAGACAGACAGCTGCTGTGTGTGACACTGCCCTGTGGC 642

Db 344 CTTCCGTTCACACCTGCGCTGTGCTGACCTCTTGTGTCATCTGCTCCCTTGTGCT 285

QY 643 AGTGACGCTGCCCTGCTCACTGCTCTTTGGCTCTGCTGCTGCAAGTGGACGTCCT 702

Db 284 GCGCGAGGCTTTGTGGGCTGCTGCGCACCGGCTCTGCAAAAGTATGATGCTCT 225

QY 703 CTTCAACATCACTCTTACGAGGAGAGCCCTCGCTGCGCTGCATAGCTTTGACCGCTA 762

Db 224 GCACAGATCACTCTTACTGACAGACGCTGCTCTGCGCTGCATTTGCTGTGACCGCTA 165

QY 763 CCGAATATGTTTCATGACCCAGCTTACCGCGCGGCGCCCGCGCGTGACCT 822

Db 164 CCGGCGCATTTGTCACACTCGCTCATACCGGCCACCGCGCTCCATTCATCCACAT 105

QY 823 CACCTGCTGCGCTGTGTGGGCGCTGCTGCTTTTGGCTCCAGACTTATCTTCT 882

Db 104 CACTGTATACCATTTGGCTGCGGCGCTCTCTTGGCTTGCAGACTTCTTCTGCG 45

QY 883 GTGCGCCACCA 894

Db 44 CAAGTCAGCCA 33

RESULT 15
AL531903
LOCUS AL531903 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM003YH06 5
DEFINITION AL531903 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM003YH06 5
prime, mRNA sequence.
ACCESSION AL531903
VERSION AL531903.1 GI:12795396
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 191 a 261 c 232 g 250 t

ORIGIN

Query Match 8.3%; Score 155; DB 9; Length 935;
Best Local Similarity 54.1%; Pred. No. 3.9e+22;
Matches 364; Conservative 0; Mismatches 300; Indels 9; Gaps 2;

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Db 319 CTTACTCTTGGCTGACCTGACCATCTGGCGCGCTCCAGGTGAATGGCTGGATTTT 378
OY 670 TGGCTGCGCTCTGCAGAGTGGCAGGTGCTCTTCACTCACTTCTAGCGAGAGC 729
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OY 730 CCTCCTGCTGGCCTGATGACCTTTGACCGCTACCTGACATAGTTCATGCCACCCAGCT 789
Db 439 CTGCTGTGGCTGCTGATGAGTGGACGCTGACCTGGCCATTGCTCATGCAACAGCAC 498
OY 790 CTACCGCGCGGCGCCCGCGCGCTGACCTCACTGCGCTGCTGGGGGCTCTG 849
Db 499 ACTGACCCAGAAAGCTC---ACTTGGTCAAGTTGTTTGTCTTGGCTGGGACTGTC 555
OY 850 CCTGCTTTTGGCCCTCCAGACTTCATCTTCTGTCGGCCACC-----ACGACGAGCG 903
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OY 904 CCTCAACGGCACCACCTGCAATACAACTTCCACAGTGGCGCGCACGCGCTGCGGGT 963
Db 616 TCCAGTTTGTATGAGGTCTCTGGAAATGACAGCAAAATGGCGGATGGTGTGGCAT 675
OY 964 GCTGACAGTGTGTGCTGCTTTCTGCTGCCCTGCTGTCATGAGCTATGCCCCA 1023
Db 676 CCGGCTTCAACACTTGTGGCTTCATCGTGGCGCTGTTGTCTGCTATGATG 735
OY 1024 CATCTGGCCGCTGCTGCTGTTTCCAGGGGCCAGCGCGCGCTGCGGCCATGCGGCTG 1083
Db 736 CACCTGCGCTACACTGTTTAAGGCCACACATGGGGCAGAAACGACCGAGCCATGAGGGT 795
OY 1084 GGTGGTGGTGGTGGTGGCGCTTGGCCCTGCTGCTGAGACCCCTATCACCCTGGTGT 1143
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OY 1144 GGACATCTCATG 1156
Db 856 AGACACCTCATG 868
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Search completed: November 2, 2002, 06:28:04
Job time : 1694 secs

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PCT-US96-00499A-1			
Sequence 1, Application PC/TUS9600499A			
GENERAL INFORMATION:			
APPLICANT: LI, YI			
TITLE OF INVENTION: Human G-Protein Chemokine Receptor			
TITLE OF INVENTION: HSAU68			
NUMBER OF SEQUENCES: 9			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Carella, Byrne, Bain, Giffillan, Cecchi,			
ADDRESSEE: Stewart & Olstein			
STREET: 6 Becker Farm Road			
CITY: Roseland			
STATE: NJ			
COUNTRY: USA			
ZIP: 07068-1739			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: PCT/US96/00499A			

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? FILING DATE: 11 JAN 1996
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: MULLINS, J.G.
? REGISTRATION NUMBER: 33,073
? REFERENCE/DOCKET NUMBER: 335800-474
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-994-1700
? TELEFAX: 201-994-1744.
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1876 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 173..1417
? PCT-US96-00499A-1

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RESULT 3
US-09-101-518-1
; Sequence 1, Application US/09101518
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSAT068
; FILE REFERENCE: PF218PCT-US
; CURRENT APPLICATION NUMBER: US/09/101,518
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (173)..(1420)
US-09-101-518-1

Query Match 99.9%; Score 1874.4; DB 15; Length 1876;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1875; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGAAGGAGAGAGAGAGAGAGAGACAGTGGCCAGAGAGGGCTGCGCACTGAGAG 60
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Db 1 CCTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
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Db 61 GACGCTCTTCTCTCCGCGCCAGAGGGTCCCTGGGCGCGATGGAATCAGCAGAAAGATGCGAG 120
QY 121 AGAAGCAGCCTTTGAGAGAGAGAGTCAATCCAGAGCCCAAGTGAAGCCGAGT 180
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Db 181 GAGGAAGTACGGCCCTGGAAGAGCTGGGGGGAGACTTAAGAGGAGGTGCTCAAGATTA 240
QY 241 ATCAGAGACTAATCAGACTCAATCACAAGAGTTCCTGCGCAGGCTTTTACAGAGCCC 300
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Db 241 ATCAGAGACTAATCAGACTCAATCACAAGAGTTCCTGCGCAGGCTTTTACAGAGCCC 300
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Db 301 TTCTCTCCCGTTCGCGCTCAGAGTGAAGTACCACCAAGTGTCTTAAATGAGCGCGAGGT 360
QY 361 TGCCGCGCCCTCGGAGAGCTTCACTTCCATATGAGAGAGAGAGAGAGAGAGTCA 420
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QY 481 GCCAGCCCTTACAGAGCTCTTTCTGCTGGGGCTGCTGGCAAGGCGGCTGGAGAGC 540
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QY 541 CGTGCTGTGAGCGCGGCGAGAGCCCTGAGAGAGCAGCAGACACTTCTGCTCCACTGAGC 600
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[illegible]

Query Match	Best Local Similarity	Matches 1872: Conservative	Score 1873.2; DB 1; Length 1877;	Pred. No. 0;	Mismatches 1; Indels 0; Gaps 0;
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DB 1681	ACTTATCTTCCCAAGTGGGGAGTACAGAGCATGGCGTATAGAGGTGTGCCCCATGA	1740			
QY 1741	ACCCACAGCCCGAGGCTCCAGCTCAGCAGTGTGTGGCCATGTGCCCAAGACCTTAT	1800			
DB 1741	ACCCACAGCCCGAGGCTCCAGCTCAGCAGTGTGTGGCCATGTGCCCAAGACCTTAT	1800			
QY 1801	ATTGGTCTTTTATTTTATGTCTTAAATCCCTTAAACTTTTCAATTAACAAGATCG	1860			
DB 1801	ATTGGTCTTTTATTTTATGTCTTAAATCCCTTAAACTTTTCAATTAACAAGATCG	1860			
QY 1861	TCAGGAAAAAAAAAAAA 1876				
DB 1861	TCAGGAAAAAAAAAAAA 1876				
RESULT 4					
PCT-US00-26524B-2115					
; Sequence 2115, Application PC/TUS0026524B					
; GENERAL INFORMATION:					
; APPLICANT: Birse et. al.					
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept					
; FILE REFERENCE: PA005PCT					
; CURRENT FILING DATE: 2000-09-28					
; PRIOR APPLICATION NUMBER: 60/157,137					
; PRIOR FILING DATE: 1999-09-29					
; PRIOR APPLICATION NUMBER: 60/163,280					
; PRIOR FILING DATE: 1999-11-03					
; NUMBER OF SEQ ID NOS: 8564					
; SOFTWARE: PatentIn Ver. 2.0					
; SEQ ID NO 2115					
; LENGTH: 1877					
; TYPE: DNA					
; ORGANISM: Homo sapiens					
PCT-US00-26524B-2115					

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Db	481	GCACGCCCTCTACAGCCCTCTCTTTCTGCTGGGGCTGCTGGGCTAAAGGCGCGTGGACG	540
OY	541	CGTCTGTGTAGCGGGGGGAGACGCGCTGAGGAGAGACCGGACACTTCCTGCTCACACTAGC	600
Db	541	CGTCTGTGTAGCGGGGGGAGACGCGCTGAGGAGAGACCGGACACTTCCTGCTCACACTAGC	600
OY	601	TGTAGAGACACGCTGCTGCTGTGCTGACACTGCGCGCTCTTGGGAGTGGAGAGCTGTGCGTCA	660
Db	601	TGTAGAGACACACTGTGCTGTGCTGTGACACTGCGCGCTCTTGGGAGTGGAGAGCGTCCGTCTCA	660
OY	661	GTGGGCTCTTTGGCTCTTGGCTCTGTGCCTCTGCCTGCAAAAGTGGAGAGTGCCTCTTCAACATCACTTCTA	720
Db	661	GTGGGCTCTTTGGGCTCTTGGCTCTGTGCCTCTGCCTGCAAAAGTGGAGAGTGCCTCTTCAACATCACTTCTA	720
OY	721	CGCAGAGAGCCCTCTCTGTGTGCTGCTGACATGACGCTTTGACGCGCTGACGCAATAGTTCAATGCT	780
Db	721	CGCAGAGAGCCCTCTCTGTGTGCTGCTGACATGACGCTTTGACGCGCTGACGCAATAGTTCAATGCT	780
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OY	841	GGGGCTCTGGCTGCTTTTGGCCTCTCCAGACTTTCATCTTCTGTGTGGGCCACAGACGA	900
Db	841	GGGGCTCTGGCTGCTTTTCCCTCCCTCCAGACTTTCATCTTCTGTGTGGGCCACAGACGA	900
OY	901	GGCGCTCAAGCCGACCCACACGACATGACAACTTCCACAGGTGGGGCGGACAGGGCTGTGCG	960
Db	901	GGCGCTCAAGCCGACCCACACGACATGACAACTTCCACAGGTGGGGCGGACAGGGCTGTGCG	960
OY	961	GGTGTGTGACGTGTGTGGCTGGCTTTTCTGTGCTGCGCCCTGTGTGATAGGCTACTGTATAGC	1020
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OY	1021	CCACATCTCTGGCGGTGCTGTGTGCTTTCAGAGGGGCGACGCGCGCGCTGCGGGCTATCGGCT	1080
Db	1021	CCACATCTCTGGCGGTGCTGTGTGCTTTCAGAGGGGCGACGCGCGCGCTGCGGGCTATCGGCT	1080
OY	1081	GGTGTGTGTGTGTGTGTGTGCTTTTCCCTGCTGTGAGACCCCTATACACTGTGTGTGCT	1140
Db	1081	GGTGTGTGTGTGTGTGTGTGCTTTTCCCTGCTGTGAGACCCCTATACACTGTGTGTGCT	1140
OY	1141	GGTGTGTGTGTGTGTGTGTGCTGGGCGCTTTTGGCGCGCACTGTGGCGCAGAAAAGCAGGT	1200
Db	1141	GGTGTGTGTGTGTGTGTGTGCTGGGCGCTTTTGGCGCGCACTGTGGCGCAGAAAAGCAGGT	1200
OY	1201	AGAGGTGGCCAAAGTGGTGTACACTCAGAGGCGCTGAGCATAGCATGCTGTCTTACCCGCT	1260
Db	1201	AGAGGTGGCCAAAGTGGTGTACACTCAGAGGCGCTGAGCATAGCATGCTGTCTTACCCGCT	1260
OY	1261	GCTCTATGACCTTTGTAGGGGTCAAGTTTCCGGGAGCGAGTGTGATGCTGCTTTGGCGCT	1320
Db	1261	GCTCTATGACCTTTGTAGGGGTCAAGTTTCCGGGAGCGAGTGTGATGCTGCTTTGGCGCT	1320
OY	1321	GGGCTGCCCAACACAGAGAGGCTCTCAGAGGCGATGCTTCGCGCGGATATATC	1380
Db	1321	GGGCTGCCCAACACAGAGAGGCTCTCAGAGGCGATGCTTCGCGCGGATATATC	1380
OY	1381	CTGGGTGAGAGCCGACAGAGGCGCTTCACACTCGGGCTTTGTAGAGGCGCGAATTCGGGCTCCCC	1440
Db	1381	CTGGGTGAGAGCCGACAGAGGCGCTTCACACTCGGGCTTTGTAGAGGCGCGAATTCGGGCTCCCC	1440
OY	1441	TTTTGGCCACAGTCTGACTTCCCGGATTTCCAGAGCTCTCCCTCTGTGCGGGGCTGTG	1500
Db	1441	TTTTGGCCACAGTCTGACTTCCCGGATTTCCAGAGCTCTCCCTCTGTGCGGGGCTGTG	1500
OY	1501	CTCTGCCCAATATCTGTGCTCCGGGAGTCTACTGTGAGCGCCAGACAGCAGAGTCTTCC	1560
Db	1501	CTCTGCCCAATATCTGTGCTCCGGGAGTCTACTGTGAGCGCCAGACAGCAGAGTCTTCC	1560

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QY 1561 GGGAGCCACCTCCCACTCTGAGAGACTGCACCACTTCTGCTGCTTGTAGTCCCAAGCC 1620
Db 1561 GGGAGCCACCTCCCACTCTGAGAGACTGCACCACTTCTGCTGCTTGTAGTCCCAAGCC 1620
QY 1621 CATTCCTGCGCCCGGAGTGGCTGCTGGAGGCCCACTGCTCCCTTCATTTGGAACTAAA 1680
Db 1621 CATTCCTGCGCCCGGAGTGGCTGCTGGAGGCCCACTGCTCCCTTCATTTGGAACTAAA 1680
QY 1681 ACTTCATCTCCCAAGTGGCGGGAGTACAMGGCATGGCGTGAAGGTTGCTGCCCATGA 1740
Db 1681 ACTTCATCTCCCAAGTGGCGGGAGTACAMGGCATGGCGTGAAGGTTGCTGCCCATGA 1740
QY 1741 AGCCACAGCCAGGCTCCAGCTCAGCAGTGTGCTGGCCATGGTCCCAAGACTCTAT 1800
Db 1741 AGCCACAGCCAGGCTCCAGCTCAGCAGTGTGCTGGCCATGGTCCCAAGACTCTAT 1800
QY 1801 ATTTGCTCTTTATTTTATGTCTAAAACTCGCTTAAACTTTTCAATTAACAAGATCG 1860
Db 1801 ATTTGCTCTTTATTTTATGTCTAAAACTCGCTTAAACTTTTCAATTAACAAGATCG 1860
QY 1861 TCAGGAAAAAAAAAAAA 1876
Db 1861 TCAGGAAAAAAAAAAAA 1876

RESULT 5
US-60-258-273-3/c
; Sequence 3, Application US/60258273
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
; TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO01042-PROV
; CURRENT APPLICATION NUMBER: US/60/258,273
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6604
; TYPE: DNA
; ORGANISM: Human
US-60-258-273-3

Query Match 98.0%; Score 1839.2; DB 64; Length 6604;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1863; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 CCTGAAGGAGAGCAGGAGAGAGAGACAGTGGCCAGAGAGGCTCTGGCACTGGAGG 60
Db 3872 CCTGAAGGAGAGCAGGAGAGAGAGAGACAGTGGCCAGAGAGGCTCTGGCACTGGAGG 3813
QY 61 GACGCTCTTCTCCGCGCCAGGGGTCCTGGGGCGATGGGATCACGCAAGAAATGGCAG 120
Db 3812 GACGCTCTTCTCTCCGCGCCAGGGGTCCTGGGGCGATGGGATCACGCAAGAAATGGCAG 3753
QY 121 AGAAGCAGCCTTTGAGAAAGGGAAGTCACTATCCAGAGCCCAAGACTGAGCGGATGAGATT 180
Db 3752 AGAAGCAGCCTTTGAGAAAGGGAAGTCACTATCCAGAGCCCAAGAGCTGAGCGGATGAGATT 3693
QY 181 GAGGAAGTACGG-CCCTGGAAAGACTGGCGGGGACAGTTATAGGAGGACTGTCAGAGTA 239
Db 3692 GAGGAAGTACGGTCCCTGGAAAGACTGGCGGGGACAGTTATAGGAGGACTGTCAGAGTA 3633
QY 240 AATCAACACTTAATCAACACTCAATCACAAAAAAGATTCTCGCAGGCGCTTTACACAGCCC 299
Db 3632 AATCAACACTTAATCAACACTCAATCACAAAAAAGATTCTCGCAGGCGCTTTACACAGCCC 3573
QY 300 CTTCCTCCCGCTTCCCGCTTCACAGGTGAGTGACACCAAGTGTCTAAATAGACGCCGAGG 359
Db 3572 CTTCCTCCCGCTTCCCGCTTCACAGGTGAGTGACACCAAGTGTCTAAATAGACGCCGAGG 3513
QY 360 TTTCGCGCTCTCTCTGGAGAACTTCAAGCTCTTCTCTTAATGATGAGAAACCAAGAACTGACT 419

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|||||
Db 3512 TTGCGCCCTCTCTGGAGAACTTCAGCTCTTCTATGACTATGAGAAAAAGAGAGTACT 3453
OY 420 CGTGGTGAACCTCCCCCGCCCTCCACAGAGACTTCAGCTGAACTTCGACCGGGCTTCC 479
Db 3452 CGTGTGAACCTCCCCCGCCCTCCACAGAGACTTCAGCTGAACTTCGACCGGGCTTCC 3393
OY 480 TGCACAGCCTCTACAGACCTCTCTTTCCTGCTGGGGCTGCTGGAGCAAGGAGGGGTGGAG 539
Db 3392 TGCACAGCCTCTACAGACCTCTCTTTCCTGCTGGGGCTGCTGGAGCAAGGAGGGGTGGAG 3333
OY 540 CCGTCTGCTGAGCGCGGGAGAGCCCTGAGAGCAGACGACCTTCCTGCTGACACTAG 599
Db 3332 CCGTCTGCTGAGCGCGGGAGAGCCCTGAGAGCAGACGACCTTCCTGCTGACACTAG 3273
OY 600 CTGTAGCAGACAGCTGCTGCTGCTGCTGACACTTCGCTGGGCACTGAGACGCTGCCCTCC 659
Db 3272 CTGTAGCAGACAGCTGCTGCTGCTGCTGACACTTCGCTGGGCACTGAGACGCTGCCCTCC 3213
OY 660 AGTGGGTCTTTGGCTCTGAGCCCTCTGCAAAAGTGGAGGTGCTCTTCAACATCAACTTCT 719
Db 3212 AGTGGGTCTTTGGCTCTGAGCCCTCTGCAAAAGTGGAGGTGCTCTTCAACATCAACTTCT 3153
OY 720 ACGCAGAGACCTCTCTGCTGCTGCTGCTGACCTTTGACCGCTACCTGAAATAGTTATG 779
Db 3152 ACGCAGAGACCTCTCTGCTGCTGCTGCTGACCTTTGACCGCTACCTGAAATAGTTATG 3093
OY 780 CCACCCAGCTCTACCGCGCGGG 839
Db 3092 CCACCCAGCTCTACCGCGGG 3033
OY 840 GGGGGCTCTGCTGCTGCTTTTCGCGCTCCAGACTTCATCTCTGTCGGGGCCACAGAGAG 899
Db 3032 GGGGGCTCTGCTGCTGCTTTTCGCGCTCCAGACTTCATCTCTGTCGGGGCCACAGAGAG 2973
OY 900 AGCGCTCAACGCCACCACTGCAATACAACTTCCACAGGTGGGGCGGACGCGCTTGC 959
Db 2972 AGCGCTCAACGCCACCACTGCAATACAACTTCCACAGGTGGGGCGGACGCGCTTGC 2913
OY 960 GGGTCTCTGAGCTGCTGCTGCTGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1019
Db 2912 GGGTCTCTGAGCTGCTGCTGCTGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2853
OY 1020 CCCACATCTCTGCGCTGCTGCTGCTGCTTTCGAGGGGGCGGCGGCGGCGGCGGCGGCG 1079
Db 2852 CCCACATCTCTGCGCTGCTGCTGCTGCTTTCGAGGGGGCGGCGGCGGCGGCGGCGGCG 2793
OY 1080 TGT 1139
Db 2792 TGT 2733
OY 1140 TGT 1199
Db 2732 TGT 2673
OY 1200 TAG-ACGTGGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1258
Db 2672 TAGTACGTGGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2613
OY 1259 CTGCTCTATGCTTTGTAGAGGGTCAAGTTCCGGGAGCGGAGTGTGATGCTGCTTGGCG 1318
Db 2612 CTGCTCTATGCTTTGTAGAGGGTCAAGTTCCGGGAGCGGAGTGTGATGCTGCTTGGCG 2553
OY 1319 CTGGGCTCTGCGCCAAACAGAGAGGGGTCCAGAGGAGCCATCTCTTCCCGCGGGATTTCA 1378
Db 2552 CTGGGCTCTGCGCCAAACAGAGAGGGGTCCAGAGGAGCCATCTCTTCCCGCGGGATTTCA 2493
OY 1379 TCTGTGTGTGAGACCTCAGAGGCTCTACTGTGGGCTTGTGAGGCGGGAATCCGGGCTCC 1438
Db 2492 TCTGTGTGTGAGACCTCAGAGGCTCTACTGTGGGCTTGTGAGGCGGGAATCCGGGCTCC 2433
OY 1439 CTTTGGCCACAGTCTGACTTCCCGGCAATTCAGGCTCTCCCTCCCTGCGGCTCT 1498
|||||

Db 2432 CCTTTCGCCACAGCTGTGACTTCCCGGCAATTCAGGCTCTCTCTCCCTGCGGCTCT 2373
OY 1499 GGCTCTCCCAATATCTCTGCTCCCGGGAGCTCATCTGGAGCCCGCCAGCCACAGGCTTC 1558
Db 2372 GGCTCTCCCAATATCTCTGCTCCCGGGAGCTCATCTGGAGCCCGCCAGCCACAGGCTTC 2313
OY 1559 CCGGGAAGCCACCTCTCCAGCTCTGAGAGACTGACACATTTGCTCTTACCTGCGCAAGC 1618
Db 2312 CCGGGAAGCCACCTCTCCAGCTCTGAGAGACTGACACATTTGCTCTTACCTGCGCAAGC 2253
OY 1619 CCATCTCTGCGCCCGGAGGTGCTGCTGAGGCCACCCACTGCTCTCTCAATTTGAAACTA 1678
Db 2252 CCATCTCTGCGCCCGGAGGTGCTGCTGAGGCCACCCACTGCTCTCTCAATTTGAAACTA 2193
OY 1679 AATCTCTATCTCCCAATGCTGGGGAGTACAGAGCATGCTGCTAGAGGTGCTGCCCAT 1738
Db 2192 AATCTCTATCTTCCCAATGCTGGGGAGTACAGAGCATGCTGCTAGAGGTGCTGCCCAT 2133
OY 1739 GAAGCCACAGCCAGGCTCTCAGCTCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1798
Db 2132 GAAGCCACAGCCAGGCTCTCAGCTCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2073
OY 1799 AATTTGCTCTTTTATTTATGCTTAAATCTCTGCTTAAATCTTTCAATTAACAGAT 1858
Db 2072 AATTTGCTCTTTTATTTATGCTTAAATCTCTGCTTAAATCTTTCAATTAACAGAT 2013
OY 1859 GGTCAAGA 1866
Db 2012 GGTCAAGA 2005

RESULT 6
US-09-023-655-980
Sequence 980, Application US/09023655
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 980:
SEQUENCE CHARACTERISTICS:
LENGTH: 1670 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: q1552845
US-09-023-655-980

Query Match 82.5%; Score 1548.4; DB 14; Length 1670;
Best Local Similarity 99.0%; Pred. No. 1.1e-313;
Matches 1558; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 303 CCGCCCCGTTCCGGCCCTACAGAGTGTGAGGACCAAGTGGCTAAATGACCGCCAGAGTTG 362
DB 58 CCAGCCCAAGCCATGTGCTTGAAGTGAAGTACCACCAAGTGTAAATGACGCGAGAGTTG 117
QY 363 CCGCCCTCCCTGGAGAACTTACACTTCTTATGACTATGAGAAACGAGAGTACTGT 422
DB 118 CCGCCCTCCCTGGAGAACTTACACTTCTTATGACTATGAGAAACGAGAGTACTGT 177
QY 423 GCTGTAACCTCCCGCCCTGCCACAGAGCTTACAGCTGAACTTGAACGCGGCTTCCTGC 482
DB 178 GCTGTACCTCCCGCCCTGCCACAGAGCTTACAGCTGAACTTGAACGCGGCTTCCTGC 237
QY 483 CAGCCCTACAGCCCTCCCTTCTGCTGGGGCTGCTGGGCAACGGCGGGTGGACGCGG 542
DB 238 CAGCCCTACAGCCCTCCCTTCTGCTGGGGCTGCTGGGCAACGGCGGGTGGACGCGG 297
QY 543 TCTGCTGAGCCGCGGAGAGCCCTGAGCAGCAGCAGCTTCTGCTCCACACTGAGCTG 602
DB 298 TCTGCTGAGCCGCGGAGAGCCCTGAGCAGCAGCAGCTTCTGCTCCACACTGAGCTG 357
QY 603 TAGCAGACACGCTGCTGTGTGTGACACTGCGCTGTGGGCAATGGAGCGCTGCCAGT 662
DB 358 TAGCAGACACGCTGCTGTGTGTGACACTGCGCTGTGGGCAATGGAGCGCTGCCAGT 417
QY 663 GGGTCTTTGGCTGTGGCTCTGCAAAAGTGGCAAGTGGCCCTTTCAACATCAACTTTAG 722
DB 418 GGGTCTTTGGCTGTGGCTCTGCAAAAGTGGCAAGTGGCCCTTTCAACATCAACTTTAG 477
QY 723 CAGGAGCCCTCTGCTGTGAGCTGCATAGCTTGTACCGCTACCTGGAACATAGTTCAATGCA 782
DB 478 CAGGAGCCCTCTGCTGTGAGCTGCATAGCTTGTACCGCTACCTGGAACATAGTTCAATGCA 537
QY 783 CCCAGCTACAGCCGCGGGGGCCCCCGGGCGGTGACCCCTCACTGCTGTGTGGG 842
DB 538 CCCAGCTACAGCCGCGGGGGCCCCCGGGCGGTGACCCCTCACTGCTGTGTGGG 597
QY 843 GGCCTGCTGCTGCTTTTCGCGCTCCAGACTTCATCTTCTGTCGGCCACACAGAGAGC 902
DB 598 GGCCTGCTGCTGCTTTTCGCGCTCCAGACTTCATCTTCTGTCGGCCACACAGAGAGC 657
QY 903 GGCCTCAAGCCCAACCACTGCAATACACTTCCACAGGTGGGCGCACAGGCTTCGCGG 962
DB 658 GGCCTCAAGCCCAACCACTGCAATACACTTCCACAGGTGGGCGCACAGGCTTCGCGG 717
QY 963 TGGTGTAGT 1022
DB 718 TGGTGTAGT 777
QY 1023 ACATCTGAGCCCTGCTGT 1082
DB 778 ACATCTGAGCCCTGCTGT 837
QY 1083 TGGT 1142
DB 838 TGGT 897
QY 1143 TGGACATCTCTCATGTGACCTGGGCGCTTTGGCCGCAACTGTGGCCGAGAAAGAGGCTAG 1202
DB 898 TGGACATCTCTCATGTGACCTGGGCGCTTTGGCCGCAACTGTGGCCGAGAAAGAGGCTAG 957
QY 1203 ACGTGCCCAAGTCGCTGACCTGAGGCTGGGCTACATGACTGTGCTGCAACCGGCTGC 1262
DB 958 ACGTGCCCAAGTCGCTGACCTGAGGCTGGGCTACATGACTGTGCTGCAACCGGCTGC 1017

QY 1263 TCTATGCTTTTGTAGGGGTCAAGTTCCGGGAGCGAGTGTGATGTCTTGTCCGCTGG 1322
DB 1018 TCTATGCTTTTGTAGGGGTCAAGTTCCGGGAGCGAGTGTGATGTCTTGTCCGCTGG 1077
QY 1323 GCTGCCCAACCAAGAGAGGCTTCAGAGCAGCAGCATGCTTCTCCGCGGATTCATCT 1382
DB 1078 GCTGCCCAACCAAGAGAGGCTTCAGAGCAGCAGCATGCTTCTCCGCGGATTCATCT 1137
QY 1383 GGTCTGAGACCTCAGAGGCTCCTACTGTGGGCTGTGAGCGCGGAATTCGGGCTCCCT 1442
DB 1138 GGTCTGAGACCTCAGAGGCTCCTACTGTGGGCTGTGAGCGCGGAATTCGGGCTCCCT 1197
QY 1443 TCGCCACAGTGTGATTTCCCGCATTTCCAGAGCTCTCCCTCTGCTGCGGCTGTGCT 1502
DB 1198 TCGCCACAGTGTGATTTCCCGCATTTCCAGAGCTCTCCCTCTGCTGCGGCTGTGCT 1257
QY 1503 CTGCCCAATATCTGCTCCCGGAGCTCACTGGCAGCCCAAGCAGCAGGCTTCCCGG 1562
DB 1258 CTGCCCAATATCTGCTCCCGGAGCTCACTGGCAGCCCAAGCAGCAGGCTTCCCGG 1317
QY 1563 GAAGCCACCTCCACAGCTGTGAGACTGCACATTGCTGCTTGTAGCTGCCAAGCCCA 1622
DB 1318 GAAGCCACCTCCACAGCTGTGAGACTGCACATTGCTGCTTGTAGCTGCCAAGCCCA 1377
QY 1623 TCTTGCGCGCCGAGGTGGCTGCTGGAGCCCACTGCCCTTCTCATTTGAAACTTAAAC 1682
DB 1378 TCTTGCGCGCCGAGGTGGCTGCTGGAGCCCACTGCCCTTCTCATTTGAAACTTAAAC 1437
QY 1683 TTCTATTTCCCAAGTGGCGGAGTACAAAGCATGGCGTGAAGAGGTGCTGCCCATGAAG 1742
DB 1438 TTCTATTTCCCAAGTGGCGGAGTACAAAGCATGGCGTGAAGAGGTGCTGCCCATGAAG 1497
QY 1743 CCACAGCCAGGCTCCACAGTCACTGAGCTGTGAGCTGAGTGGCCCAAGACCTATAT 1802
DB 1498 CCACAGCCAGGCTCCACAGTCACTGAGCTGTGAGCTGAGTGGCCCAAGACCTATAT 1557
QY 1803 TTGCTTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1862
DB 1558 TTGCTTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1617
QY 1863 AGGAAAAAAGAAAA 1876
DB 1618 AGGACCAAAAAA 1631

RESULT 7
US-09-880-107-3833
; Sequence 3833, Application US/09880107
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3833
; LENGTH: 1670
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. X95876
US-09-880-107-3833
Query Match 82.5%; Score 1548.4; DB 33; Length 1670;

Best Local Similarity 99.0%; Pred. No. 1,1e-313;
Matches 1558; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Oy 303 COTCCCGCTTCCCGCCCTGACAGAGTGAACACCAAGTGTAAATACGCGGAGTTG 362
Db 58 CCAGCCCAAGCCACTGTGAGTGAACACCAAGTGTAAATACGCGGAGTTG 117
Oy 363 CCGCCCTCTGAGAGACTTCAAGCTTCTTATGACTATGAGAAAGAGAGTGAAGT 422
Db 118 CCGCCCTCTGAGAGACTTCAAGCTTCTTATGACTATGAGAAAGAGAGTGAAGT 177
Oy 423 GCTGTACCTCCCGCCCTGACAGAGACTTCAAGCTTCAAGCTTCAAGCGGCTTCTGC 482
Db 178 GCTGTACCTCCCGCCCTGACAGAGACTTCAAGCTTCAAGCTTCAAGCGGCTTCTGC 237
Oy 483 CAGCCCTTACAGCTCTCTTCTTCTGCTGGGGCTGCTGGGCAAGCGGCGGAGAGCG 542
Db 238 CAGCCCTTACAGCTCTCTTCTTCTGCTGGGGCTGCTGGGCAAGCGGCGGAGAGCG 297
Oy 543 TGTGTGAGCGCGGAGAGAGCTTGAAGAGACACCAAGCTTCTGCTCAAGCTAGCTG 602
Db 298 TGTGTGAGCGCGGAGAGAGCTTGAAGAGACACCAAGCTTCTGCTCAAGCTAGCTG 357
Oy 603 TAGCAGACACCTGCTGCTGCTGACACTGCGCTGCGGAGTGAAGCGCTGCGCTCAGT 662
Db 358 TAGCAGACACCTGCTGCTGCTGACACTGCGCTGCGGAGTGAAGCGCTGCGCTCAGT 417
Oy 663 GGGCTTTTGGGCTTGGGCTTGGCAAGTGAAGTGGCTTCTTCAACATCACTTCTAG 722
Db 418 GGGCTTTTGGGCTTGGGCTTGGCAAGTGAAGTGGCTTCTTCAACATCACTTCTAG 477
Oy 723 CAGAGAGCCCTCTGCTGCTGATGACACTTGAAGCGCTTGAAGTGAAGTGAAGTGA 782
Db 478 CAGAGAGCCCTCTGCTGCTGATGACACTTGAAGCGCTTGAAGTGAAGTGAAGTGA 537
Oy 783 CCCAGCTTACCGCGGCGGCGCGCGCGCGCTGACCTGCTGCTGCTGCTGCTGCTG 842
Db 538 CCCAGCTTACCGCGGCGGCGCGCGCGCGCTGACCTGCTGCTGCTGCTGCTGCTG 597
Oy 843 GGGCTTGGCTTGGCTTGGGCTTGGCAAGTGAAGTGGCTTCTTCAACATCACTTCTAG 902
Db 598 GGGCTTGGCTTGGCTTGGGCTTGGCAAGTGAAGTGGCTTCTTCAACATCACTTCTAG 657
Oy 903 GCGTCAAGCGCACCACTGCGCAATACACTTCCACAGTGGGCGGAGCGCTGCGGAG 962
Db 658 GCGTCAAGCGCACCACTGCGCAATACACTTCCACAGTGGGCGGAGCGCTGCGGAG 717
Oy 963 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1022
Db 718 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777
Oy 1023 ACATCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1082
Db 778 ACATCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
Oy 1083 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1142
Db 838 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
Oy 1143 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1202
Db 898 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
Oy 1203 ACATCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1262
Db 958 ACATCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1017
Oy 1263 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1322
Db 1018 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1077
Oy 1323 GCTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1382

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Db 1078 GCTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1137
Oy 1383 GGTGTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1442
Db 1138 GGTGTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1197
Oy 1443 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1502
Db 1138 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1257
Oy 1503 CTCCCAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1562
Db 1258 CTCCCAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1317
Oy 1563 GAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1622
Db 1318 GAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1377
Oy 1623 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1682
Db 1378 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1437
Oy 1683 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1742
Db 1438 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1497
Oy 1743 CCACAGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1802
Db 1498 CCACAGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1557
Oy 1803 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1862
Db 1558 TGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1617
Oy 1863 AGCAAAAAAAAAA 1876
Db 1618 AGCAAAAAAAAAA 1631

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RESULT 8
US-09-624-594-1
; Sequence 1, Application US/09624594
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Marcel
; APPLICANT: Moser, Bernhard
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CYCR3,
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Mallitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentlin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/624,594
; FILING DATE: 25-JUL-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,838
; FILING DATE: 10-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: TK196-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1670 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: unknown
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 69..1172
; US-09-624-594-1

Query Match      82.2%; Score 1541.6; DB 24; Length 1670;
Best Local Similarity 99.1%; Pred. No. 3.6e-312;
Matches 1550; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 303 CCTCCCGTTCGCCGCTCAGAGTGAGGACCAAGTGTCTAATGAGCGCGAGTTG 362
Db 58 CCAGCCCAAGCATGTGCTCTTGAAGTGAAGACCAAGTGTCTAATGAGCGCGAGTTG 117
OY 363 CCGCCCTCTGAGAGACTTCAAGCTTCTCTATGACTATGAGAAAAAGAGAGTGACTGT 422
Db 118 CCGCCCTCTGAGAGACTTCAAGCTTCTCTATGACTATGAGAAAAAGAGAGTGACTGT 177
OY 423 GGTGACTCTCCCGCCCTGAGGAGAGAGTGTAGCTTGAAGTGAAGCGGCTTCTGTC 482
Db 178 GGTGACTCTCCCGCCCTGAGGAGAGTGTAGCTTGAAGTGAAGCGGCTTCTGTC 237
OY 483 CAGCCCTCTACAGCTCTCTTCTGCTGAGGAGTGTGAGGAGGAGGAGGAGGAGGAG 542
Db 238 CAGCCCTCTACAGCTCTCTTCTGCTGAGGAGTGTGAGGAGGAGGAGGAGGAGGAG 297
OY 543 TGTCTGCTAGAGCGGCGGAGAGAGCTTGAAGAGCAGCAGCAGCAGCTTCTGCTGCTAG 602
Db 298 TGTCTGCTAGAGCGGCGGAGAGAGCTTGAAGAGCAGCAGCAGCAGCTTCTGCTGCTAG 357
OY 603 TAGCAGAGACGCTGCTGCTGCTGAGACATGCGCTGTGGGAGATGAGAGCTGCGCTCAG 662
Db 358 TAGCAGAGACGCTGCTGCTGCTGAGACATGCGCTGTGGGAGATGAGAGCTGCGCTCAG 417
OY 663 GGGTCTTTGGCTCTGAGCTGCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 722
Db 418 GGGTCTTTGGCTCTGAGCTGCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 477
OY 723 CAGAGAGCTCTGCTGCTGCTGAGCTGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 782
Db 478 CAGAGAGCTCTGCTGCTGCTGAGCTGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 537
OY 783 CCCAGCTGTACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 842
Db 538 CCCAGCTGTACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 597
OY 843 GAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
Db 598 GAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657
OY 903 GCGTCAACGCAACCACTGCAATCAACTTCCACAGAGTGGGCGCAGCGCTGCGGG 962
Db 658 GCGTCAACGCAACCACTGCAATCAACTTCCACAGAGTGGGCGCAGCGCTGCGGG 717
OY 963 TGTCTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
Db 718 TGTCTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
OY 1023 ACATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1082
Db 778 ACATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
OY 1083 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1142
Db 838 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 897
OY 1143 TGGACATCTCATGAGACTGGGCGCTTTGGCGCCGCAACTGTGAGCGAGAAAGAGGTAG 1202
Db 1143 TGGACATCTCATGAGACTGGGCGCTTTGGCGCCGCAACTGTGAGCGAGAAAGAGGTAG 1202
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Db 898 TGGACATCTCATGAGACTGGGCGCTTTGGCGCCGCAACTGTGAGCGAGAAAGAGGTAG 957
OY 1203 ACATGCGCAAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1262
Db 958 ACATGCGCAAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1017
OY 1263 TCTATGCTTTGTAGAGGCTCAAGTGTGCGGAGCGGAGTGTGATGCTGCTTGTGCGCTG 1322
Db 1018 TCTATGCTTTGTAGAGGCTCAAGTGTGCGGAGCGGAGTGTGATGCTGCTTGTGCGCTG 1077
OY 1323 GCTGCGCCCAACAGAGAGGCTTCCAGAGGCAAGCTGCTTCTCCCGCGGATTTATCT 1382
Db 1078 GCTGCGCCCAACAGAGAGGCTTCCAGAGGCAAGCTGCTTCTCCCGCGGATTTATCT 1137
OY 1383 GGTCTGAGACCTCAGAGGCTCTCTACTGCGGCTGTGTGAGGCGGAGTCCGGGCTCCCT 1442
Db 1138 GGTCTGAGACCTCAGAGGCTCTCTACTGCGGCTGTGTGAGGCGGAGTCCGGGCTCCCT 1197
OY 1443 TCGCCCAAGTCTGACTTCCCGCATTCAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1502
Db 1198 TCGCCCAAGTCTGACTTCCCGCATTCAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1257
OY 1503 CTCCCAATATCTCTGCTCTCCGAGACTCACTGAGCAGCCAGACACACAGTCTCTCCG 1562
Db 1258 CTCCCAATATCTCTGCTCTCCGAGACTCACTGAGCAGCCAGACACACAGTCTCTCCG 1317
OY 1563 GAAGCAGCCCTCCAGCTCTGAGACTCAGCATTTGCTGCTCTTACGCTGCGCAAGCCCA 1622
Db 1318 GAAGCAGCCCTCCAGCTCTGAGACTCAGCATTTGCTGCTCTTACGCTGCGCAAGCCCA 1377
OY 1623 TCTGCGCGCGGAGGCTGCTGCTGAGCGCCCATGCGCTTCTCTATTTGAAACTAAAC 1682
Db 1378 TCTGCGCGCGGAGGCTGCTGCTGAGCGCCCATGCGCTTCTCTATTTGAAACTAAAC 1437
OY 1683 TTGATCTTCCCAAGTGTGCGGAGTACAAAGATGTGGCTAGAGGCTGTGCGCCCATGAAG 1742
Db 1438 TTGATCTTCCCAAGTGTGCGGAGTACAAAGATGTGGCTAGAGGCTGTGCGCCCATGAAG 1497
OY 1743 CCACAGCCAGGCTCTCAGACTGAGAGTGTGAGGATGTGGCTGCGCCCAAGACTTATAT 1802
Db 1498 CCACAGCCAGGCTCTCAGACTGAGAGTGTGAGGATGTGGCTGCGCCCAAGACTTATAT 1557
OY 1803 TTGCTCTTTTATTTTATGCTTAAATCTGCTTAAACTTTTCAATTAACAAGATGCTC 1862
Db 1558 TTGCTCTTTTATTTTATGCTTAAATCTGCTTAAACTTTTCAATTAACAAGATGCTC 1617
OY 1863 AGGA 1866
Db 1618 AGGA 1621

RESULT 9
US-09-633-541-1
; Sequence 1, Application US/09633541
; GENERAL INFORMATION:
; APPLICANT: Loelscher, Marcel
; APPLICANT: Moser, Bernhard
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3.
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/633,541
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/709,838
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TK196-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1670 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
FEATURE:
NAME/KEY: CDS
LOCATION: 69..1172
US-09-633-341-1

Query Match 82.2%; Score 1541.6; DB 24; Length 1670;
Best Local Similarity 99.1%; Pred. No. 3,6e-312;
Matches 1550; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

303 CCTCCCGGTTCCCGCCCTCCACAGGTGAGTACACCAAGTGTAAATGACGCCGAGGTTG 362
Db 58 CCAGCCGACGCTATGGTCTTGTGAGTGAGTACACCAAGTGTAAATGACGCCGAGGTTG 117
363 CGGCGCTCTGTGAGAACTTACGCTCTCTATGACTATGAGAAAAAGAGTACTGCT 422
Db 118 CGGCGCTCTGTGAGAACTTACGCTCTCTATGACTATGAGAAAAAGAGTACTGCT 177
423 GCTGTACTCCCGCCGCTGACCACAGAGTACTGAGCTGAACCTTCGACGGGCTTCTGC 482
Db 178 GGTGTACTCCCGCCGCTGACCACAGAGTACTGAGCTGAACCTTCGACGGGCTTCTGC 237
483 CAGCCCTTACAGGCTCCTCTTCTGTGCTGGGCTGCTGGCAAGGGCGGCTGGCAGCCG 542
Db 238 CAGCCCTTACAGGCTCCTCTTCTGTGCTGGGCTGCTGGCAAGGGCGGCTGGCAGCCG 297
543 TGTCTGTAGCGGGGGGAGAGGCTGAGAGACGACACGACCTTCTGCTCCACATGACTG 602
Db 298 TGTCTGTAGCGGGGGGAGAGGCTGAGAGACGACACGACCTTCTGCTCCACATGACTG 357
603 TAGCAGACAGGCTGCTGTGCTGACACTGCGCTGAGGAGTGAAGGCTGCGCTCAGT 662
Db 358 TAGCAGACAGGCTGCTGTGCTGACACTGCGCTGAGGAGTGAAGGCTGCGCTCAGT 417
663 GGGCTTTGGCTGTGAGCTGTGCAAGTGGAGGTGCCCTTCAACATCAACTTCTAG 722
Db 418 GGGCTTTGGCTGTGAGCTGTGCAAGTGGAGGTGCCCTTCAACATCAACTTCTAG 477
723 CAGGAGCCCTCTCTGTGAGCTGATCAGTTTGGACCGCTACTGAACATGATTCATGCA 782
Db 478 CAGGAGCCCTCTCTGTGAGCTGATCAGTTTGGACCGCTACTGAACATGATTCATGCA 537
783 CCCAGCTTACCGCGGGGGGGCGCGCGGCTGACCTTCACTGCTGCGGCCACAGAGAGC 842
Db 538 CCCAGCTTACCGCGGGGGGGCGCGCGGCTGACCTTCACTGCTGCGGCCACAGAGAGC 597
843 GGGCTGCTGCTTTTGGCGCTTCCAGACTTATCTTCTGCTGCGGCCACAGAGAGC 902
Db 598 GGGCTGCTGCTTTTGGCGCTTCCAGACTTATCTTCTGCTGCGGCCACAGAGAGC 657
903 GCGTCAAGCCACCCACAGTGCATACAACTTCCACAGAGTGGGCGGACAGGCTTGGGG 962
Db 658 GCGTCAAGCCACCCACAGTGCATACAACTTCCACAGAGTGGGCGGACAGGCTTGGGG 717
963 TCGTCAAGCTGTGCTGCTTCTGCTGCTCCCTGCTGCTATGGGCTACTGCTATGCC 1022

Db 718 TCGTCAAGCTGTGCTGCTTCTGCTGCTCCCTGCTGCTATGGCTACTGCTATGCC 777
1023 ACATCTGCGCGCTGCTGCTGCTTCCAGAGGCGCAGCGGCGCTGCGGCGCTGCTG 1082
Db 778 ACATCTGCGCGCTGCTGCTTCCAGAGGCGCAGCGGCGCTGCGGCGCTGCTG 837
1083 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1142
Db 838 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
1143 TGGACATCTTCATGACCTGCGGCTTGGCCGCACTGTGGCCGAGAAAGAGGCTAG 1202
Db 898 TGGACATCTTCATGACCTGCGGCTTGGCCGCACTGTGGCCGAGAAAGAGGCTAG 957
1203 AGTGGCCAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1262
Db 958 AGTGGCCAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1017
1263 TGTATGCTTTGTAGGGGTCAGTTCGCGGAGCGATGTGATGCTGCTGCTGCTGCTG 1322
Db 1018 TGTATGCTTTGTAGGGGTCAGTTCGCGGAGCGATGTGATGCTGCTGCTGCTGCTG 1077
1323 GGTGCCCAACAGAGAGGGCTCCAGAGGACGCTGCTTCCGCGGAGATTCATCT 1382
Db 1078 GGTGCCCAACAGAGAGGGCTCCAGAGGACGCTGCTTCCGCGGAGATTCATCT 1137
1383 GGTGTGAGACTGAGAGGCTCTCTACTGCGGCTTGTGAGGCGGAAATCCGGGCTCCCTT 1442
Db 1138 GGTGTGAGACTGAGAGGCTCTCTACTGCGGCTTGTGAGGCGGAAATCCGGGCTCCCTT 1197
1443 TGGCCCAAGTGTGATTCGCGGATTCAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTG 1502
Db 1198 TGGCCCAAGTGTGATTCGCGGATTCAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTG 1257
1503 CTCCCAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1562
Db 1258 CTCCCAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1317
1563 GAAGCCACCTCCAGCTGTGAGAGTGCACCAATGCTGCTGCTGCTGCTGCTGCTGCTG 1622
Db 1318 GAAGCCACCTCCAGCTGTGAGAGTGCACCAATGCTGCTGCTGCTGCTGCTGCTGCTG 1377
1623 TCGTGGCGGCGAGTGTGCTGCTGAGGCGCCATGCTGCTGCTGCTGCTGCTGCTGCTG 1682
Db 1378 TCGTGGCGGCGAGTGTGCTGCTGAGGCGCCATGCTGCTGCTGCTGCTGCTGCTGCTG 1437
1683 TTCAATCTCCCAAGTGTGCTGCTGAGAGTGCATGAGAGGCTGCTGCTGCTGCTGCTG 1742
Db 1438 TTCAATCTCCCAAGTGTGCTGCTGAGAGTGCATGAGAGGCTGCTGCTGCTGCTGCTG 1497
1743 CCACAGCCAGGCTCCAGCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1802
Db 1498 CCACAGCCAGGCTCCAGCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1557
1803 TTGCTCTTTTATTTATGCTTAAATCTGCTTAAACTTTTCAATTAACAAGATGCTG 1862
Db 1558 TTGCTCTTTTATTTATGCTTAAATCTGCTTAAACTTTTCAATTAACAAGATGCTG 1617
1863 AGGA 1866
Db 1618 AGGA 1621

RESULT 10
US-09-663-702-1
Sequence 1, Application us/09663702
GENERAL INFORMATION:
APPLICANT: Loetscher, Marcel
Moser, Bernhard
Qin, Shixin
Mackay, Charles R.
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,

Db 1558 TTGCTCTTTATTTTATGCTAAATCCTGCTTAAACTTTTCAATAACAGATCGTC 1617
Oy 1863 AGGA 1866
Db 1618 AGGA 1621

RESULT 11
US-09-663-799-1

; Sequence 1, Application us/09663799
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Marcel
; Moser, Bernhard
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
; NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/663,799
; FILING DATE: 15-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/709,838
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: TK196-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1670 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 69..1172
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-663-799-1

Query Match 82.2%; Score 1541.6; DB 26; Length 1670;
Best Local Similarity 99.1%; Pred. No. 3,6e-312;
Matches 1550; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 303 CCTCCCGCTTCCCGCTCAGAGTGAACACCAAGTCTAAATGACCGGAGTTG 362
Db 58 CCACCCCGCATGCTGCTGAGTGAACACCAAGTCTAAATGACCGGAGTTG 117
Oy 363 CCGCCCTCCCTGAGAACTTGAAGTCTTCTATGACTATGAGAAAGAGAGTGAAGT 422
Db 118 CCGCCCTCTCTGAGAACTTGAAGTCTTCTATGACTATGAGAAAGAGAGTGAAGT 177
Oy 423 GCTTACCTCCCGCTTCCCGCTCAGAGTGAACCTGAGCTTGAACCGGAGCTTCTGC 482
Db 178 GCTTACCTCCCGCTTCCCGCTCAGAGTGAACCTGAGCTTGAACCGGAGCTTCTGC 237
Oy 483 CAGCCCTTACAGCTCTCTTTTCTGCTGGGAGTCTGAGGCAAGCGGCGGTGCGACCG 542
Db 238 CAGCCCTTACAGCTCTCTTTTCTGCTGGGAGTCTGAGGCAAGCGGCGGTGCGACCG 297

Oy 543 TCGCTGAGCCGGGAGACGCTGAGCAGACCGACACTTCCGTCTCAGCTAGCTG 602
Db 298 TCGCTGAGCCGGGAGACGCTGAGCAGACCGACACTTCCGTCTCAGCTAGCTG 357
Oy 603 TAGCAGACAGCTGCTGCTGCTGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
Db 358 TAGCAGACAGCTGCTGCTGCTGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
Oy 663 GGGTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
Db 418 GGGTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
Oy 723 CAGGAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
Db 478 CAGGAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537
Oy 783 CCGACCTTACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 842
Db 538 CCGACCTTACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 597
Oy 843 GGGTCTGCTGCTTTCGCGCTCCAGACTTATCTTCTGCTGCGGCCACACAGAGAC 902
Db 598 GGGTCTGCTGCTTTCGCGCTCCAGACTTATCTTCTGCTGCGGCCACACAGAGAC 657
Oy 903 GCGTCAAGCGCCACCCAGTCCCAATCAACTTCCCAAGTGGGCGGCGGCGGCGGCGG 962
Db 658 GCGTCAAGCGCCACCCAGTCCCAATCAACTTCCCAAGTGGGCGGCGGCGGCGGCGG 717
Oy 963 TCGCTCAGCTGCTGCTGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
Db 718 TCGCTCAGCTGCTGCTGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
Oy 1023 ACATCTGCGCGTCTGCTGCTTTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1082
Db 778 ACATCTGCGCGTCTGCTGCTTTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCT 837
Oy 1083 TGGTGTGCTGCTGCTGCTGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1142
Db 838 TGGTGTGCTGCTGCTGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
Oy 1143 TGGACATCTCATGAGACCTGCGGCTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCT 1202
Db 898 TGGACATCTCATGAGACCTGCGGCTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCT 957
Oy 1203 ACGTGGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1262
Db 958 ACGTGGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1017
Oy 1263 TGTATGCTTGTAGGGGCTGAGTCCGGGAGCGGAGTGGAGTGGCTGCTGCGGCTGG 1322
Db 1018 TGTATGCTTGTAGGGGCTGAGTCCGGGAGCGGAGTGGAGTGGCTGCTGCGGCTGG 1077
Oy 1323 GCTGCCCAACACGAGAGGCTTTCAGAGGACGACATCGTCTTCCCGCGGAGTTATCT 1382
Db 1078 GCTGCCCAACACGAGAGGCTTTCAGAGGACGACATCGTCTTCCCGCGGAGTTATCT 1137
Oy 1383 GGTCTGAGACCTCAAGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1442
Db 1138 GGTCTGAGACCTCAAGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
Oy 1443 TCGCCACAGTCTGACTTCCCGGCAATCCAGGCTCTCTCCCTGCTGCGGCTGCGGT 1502
Db 1198 TCGCCACAGTCTGACTTCCCGGCAATCCAGGCTCTCTCCCTGCTGCGGCTGCGGT 1257
Oy 1503 CTGCCCAATATCTGCTTCCCGGAGTCACTGCGAGCCGACACACACAGGCTTCCCGG 1562
Db 1258 CTGCCCAATATCTGCTTCCCGGAGTCACTGCGAGCCGACACACACAGGCTTCCCGG 1317
Oy 1563 CAGCCACCTTCCAGCTCTGAGACTGACATTTGCTGCTTATAGTCCCAAGCCCA 1622
Db 1318 CAGCCACCTTCCAGCTCTGAGACTGACATTTGCTGCTTATAGTCCCAAGCCCA 1377

Db 1559 TTGCTCTTTATTTATGCTAAATCTGCTAAACCTTTCAATTAACAAGATGCT 1618
QY 1862 CAGCA 1866
Db 1619 CAGCA 1623

RESULT 13
US-09-016-434-1052
Sequence 1052, Application US/09016434
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1052:
SEQUENCE CHARACTERISTICS:
LENGTH: 1293 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1002740
US-09-016-434-1052

Query Match 68.9%; Score 1293; DB 14; Length 1293;
Best Local Similarity 100.0%; Pred. No. 3.6e-260;
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 ATAGAGAGAGCTGCTCAGATTAATCAGACTAAATCAGACTCAATCACAAGAGTTC 277
Db 1 ATAGAGAGAGCTGCTCAGATTAATCAGACTAAATCAGACTCAATCACAAGAGTTC 60
QY 278 CTGGCAGGCTTTTACACAGCCCCCTTCCCTCCCGTTCCCGCCCTCAGAGTGTAGTAC 337
Db 61 CTGGCAGGCTTTTACACAGCCCCCTTCCCTCCCGTTCCCGCCCTCAGAGTGTAGTAC 120
QY 338 CAAAGTCAATGAAGCGGAGGTTGCGCCCTCTGAGAACTTCAAGCTTCTATGAC 397
Db 121 CAAAGTCAATGAAGCGGAGGTTGCGCCCTCTGAGAACTTCAAGCTTCTATGAC 180
QY 398 TATGGAGAAAAGAGAGTGTGCTGTACCTCCCGCCCTGCGCCACAGAGACTTCAAGC 457
Db 181 TATGGAGAAAAGAGAGTGTGCTGTACCTCCCGCCCTGCGCCACAGAGACTTCAAGC 240

QY 458 CTGAACCTTGACCGGCGCTTCTCCGACAGCCCTTACAGGCTCTCTTTCTGCTGGGCTG 517
Db 241 CTGAACCTTGACCGGCGCTTCTCCGACAGCCCTTCTGCTGGGCTG 300
QY 518 CTGGGCAACGGCGGCTGAGCGGCTGCTGAGCGGCGGACAGCCCTGAGACAGCACC 577
Db 301 CTGGGCAACGGCGGCTGAGCGGCTGCTGAGCGGCGGACAGCCCTGAGACAGCACC 360
QY 578 GACACCTTCTGCTCCACCTAGCTGTAGAGACAGAGCTGTGTGACTGTGACCTGCTG 637
Db 361 GACACCTTCTGCTCCACCTAGCTGTAGAGACAGAGCTGTGTGACTGTGACCTGCTG 420
QY 638 TGGGAGTGGAGGCTGCGCTCCAGTGGGCTTTGGCTGTGCGCTCTGCAAACTGGAGGT 697
Db 421 TGGGAGTGGAGGCTGCGCTCCAGTGGGCTTTGGCTGTGCGCTCTGCAAACTGGAGGT 480
QY 698 GCCCTCTTCAATCAATCAATCTTACGAGAGAGCCCTCTGAGCTGATCAAGCTTTGAC 757
Db 481 GCCCTCTTCAATCAATCAATCTTACGAGAGAGCCCTCTGAGCTGATCAAGCTTTGAC 540
QY 758 CGCTACCTGAACATAGTTTCATGCCACCCAGCTTACCGCGGGGGGCCCGCGCGTG 817
Db 541 CGCTACCTGAACATAGTTTCATGCCACCCAGCTTACCGCGGGGGGCCCGCGCGTG 600
QY 818 ACCCTACCTGCTGCTGCTGTGAGGGGCTGCTGCTGCTTTTGGCCCTCCACACTTGCATC 877
Db 601 ACCCTACCTGCTGCTGCTGTGAGGGGCTGCTGCTGCTTTTGGCCCTCCACACTTGCATC 660
QY 878 TTCTGTGCGGCCACACAGAGAGCGGCTTCAAGCGCCACCTGCAATCAACTTCCCA 937
Db 661 TTCTGTGCGGCCACACAGAGAGCGGCTTCAAGCGCCACCTGCAATCAACTTCCCA 720
QY 938 CAGGTGGGCGGACGCGCTTCTGCGGCTGCTGAGCTGTGTGCTGCTGCTGCTGCTG 997
Db 721 CAGGTGGGCGGACGCGCTTCTGCGGCTGCTGAGCTGTGTGCTGCTGCTGCTGCTG 780
QY 998 CTGCTCATGCGCTTACTGCTATGCCACATCTGCGGCTGCTGCTGCTGCTGCTGCTG 1057
Db 781 CTGCTCATGCGCTTACTGCTATGCCACATCTGCGGCTGCTGCTGCTGCTGCTGCTG 840
QY 1058 CGGCGCTGCGGCGGCTGAGGGGCTGAGGGGCTGAGGGGCTGAGGGGCTGAGGGGCTG 1117
Db 841 CGGCGCTGCGGCGGCTGAGGGGCTGAGGGGCTGAGGGGCTGAGGGGCTGAGGGGCTG 900
QY 1118 ACCCCCTATCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1177
Db 901 ACCCCCTATCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 1178 AACTGTGGCGGAGAAAGCAGGGGTAGACGTGGGCAAGTGGGTACCTCAGGCTGGGCTAC 1237
Db 961 AACTGTGGCGGAGAAAGCAGGGGTAGACGTGGGCAAGTGGGTACCTCAGGCTGGGCTAC 1020
QY 1238 ATGCACTGCTGCTCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1297
Db 1021 ATGCACTGCTGCTCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1298 ATGTGGATGCTGCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1357
Db 1081 ATGTGGATGCTGCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1358 TCGTCTTCCCGCGGAGTTTCATCTGCTGTGAGACTCAGAGAGCTCTCTACTGCGGCTTG 1417
Db 1141 TCGTCTTCCCGCGGAGTTTCATCTGCTGTGAGACTCAGAGAGCTCTCTACTGCGGCTTG 1200
QY 1418 TGAGGCGGGAATCCGGGCTCCCTTTCGCGCACAGTGTACTTCCCGGATTCAGAGGCTC 1477
Db 1201 TGAGGCGGGAATCCGGGCTCCCTTTCGCGCACAGTGTACTTCCCGGATTCAGAGGCTC 1260
QY 1478 CTCCCTCCCTTTCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1510
Db 1261 CTCCCTCCCTTTCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1293

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RESULT 14
US-09-960-706-962
; Sequence 962, Application US/09960706
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 962
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U32674
US-09-960-706-962

Query Match          68.9%; Score 1293; DB 36; Length 1293;
Best Local Similarity 100.0%; Pred. No. 3.6e-260;
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 ATAGAGGAGGCTGCTCAGAGTAATACAGACTAATATCAGACTCAATCAAAAGAGTTG 277
DB 1 ATAGAGGAGGCTGCTCAGAGTAATACAGACTAATATCAGACTCAATCAAAAGAGTTG 60
QY 278 CTGCAGGCTTTTACACAGCCCTCTCTCCGTTCCCGCCCTCAGAGGTGAGTACAC 337
DB 61 CTGCAGGCTTTTACACAGCCCTCTCTCCGTTCCCGCCCTCAGAGGTGAGTACAC 120
QY 338 CAAGTGTAAATGAGCGGAGGTGGCGCCCTCTGAGAGACTTCAAGCTTTCTATGAC 397
DB 121 CAAGTGTAAATGAGCGGAGGTGGCGCCCTCTGAGAGACTTCAAGCTTTCTATGAC 180
QY 398 TATGAGAAAGAGAGTGTCTGTCTGTACTCCCGCCCTGCGCAAGAGACTTCAAG 457
DB 181 TATGAGAAAGAGAGTGTCTGTCTGTACTCCCGCCCTGCGCAAGAGACTTCAAG 240
QY 458 CTGAACCTTGACCGGCGCTCTCTGCGACGCCCTTACAGGCTCTCTTCTGCTGGGCTG 517
DB 241 CTGAACCTTGACCGGCGCTCTCTGCGACGCCCTTACAGGCTCTCTTCTGCTGGGCTG 300
QY 518 CTGGGCAAGCGCGGCTGCGACGCCCTGCTGTGAGCGCGGAGACCCCTGAGACAC 577
DB 301 CTGGGCAAGCGCGGCTGCGACGCCCTGCTGTGAGCGCGGAGACCCCTGAGACAC 360
QY 578 GACACCTTCTCTCAGCTAGCTAGTACAGAGAGCTGTGTGTGTGACTGTGCGCTG 637
DB 361 GACACCTTCTCTCAGCTAGCTAGTACAGAGAGCTGTGTGTGTGACTGTGCGCTG 420
QY 638 TGGGAGTGTGAGCGTCCGCTCCAGTGGGTCTTGGCTGTGCGCTGTGCAAAAGTGGAG 697
DB 421 TGGGAGTGTGAGCGTCCGCTCCAGTGGGTCTTGGCTGTGCGCTGTGCAAAAGTGGAG 480
QY 698 GCGCTCTTTCACATCACTTCTAGCGAGAGCGCTCTGCTGGCTGTGCAAGCTTTGAC 757
DB 481 GCGCTCTTTCACATCACTTCTAGCGAGAGCGCTCTGCTGGCTGTGCAAGCTTTGAC 540
QY 758 CGCTACCTGAATATGTTATGCCACCGACTACCGCGGGGGGCGCGCGCGCGGCTG 817
DB 541 CGCTACCTGAATATGTTATGCCACCGACTACCGCGGGGGGCGCGCGCGCGGCTG 600
QY 818 ACCCTACCTGCTGCTGTGTGGGGGCTCTGCTGCTTTTGCCCTCCAGACTTCAATC 877
DB 601 ACCCTACCTGCTGCTGTGTGGGGGCTCTGCTGCTTTTGCCCTCCAGACTTCAATC 660
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QY 878 TTCCTGTGGCCCGACAGAGAGCGCTCAACGCCACCCACTGCCATATCACTTCCCA 937
DB 661 TTCCTGTGGCCCGACAGAGAGCGCTCAACGCCACCCACTGCCATATCACTTCCCA 720
QY 938 CAGGTGGGCGGACGCGCTGTGGGGGTGCTGAGCTGTGGGTGGCTTCTGTGCCCCG 997
DB 721 CAGGTGGGCGGACGCGCTGTGGGGGTGCTGAGCTGTGGGTGGCTTCTGTGCCCCG 780
QY 998 CTGTTCATGAGCTTACTGTATGCCACATCTGAGCGCTGTGCTGTGTTCCAGGGCCAG 1057
DB 781 CTGTTCATGAGCTTACTGTATGCCACATCTGAGCGCTGTGCTGTGTTCCAGGGCCAG 840
QY 1058 CGGCGCTGCGGGCCATGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1117
DB 841 CGGCGCTGCGGGCCATGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 1118 ACCCCCTATCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1177
DB 901 ACCCCCTATCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
QY 1178 AACTGTGGCGGAGAAAGCAGGCTAGACGTGCGCAAGTCCGTACCTCAGAGCTGGGCTAC 1237
DB 961 AACTGTGGCGGAGAAAGCAGGCTAGACGTGCGCAAGTCCGTACCTCAGAGCTGGGCTAC 1020
QY 1238 ATGCACTGCTGCTCAACCCGCTCTATAGCTTTTGAAGGCTCAAGTCCGGAAGCG 1297
DB 1021 ATGCACTGCTGCTCAACCCGCTCTATAGCTTTTGAAGGCTCAAGTCCGGAAGCG 1080
QY 1298 ATGTGATGCTGCTCTTGGGCTGTGGCTGCGCCCAACAGAGAGGCTCCAGAGGCCA 1357
DB 1081 ATGTGATGCTGCTCTTGGGCTGTGGCTGCGCCCAACAGAGAGGCTCCAGAGGCCA 1140
QY 1358 TCGTCTCCGCGGGGATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1417
DB 1141 TCGTCTCCGCGGGGATTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
QY 1418 TGAAGCGGGAATTCGCGGCTCCCTTTGCGCCACAGTGTGACTTCCCGGATTCAGGCTC 1477
DB 1201 TGAAGCGGGAATTCGCGGCTCCCTTTGCGCCACAGTGTGACTTCCCGGATTCAGGCTC 1260
QY 1478 CTCCCTCCCTGCGGGCTGTGGCTGTCCCA 1510
DB 1261 CTCCCTCCCTGCGGGCTGTGGCTGTCCCA 1293

RESULT 15
US-09-170-496-19
; Sequence 19, Application US/09170496
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496-19

Query Match          58.5%; Score 1097; DB 15; Length 1107;
Best Local Similarity 100.0%; Pred. No. 3.7e-219;
Matches 1097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 AGGTGATGACCAACAGTGAATATGAGCGGAGGTTGCGCGCTGGAGAACTTCA 383
DB 11 AGGTGATGACCAACAGTGAATATGAGCGGAGGTTGCGCGCGCTGGAGAACTTCA 70
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QY	1	CCTGAAGGAGAGCAGGGAGAGAGAGACACTGGCCAGAGAGGGCTCTGGGCACTGGAGG	60
QY	1	CCTGAAGGAGAGCAGGGAGAGAGAGACACTGGCCAGAGAGGGCTCTGGGCACTGGAGG <td>60</td>	60
Db	1	CCTGAAGGAGAGCAGGGAGAGAGAGACACTGGCCAGAGAGGGCTCTGGGCACTGGAGG	60
QY	61	GACGCTCTTCTTCTCTGCCAGAGGGGTCTCTGGGCGCAGTGGATCAGCAGAGAAATGGGAG	120
Db	61	GACGCTCTTCTTCTCTGCCAGAGGGGTCTCTGGGCGGATGGATCAGCAGAGAAATGGGAG	120
QY	121	AGAACACACCTTTGAGAGGAGAGCACAATTATCCAGACCAGACTGAGCGGATGGAGATT	180
Db	121	AGAACACACCTTTGAGAGGAGAGCACAATTATCCAGACCAGACTGAGCGGATGGAGATT	180
QY	181	GAGGAAGTACGGCCCTGGAGAGCTGGCGGGACAGATTATAGGAGAGCTGCTCAGAGTAA	240

D	b	181	GAGAACTACGGCCCTGGAAAGACTGGCGGGGACAGTTATAGAGGAGACTGCTCAGAGTAA	240
Q	y	241	ATCACAGACTAAATCAGACTCAATTCACAAAGAAGTTCGCGCAGGCGTTTACACAGCCCC	300
D	b	241	ATCACAGACTAAATCAGACTCAATTCACAAAGAAGTTCGCGCAGGCGTTTACACAGCCCC	300
Q	y	301	TTTCTCCCCGTTCCCGGCTCACAGGTGAGTGAACCAACCAATGCTAAATGACCGGAGGT	360
D	b	301	TTTCTCCCCGTTCCCGGCTCACAGGTGAGTGAACCAACCAATGCTAAATGACCGGAGGT	360
Q	y	361	TGCGGCGCTCTGGAGAACTTCAGCTCTTCATGACTATGGAGAAAAGAGAGTAC	420
D	b	361	TGCGGCGCTCTGGAGAACTTCAGCTCTTCATGACTATGGAGAAAAGAGAGTAC	420
Q	y	421	GTCGCTACCTCCCGGCGCTGCCACAGGACTTCACCCCTGAACTTCGACCGGGCGTTCT	480
D	b	421	GTCGCTACCTCCCGGCGCTGCCACAGGACTTCACCCCTGAACTTCGACCGGGCGTTCT	480
Q	y	481	GCCAGCCCTCTACAGCCTCTCTTTTGCTGGGGGCTGCTGGCCAAAGGGCGGTGGCAGC	540
D	b	481	GCCAGCCCTCTACAGCCTCTCTTTTGCTGGGGGCTGCTGGCCAAAGGGCGGTGGCAGC	540
Q	y	541	CGTCTCTGTGAGCGGGGGGAGACCCGCGAGACAGACCCGACCTTCGTCCTACCTATGC	600
D	b	541	CGTCTCTGTGAGCGGGGGGAGACCCGCGAGACAGACCCGACCTTCGTCCTACCTATGC	600
Q	y	601	TGTAGCAGACACGCTGCTGGTGTGACACTGCGCGCTCTGGGAGTGGAGCGCTGCCA	660
D	b	601	TGTAGCAGACACGCTGCTGGTGTGACACTGCGCGCTCTGGGAGTGGAGCGCTGCCA	660
Q	y	661	GTTGGGCTTTGGCTCTTGCGCTCTGCAAAAGTGGAGGTGCCCTTCAACATCAACTTTA	720
D	b	661	GTTGGGCTTTGGCTCTTGCGCTCTGCAAAAGTGGAGGTGCCCTTCAACATCAACTTTA	720
Q	y	721	CGCAGAGACCCCTCGCTGCTGCGCTGCAATCAGCTTTGACGCTATCGAATATGTTCAATGC	780
D	b	721	CGCAGAGACCCCTCGCTGCTGCGCTGCAATCAGCTTTGACGCTATCGAATATGTTCAATGC	780
Q	y	781	CACCCAGCTTACCGCGCGGGGGCCCCCGCGCGCTGACCTCACCCTGCGTGGCTGTG	840
D	b	781	CACCCAGCTTACCGCGCGGGGGCCCCCGCGCGCTGACCTCACCCTGCGTGGCTGTG	840
Q	y	841	GGGGCTTGCGCTGCTTTTGCGCCCTCCCAAGCTTCACTTCTGTCGGCCACACAGAGA	900
D	b	841	GGGGCTTGCGCTGCTTTTGCGCCCTCCCAAGCTTCACTTCTGTCGGCCACACAGAGA	900
Q	y	901	GCGGCTCAAGCCACCCACTGSCCAATCAAACTTCCACAGGTGGGGCCGACGCGCTCGG	960
D	b	901	GCGGCTCAAGCCACCCACTGSCCAATCAAACTTCCACAGGTGGGGCCGACGCGCTCGG	960
Q	y	961	GGTGCTCAGCTGGTGGCTGGCTTCTGCTGGCCCCGCTGAGTGCATAGGCTACTGTATGC	1020
D	b	961	GGTGCTCAGCTGGTGGCTGGCTTCTGCTGGCCCCGCTGAGTGCATAGGCTACTGTATGC	1020
Q	y	1021	CCACATCTTGCGCTGCTGTTTTCAGGGGGCAGCGGGCGCTGCGGGCCATCGGCT	1080
D	b	1021	CCACATCTTGCGCTGCTGTTTTCAGGGGGCAGCGGGCGCTGCGGGCCATCGGCT	1080
Q	y	1081	GGTGGTGGTGGTGGTGGCTTTTCCCTCTGCTGAGACCCCTATCACTGTGTGTCT	1140
D	b	1081	GGTGGTGGTGGTGGTGGCTTTTCCCTCTGCTGAGACCCCTATCACTGTGTGTCT	1140
Q	y	1141	GGTGGACATCTCATGGACCTTGGGGCGCTTGGCGCGCACTGGCCGAGAAAGAGAGGT	1200
D	b	1141	GGTGGACATCTCATGGACCTTGGGGCGCTTGGCGCGCACTGGCCGAGAAAGAGAGGT	1200
Q	y	1201	AGAGCTGGCAAGTCGCTCACTCAGGCGCTGGGCTACATGCACTGCTGCTCAACCCCT	1260
D	b	1201	AGAGCTGGCAAGTCGCTCACTCAGGCGCTGGGCTACATGCACTGCTGCTCAACCCCT	1260
Q	y	1261	GCTCTATGCCCTTTGTAGGGTCAAGTTCCGGGAGCGGAGATGTGGATGCTCTTTCGCGCT	1320
D	b	1261	GCTCTATGCCCTTTGTAGGGTCAAGTTCCGGGAGCGGAGATGTGGATGCTCTTTCGCGCT	1320

QY	1321	GGGCTGCCACACGAGAGGGCTCCAGAGGACGCCATGTTCTTCCGCGGGATTATC	1380
Db	1321	GGGGTGGCCCCAACCGAGAGAGGGCTCCAGAGGCGCCGCTTCGCCCGCGGATTATC	1380
QY	1381	CTGGCTGAGACCTCAGAGGGCTCTACCTACCTGGGCTGTGAGGCGGGAAATCGGGGCTCCC	1440
Db	1381	CTGGCTGAGACCTCAGAGGGCTCTACCTACCTGGGCTGTGAGGCGGGAAATCGGGGCTCCC	1440
QY	1441	TTTTGCCACAGTCTGACTTCCCGGCAATTCAGAGGCTCCCTCCCTGCGGGCTGG	1500
Db	1441	TTTTGCCACAGTCTGACTTCCCGGCAATTCAGAGGCTCCCTCCCTGCGGGCTGG	1500
QY	1501	CTCTCCCAATATCTCTGCTCCCGGGACTACTGGCAGCCAGACACCAAGTCTCC	1560
Db	1501	CTCTCCCAATATCTCTGCTCCCGGGACTACTGGCAGCCAGACACCAAGTCTCC	1560
QY	1561	GGGAAGCACCCTCCAGCTGTAGGACATGCTGTCTTATGCTGCGCAAGCC	1620
Db	1561	GGGAAGCACCCTCCAGCTGTAGGACATGCTGTCTTATGCTGCGCAAGCC	1620
QY	1621	CATCTGCGCGCCGAGGTGGCTGCTGGAGCCCACTGCGCTTTCATTGTTGGAACTAAA	1680
Db	1621	CATCTGCGCGCGAGGTGGCTGCTGGAGCCCACTGCGCTTTCATTGTTGGAACTAAA	1680
QY	1681	ACTTCATCTCCCACTGCGGGAGTACAAAGGCATGGCTGTAGAGGGTGTGCCCATGA	1740
Db	1681	ACTTCATCTCCCACTGCGGGAGTACAAAGGCATGGCTGTAGAGGGTGTGCCCATGA	1740
QY	1741	AGCCACAGCCCGAGGCTCCAGACTCAGAGTGTGGCATAGTGTCCCAAGACTCTAT	1800
Db	1741	AGCCACAGCCCGAGGCTCCAGACTCAGAGTGTGGCATAGTGTCCCAAGACTCTAT	1800
QY	1801	ATTGGCTCTTTATTTTATGTCTAAATCTGCTTTAAACTTTTCAATTAACAAGATCG	1860
Db	1801	ATTGGCTCTTTATTTTATGTCTAAATCTGCTTTAAACTTTTCAATTAACAAGATCG	1860
QY	1861	TCAGAAAAAATAA 1876	
Db	1861	TCAGAAAAAATAA 1876	

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RESULT 2
US-10-106-698-2125
; Sequence 2125, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA00561
; CURRENT APPLICATION NUMBER: US/10/106, 698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 2125
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-2125

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Query Match	99.9%	Score 1873.2	DB 12	Length 1877
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1872: Conservative	3	Mismatches	1	Indels 0; Gaps 0;
QY 1 CCTGAGGAGAGCAGGAGAGAGAGAGACACAGCGCCACAGAGAGGCTCTTGGGCACTTGGAGC	60			
DB 1 CCTGAGGAGAGCAGGAGAGAGAGAGAGACACAGCGCCACAGAGAGGCTCTTGGGCACTTGGAGC	60			

OY	61	GACGCTCTTCTCTCTGCCACAGGGTCCCTTGCGCCATGSGATCTACGCGAGAAATGCGAG	120
Db	61	GACGCTCTTCTCTCTCTGCCACAGGGTCCCTTGCGCCATGSGATCTACGCGAGAAATGCGAG	120
OY	121	AGAAAGCACCCCTTTTAGAAAGGAAGTCACTATCCACAGGCCACAGACTGAGCGGATGAGATT	180
Db	121	AGAAAGCACCCCTTTTAGAAAGGAAGTCACTATCCACAGGCCACAGACTGAGCGGATGAGATT	180
OY	181	GAGGAAGTACGGCCCTGGAAAGTCTGGCGGGAGCATTTATAGAGAGAGCGTCTCAAGATTA	240
Db	181	GAGGAAGTACGGCCCTGGAAAGTCTGGCGGGAGCATTTATAGAGAGAGCGTCTCAAGATTA	240
OY	241	ATCACACGCTAAATCAGACTCTATCACAAAAGATTCTGCCAGGCCCTTTACACAGCCCC	300
Db	241	ATCACAGACTAAATCAGACTCTATCACAAAAGATTCTGCCAGGCCCTTTACACAGCCCC	300
OY	301	TTCCGCCCCCGTTCCCGCCCTCACAGGTAATGACACAAAGTGTAAATGAGCCGAGGT	360
Db	301	TTCCGCCCCCGTTCCCGCCCTCACAGGTAATGACACAAAGTGTAAATGAGCCGAGGT	360
OY	361	TGCCGCCCTCTTGAGAGAACTTTCAGCTTTCTGTACTATGAGAAAACGAGAGTGACTC	420
Db	361	TGCCGCCCTCTTGAGAGAACTTTCAGCTTTCTGTACTATGAGAAAACGAGAGTGACTC	420
OY	421	GTCGCTTACCTCCCGCCGCTTGCCACAGACTTCAGCCGTAACCTTGACCCGGCCCTTCT	480
Db	421	GTCGCTTACCTCCCGCCGCTTGCCACAGACTTCAGCCGTAACCTTGACCCGGCCCTTCT	480
OY	481	GCCAGCCCTCTACAGGCTCCTCTTTCTGCTGGGGGCTGCTGGGCAACGGCGGGTGGACG	540
Db	481	GCCAGCCCTCTACAGGCTCCTCTTTCTGCTGGGGGCTGCTGGGCAACGGCGGGTGGACG	540
OY	541	CGTACTGCTGAGCCGGGGGAGACGCCGTGAGACACACGACACTTCCTGCTCACACTAGC	600
Db	541	CGTACTGCTGAGCCGGGGGAGACGCCGTGAGACACACGACACTTCCTGCTCACACTAGC	600
OY	601	TGTAGACAGACAGCTGCTGTGTGTGACACTGCCGCTGTGGGAGTGGAGCGTGGCGTCA	660
Db	601	TGTAGACAGACAGCTGCTGTGTGTGACACTGCCGCTGTGGGAGTGGAGCGTGGCGTCA	660
OY	661	GTTGGGCTTTTGGGCTCTGTCGCTGTCGAAAGTGGAGGTTGGCCCTTTCACATTAATTCTTA	720
Db	661	GTTGGGCTTTTGGGCTCTGTCGCTGTCGAAAGTGGAGGTTGGCCCTTTCACATTAATTCTTA	720
OY	721	CGCAGAGACCCCTCTGCTGTGACTGCATACACTTTGAACGCTTACGTGACATATGTTCAATG	780
Db	721	CGCAGAGACCCCTCTGCTGTGACTGCATACACTTTGAACGCTTACGTGACATATGTTCAATG	780
OY	781	CACCCAGCTTACCGCGCGGGGGGCCCGCGCGCGGTGACCCCTACACTGCTGGCTGTGTG	840
Db	781	CACCCAGCTTACCGCGCGGGGGGCCCGCGCGCGGTGACCCCTACACTGCTGGCTGTGTG	840
OY	841	GGGGCTCTGGCTGCTTTTGGCCCTCCAGACTTCATCTTCTGTGGGCCACACAGACGA	900
Db	841	GGGGCTCTGGCTGCTTTTGGCCCTCCAGACTTCATCTTCTGTGGGCCACACAGACGA	900
OY	901	GGCGCTCAAGCCCAACCCACTGTCGCAATACAACTTCCACAGGGGGGGCGAGCGGCTCTCG	960
Db	901	GGCGCTCAAGCCCAACCCACTGTCGCAATACAACTTCCACAGGGGGGGCGAGCGGCTCTCG	960
OY	961	GGTGCTCAGACTGTGTGGCTGGCTTTTCTGTGTCGCCCTGTGCTGATAGGCTTACTGCTATGC	1020
Db	961	GGTGCTCAGACTGTGTGGCTGGCTTTTCTGTGTCGCCCTGTGCTGATAGGCTTACTGCTATGC	1020
OY	1021	CCAATCTCTGGCCGTGCTGCTGGTTTTCAGAGGGGCACAGCGGCCCTTGCGGGCCATCGGCT	1080
Db	1021	CCAATCTCTGGCCGTGCTGCTGGTTTTCAGAGGGGCACAGCGGCCCTTGCGGGCCATCGGCT	1080
OY	1081	GGTGGTGGTGTGTGTGTGGCTTTTGCCCTGTGAGACCCCTTATACACTGTGGTGTGCT	1140
Db	1081	GGTGGTGGTGTGTGTGTGGCTTTTGCCCTGTGAGACCCCTTATACACTGTGGTGTGCT	1140
OY	1141	GGTGGACATCTCTCATGTGACCTGGGCGCTTTTGGCCCCCACTGTGGCCGAGAAAGCAGGCT	1200

Db	1141	GGTGGACATCTCTCAATGGACCTGGGCGCTTTTGGCCGCAACTGTGGCCGAGAAAGCAGAGGT	1200
QY	1201	AGAGCTGGCCCAAGTCGGGTCACTCAGAGCCCTGGGCTTCATGACTCTGTGCTCCACACCCGCT	1260
Db	1201	AGACGTGGCCCAAGTCGGGTCACTCAGAGCCCTGGGCTTCATGACTCTGTGCTCCACACCCGCT	1260
QY	1261	GCCTCATGCCCTTTTGTAGGGGTCAAGTTTCCGGGAGCGGATGTGGATGTCTCTTGTGGCGCT	1320
Db	1261	GCTCATATGCCCTTTTGTAGGGGTCAAGTTTCCGGGAGCGGATGTGGATGTCTCTTGTGGCGCT	1320
QY	1321	GGGCTGCCCCACAGAGAGAGGGCTCCAGAGAGCAGCATGTGTTCTTCCCGCGGGATTATATC	1380
Db	1321	GGGCTGCCCCACAGAGAGAGGGCTCCAGAGAGCAGCATGTGTTCTTCCCGCGGGATTATATC	1380
QY	1381	CTGGCTGTAGACCTCAAGAGGCTCTCTCACTACACGGGCTTGTAGAGCCGGAAATCCGGGCTCCC	1440
Db	1381	CTGGCTGTAGACCTCAAGAGGCTCTCTCACTACACGGGCTTGTAGAGCCGGAAATCCGGGCTCCC	1440
QY	1441	TTTGGCCCAAGTCGACTTCCCGGCAATTCAGAGGCTCTCCCTCCCTGTGGCGGCTGTGG	1500
Db	1441	TTTGGCCCAAGTCGACTTCCCGGCAATTCAGAGGCTCTCCCTCCCTGTGGCGGCTGTGG	1500
QY	1501	CTCTCCCAATATCTCTGGCTTCCCGGCACTCACTGGGAGGCCACAGCACCACAGGTCTGCC	1560
Db	1501	CTCTCCCAATATCTCTGGCTTCCCGGCACTCACTGGGAGGCCACAGCACCACAGGTCTGCC	1560
QY	1561	GGGAAAGCCACCCCTCCAGCTCTGAGAGACTGACACATTTGCTGCTCTTATGTAGTCCAAAGCC	1620
Db	1561	GGGAAAGCCACCCCTCCAGCTCTGAGAGACTGACACATTTGCTGCTCTTATGTAGTCCAAAGCC	1620
QY	1621	CATCCTGGCCGCGGAGGTGCTGCTGAGAGACCCCACTGCGCTTCTCATTTGGAAACTTAA	1680
Db	1621	CATCCTGGCCGCGGAGGTGCTGCTGAGAGACCCCACTGCGCTTCTCATTTGGAAACTTAA	1680
QY	1681	ACTTCATTTTCCCAAGTGGGGGAGTACAAAGGCAATGGGTAGAGGGTGTGGCCCATGA	1740
Db	1681	ACTTCATTTTCCCAAGTGGGGGAGTACAAAGGCAATGGGTAGAGGGTGTGGCCCATGA	1740
QY	1741	AGCCACAGCCCAAGGCTCCAGCTCAGCAGTGAAGTGTGGCATGTGCCCAAGACTCTAT	1800
Db	1741	AGCCACAGCCCAAGGCTCCAGCTCAGCAGTGAAGTGTGGCATGTGCCCAAGACTCTAT	1800
QY	1801	ATTGTGCTTTTATTTTATGTATGTCTAAATCTCTGCTTAAACTTTTCAATAAACAAGATCG	1860
Db	1801	ATTGTGCTTTTATTTTATGTATGTCTAAATCTCTGCTTAAACTTTTCAATAAACAAGATCG	1860
QY	1861	TCAGAGAAAAAATAAATA 1876	
Db	1861	TCAGAGAAAAAATAAATA 1876	
RESULT 3			
PCT-US02-18947-620			
Sequence 620, Application PC/TUS0218947			
GENERAL INFORMATION:			
APPLICANT: Rosetta Inpharmatics			
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients			
FILE REFERENCE: 9301-175-228			
CURRENT APPLICATION NUMBER: PCT/US02/18947			
CURRENT FILING DATE: 2002-06-14			
PRIOR APPLICATION NUMBER: 60/280,770			
PRIOR FILING DATE: 2002-05-14			
NUMBER OF SEQ ID NOS: 2699			
SEQ ID NO 620			
LENGTH: 1670			
TYPE: DNA			
ORGANISM: Homo sapiens			
PUBLICATION INFORMATION:			
DATABASE ACCESSION NUMBER: NM_001504			
DATABASE ENTRY DATE: 2001-06-18			
PCT-US02-18947-620			

Query Match 82.5%; Score 1548.4; DB 2; Length 1670;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1558; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 303 CCTCCCGCTTCCCGCCCTCAGAGTGAGTGACACCAAGTGTGTAATGACCCGAGGTTG 362
DB 58 CCAGCCCTCAGAGCTGCTCTTGGAGTGAGTACACCAAGTGTGTAATGACCCGAGGTTG 117
QY 363 CCGCCCTCTGAGAGAACTTCAAGCTCTTCTATGACTATGAGAAAAGAGAGTGAAGT 422
DB 118 CCGCCCTCTGAGAGAACTTCAAGCTCTTCTATGACTATGAGAAAAGAGAGTGAAGT 177
QY 423 GCTGACTCTCCCGCCCTGAGAGAACTTCAAGCTCTTCTATGACTATGAGAAAAGAG 482
DB 178 GCTGACTCTCCCGCCCTGAGAGAACTTCAAGCTCTTCTATGACTATGAGAAAAGAG 237
QY 483 CAGCCCTCTAGAGCTCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542
DB 238 CAGCCCTCTAGAGCTCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 297
QY 543 TGTGCTGAG 602
DB 298 TGTGCTGAG 357
QY 603 TAGCAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
DB 358 TAGCAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
QY 663 GAGTCTTGGGCTGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 722
DB 418 GAGTCTTGGGCTGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
QY 723 CAG 782
DB 478 CAG 537
QY 783 CCGAGCTTACCGCGGG 842
DB 538 CCGAGCTTACCGCGGG 597
QY 843 GAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902
DB 598 GAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
QY 903 GCGTCAAGCGAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 962
DB 658 GCGTCAAGCGAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
QY 963 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1022
DB 718 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777
QY 1023 ACATCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1082
DB 778 ACATCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
QY 1083 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1142
DB 838 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
QY 1143 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1202
DB 898 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
QY 1203 ACATCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1262
DB 958 ACATCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1017
QY 1263 TGTATGCTTTGTAGAGGCTCAAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1322
DB 1018 TGTATGCTTTGTAGAGGCTCAAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1077
QY 1323 GCTGCGCCCAACCGAGAGAGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1382

DB 1078 GCTGCGCCCAACCGAGAGAGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1137
QY 1383 GGTGAG 1442
DB 1138 GGTGAG 1197
QY 1443 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1502
DB 1198 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1257
QY 1503 CTGCGCAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1562
DB 1258 CTGCGCAATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
QY 1563 GAAGGACCGCTGAG 1622
DB 1318 GAAGGACCGCTGAG 1377
QY 1623 TGTGCTGCGGCGAGAGTGGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1682
DB 1378 TGTGCTGCGGCGAGAGTGGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1437
QY 1683 TTTATCTTCCCAAGTGGGAGAGTCAAGAGCATGAGAGAGTGTGCTGCTGCTGCTG 1742
DB 1438 TTTATCTTCCCAAGTGGGAGAGTCAAGAGCATGAGAGAGTGTGCTGCTGCTGCTG 1497
QY 1743 CCAGAGCCAGGCTGCGAG 1802
DB 1498 CCAGAGCCAGGCTGCGAG 1557
QY 1803 TTTGCTCTTTATTTTATGCTAAATCTGCTTAAATCTTCAATAAACAAGATGCTC 1862
DB 1558 TTTGCTCTTTATTTTATGCTAAATCTGCTTAAATCTTCAATAAACAAGATGCTC 1617
QY 1863 AGGAAAAAAAAA 1876
DB 1618 AGGACCAAAAAAAAA 1631

RESULT 4
PCT-US02-25766-2790
Sequence 2790, Application PC/TUS0225766
GENERAL INFORMATION:
APPLICANT: GENE LOGIC, INC.
APPLICANT: MUNGER, William E
APPLICANT: FAULK, Ronald
APPLICANT: SUN, Hongwei
APPLICANT: SASAI, Hitoshi
APPLICANT: WAGA, Iwao
APPLICANT: YAMAMOTO, Jun
TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
FILE REFERENCE: 44921-5068-NO
CURRENT APPLICATION NUMBER: PCT/US02/25766
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 60/311,837
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 13946
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2790
LENGTH: 1670
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. X95876
PCT-US02-25766-2790

Query Match 82.5%; Score 1548.4; DB 2; Length 1670;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1558; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 303 CCTCCCGCTTCCCGCCCTCAGAGTGAGTGACACCAAGTGTGTAATGACCCGAGGTTG 362
DB 58 CCAGCCCTCAGAGCTGCTCTTGGAGTGAGTACACCAAGTGTGTAATGACCCGAGGTTG 117
QY 363 CCGCCCTCTGAGAGAACTTCAAGCTCTTCTATGACTATGAGAAAAGAGAGTGAAGT 422
DB 118 CCGCCCTCTGAGAGAACTTCAAGCTCTTCTATGACTATGAGAAAAGAGAGTGAAGT 177
QY 423 GCTGACTCTCCCGCCCTGAGAGAACTTCAAGCTCTTCTATGACTATGAGAAAAGAG 482
DB 178 GCTGACTCTCCCGCCCTGAGAGAACTTCAAGCTCTTCTATGACTATGAGAAAAGAG 237
QY 483 CAGCCCTCTAGAGCTCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542
DB 238 CAGCCCTCTAGAGCTCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 297
QY 543 TGTGCTGAG 602
DB 298 TGTGCTGAG 357
QY 603 TAGCAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
DB 358 TAGCAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
QY 663 GAGTCTTGGGCTGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 722
DB 418 GAGTCTTGGGCTGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
QY 723 CAG 782
DB 478 CAG 537
QY 783 CCGAGCTTACCGCGGG 842
DB 538 CCGAGCTTACCGCGGG 597
QY 843 GAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902
DB 598 GAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
QY 903 GCGTCAAGCGAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 962
DB 658 GCGTCAAGCGAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
QY 963 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1022
DB 718 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777
QY 1023 ACATCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1082
DB 778 ACATCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
QY 1083 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1142
DB 838 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
QY 1143 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1202
DB 898 TGTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
QY 1203 ACATCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1262
DB 958 ACATCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1017
QY 1263 TGTATGCTTTGTAGAGGCTCAAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1322
DB 1018 TGTATGCTTTGTAGAGGCTCAAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1077
QY 1323 GCTGCGCCCAACCGAGAGAGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1382

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Db 58 CCAGCCCAAGCCATGCTCTTGAAGGTGAGTGAACACCAAGTGTCTAAATGACCCGAGGTG 117
Qy 363 CCGCCCTCTGAGAACTTACGCTCTTCTATGACTATGAGAAAGAGAGTGACTGCT 422
Db 118 CCGCCCTCTGAGAACTTACGCTCTTCTATGACTATGAGAAAGAGAGTGACTGCT 177
Qy 423 GCTGTACCTCCCGCCCTGCCCCAGAGACTTCAAGCTGAATCTGACGGGCTTCTCCG 482
Db 178 GCTGTACCTCCCGCCCTGCCCCAGAGACTTCAAGCTGAATCTGACGGGCTTCTCCG 237
Qy 483 CAGCCCTCTACAGCTCTCTTCTGCTGAGGCTGCTGGGCAAGCGCGGTGCGACGC 542
Db 238 CAGCCCTCTACAGCTCTCTTCTGCTGAGGCTGCTGGGCAAGCGCGGTGCGACGC 297
Qy 543 TGTGCTGAGCGGGGGGAGCAGCCCTGAGACAGCAGACACCTTCTGCTGCTGACCTAGCT 602
Db 298 TGTGCTGAGCGGGGGGAGCAGCCCTGAGACAGCAGACACCTTCTGCTGCTGACCTAGCT 357
Qy 603 TAGCAGACAGCCTGCTGCTGCTGACACTGCGCTCTGAGGAGTGGAGCCTGCGCTCAGT 662
Db 358 TAGCAGACAGCCTGCTGCTGCTGACACTGCGCTCTGAGGAGTGGAGCCTGCGCTCAGT 417
Qy 663 GGGCTTTGGCTGTGCGCTCTGCAAAAGTGGCAGGTGCCCTTCAACATCAACTTCTAG 722
Db 418 GGGCTTTGGCTGTGCGCTCTGCAAAAGTGGCAGGTGCCCTTCAACATCAACTTCTAG 477
Qy 723 CAGAGGCCCTCTGCTGCGCTGCAATGAGCTTGAACCGCTGACTGAACTAGTTATGCA 782
Db 478 CAGAGGCCCTCTGCTGCGCTGCAATGAGCTTGAACCGCTGACTGAACTAGTTATGCA 537
Qy 783 CCCAGCTTACCGCGGGGGGCCCCCGGCGCTGACCTCAGCTGCGCTGCTGCTGG 842
Db 538 CCCAGCTTACCGCGGGGGGCCCCCGGCGCTGACCTCAGCTGCGCTGCTGCTGG 597
Qy 843 GGGCTGTGCTGCTTTTGGCCCTCCAGACTTCAATCTTCTGCTGCGCCACAGCAGAGC 902
Db 598 GGGCTGTGCTGCTTTTGGCCCTCCAGACTTCAATCTTCTGCTGCGCCACAGCAGAGC 657
Qy 903 GCCCAAGGCCAGCCAGCTGCCAATACAACTCCACAGGTGGGCGGCGGCTGCGGG 962
Db 658 GCCCAAGGCCAGCCAGCTGCCAATACAACTCCACAGGTGGGCGGCGGCTGCGGG 717
Qy 963 TGCTGAGACTGGTGGCTGCTTCTGCTGCGCCCTGCTGCTGATGGCCATGCTATGCCC 1022
Db 718 TGCTGAGACTGGTGGCTGCTTCTGCTGCGCCCTGCTGCTGATGGCCATGCTATGCCC 777
Qy 1023 ACATCTGGCCGCTGCTGCTGCTTCCAGAGGGGCAAGCGCGCTGCGGGCATGCGGCTGG 1082
Db 778 ACATCTGGCCGCTGCTGCTGCTTCCAGAGGGGCAAGCGCGCTGCGGGCATGCGGCTGG 837
Qy 1083 TGTGAGTGGTGGTGGCTTGGCCCTTGGCTGCTGAGACCCCTATCAGCTGGTGGTGG 1142
Db 838 TGTGAGTGGTGGTGGCTTGGCCCTTGGCTGCTGAGACCCCTATCAGCTGGTGGTGG 897
Qy 1143 TGGACATCTCATGAGACTGGGCGCTTGGCGCCCAACTGTGGCGGAGAAAGAGAGTAG 1202
Db 898 TGGACATCTCATGAGACTGGGCGCTTGGCGCCCAACTGTGGCGGAGAAAGAGAGTAG 957
Qy 1203 ACGTGGCCAAAGTGGTCACTCAGGCGCTGGGCTACATGCACTGCTGCCCTCAACCGGCTGC 1262
Db 958 ACGTGGCCAAAGTGGTCACTCAGGCGCTGGGCTACATGCACTGCTGCCCTCAACCGGCTGC 1017
Qy 1263 TCTATGCTTTGTATGGGGTCAAGTTCCGGGAGGGAGTGAATGATGCTGCTTGGGCTGG 1322
Db 1018 TCTATGCTTTGTATGGGGTCAAGTTCCGGGAGGGAGTGAATGATGCTGCTTGGGCTGG 1077
Qy 1323 GCTGCCCCCAACAGAGAGGGCTCCAGAGGAGAGCATGCTTCCCGCGGAGTTCATCT 1382
Db 1078 GCTGCCCCCAACAGAGAGGGCTCCAGAGGAGAGCATGCTTCCCGCGGAGTTCATCT 1137
Qy 1383 GGTGTGAGACTTGAAGGCTCTACTGCGGGCTGTGAGGCGGGAATCCGGGCTGCCCTT 1442
Db 1138 GGTGTGAGACTTGAAGGCTCTACTGCGGGCTGTGAGGCGGGAATCCGGGCTGCCCTT 1197
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Qy 1443 TCGCCACAGTGTGACTTCCCGCATTCAGGCTGCTCCCTCCCTGCGGCTGCGCT 1502
Db 1138 TCGCCACAGTGTGACTTCCCGCATTCAGGCTGCTCCCTCCCTGCGGCTGCGCT 1257
Qy 1503 CTCCCAATATCTGCTGCTGCTGCGGAGTCACTGAGGAGCCAGCCACAGAGTTCGCCG 1562
Db 1258 CTCCCAATATCTGCTGCTGCTGCGGAGTCACTGAGGAGCCAGCCACAGAGTTCGCCG 1317
Qy 1563 GAAGCCACCTTCCAGCTGTGAGAGTGCACCATTTGCTGCTTAACTGCCAAGCCCCA 1622
Db 1318 GAAGCCACCTTCCAGCTGTGAGAGTGCACCATTTGCTGCTTAACTGCCAAGCCCCA 1377
Qy 1623 TCTGCGCCCGAGGTGGCTGCTGAGAGCCCGACATGCCCTTCTCATTTGGAACATTAAC 1682
Db 1378 TCTGCGCCCGAGGTGGCTGCTGAGAGCCCGACATGCCCTTCTCATTTGGAACATTAAC 1437
Qy 1683 TTCACTTTCCTCCAAAGTGGGAGTACAAAGCATGAGGAGTGGTGGCCCATGAAG 1742
Db 1438 TTCACTTTCCTCCAAAGTGGGAGTACAAAGCATGAGGAGTGGTGGCCCATGAAG 1497
Qy 1743 CCACAGCCAGGCTTCCAGCTCAGCACTGAGTGTGGCATGGTCCCAAGACTTATAT 1802
Db 1498 CCACAGCCAGGCTTCCAGCTCAGCACTGAGTGTGGCATGGTCCCAAGACTTATAT 1557
Qy 1803 TTGCTTTTATTTTATGCTAAATAATCTGCTTAAACTTTTCAATAAACAAGATGCTC 1862
Db 1558 TTGCTTTTATTTTATGCTAAATAATCTGCTTAAACTTTTCAATAAACAAGATGCTC 1617
Qy 1863 AGAAAAAAAAAAAA 1876
Db 1618 AGGACCAAAAAAAA 1631
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RESULT 5
US-10-172-118-620
: Sequence 620, Application US/10172118
: GENERAL INFORMATION:
: APPLICANT: Dai, Hongyue
: APPLICANT: He, Yudong
: APPLICANT: Linsley, Peter
: APPLICANT: Mao, Mao
: APPLICANT: Roberts, Chris
: APPLICANT: Van de Vijver, Marc
: APPLICANT: Bernards, Rene
: TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
: FILE REFERENCE: 9301-175-999
: CURRENT APPLICATION NUMBER: US/10/172,118
: CURRENT FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: 60/380,770
: PRIOR FILING DATE: 2002-05-14
: NUMBER OF SEQ ID NOS: 2699
: SEQ ID NO 620
: LENGTH: 1670
: TYPE: DNA
: ORGANISM: Homo sapiens
: PUBLICATON INFORMATION:
: DATABASE ACCESSION NUMBER: NM_001504
: DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-620
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Query Match 82.5%: Score 1548.4: DB 12: Length 1670:
Best Local Similarity 99.0%: Pred. No. 0:
Matches 1558: Conservative 0: Mismatches 16: Indels 0: Gaps 0:
Qy 303 CTTCCCGCTTCCCGCTCACAGGTGAGTGAACACCAAGTGTAAATGACGCCGAGTTG 362
Db 58 CCAGCCCAAGCATGTCTTGAAGTGAAGTGAACCAACCAAGTGTAAATGACGCCGAGTTG 117
Qy 363 CCGCCCTCTGAGAACTTACGCTCTTCTATGACTATGAGAAACAGAGTGACTGCT 422
Db 118 CCGCCCTCTGAGAACTTACGCTCTTCTATGACTATGAGAAACAGAGTGACTGCT 177
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OY	423	GCCTACCTCCCGCCCTTGGCCACAGACTTCAGCTGAACCTTCACCGCGGCTTCCTG	482
Db	178	GCTGACTCCCGCCCTTGGCCACAGACTTCAGCTGAACCTTCACCGCGGCTTCCTG	237
OY	483	CAGCCCTCTACAGCTCTCTTTCCTGCTGGGGGCTGTGGGGCAACGGCGGTGGCAGCG	542
Db	238	CAGCCCTCTACAGCTCTCTTTCCTGCTGGGGGCTGTGGGGCAACGGCGGTGGCAGCG	297
OY	543	TGCTGTGAGCGCGGGCGACACAGCCTGAGCAGACCGACACTTTCCTGCTCACCTAGCTG	602
Db	298	TGCTGTGAGCGCGGGCGACACAGCCTGAGCAGACCGACACTTTCCTGCTCACCTAGCTG	357
OY	603	TAGCAGACACGCTCTGTGCTGACACTGCGGCTGTGGGCAAGGAGAGCGCTGCGCTCAGT	662
Db	358	TAGCAGACACGCTCTGTGCTGACACTGCGGCTGTGGGCAAGGAGAGCGCTGCGCTCAGT	417
OY	663	GGGTCTTTGGCTCTGCGCTCTGCAAAAGTGGAGAGTCCCTTTCACATCAACTTCTACG	722
Db	418	GGGTCTTTGGCTCTGCGCTCTGCAAAAGTGGAGAGTCCCTTTCACATCAACTTCTACG	477
OY	723	CAGAGGCGCTCTGCTGCGCTGATGATAGCTTGACCGGTACCTGSAACATAGTTCAATGCA	782
Db	478	CAGAGGCGCTCTGCTGCGCTGATGATAGCTTGACCGGTACCTGSAACATAGTTCAATGCA	537
OY	783	CCCAAGCTCTACCGCGCGGGGGCCCCGGCCGCGCTGAGACCTTACCTACCTGCGGTGTCTGG	842
Db	538	CCCAAGCTCTACCGCGCGGGGGCCCCGGCCGCGGTGAGACCTTACCTACCTGCGGTGTCTGG	597
OY	843	GGCTCTGCGCTCTTTCCTGCGCTCCACAGACTTCATCTCTGTGCGGCCACACAGCAGAC	902
Db	598	GGCTCTGCGCTCTTTCCTGCGCTCCACAGACTTCATCTCTGTGCGGCCACACAGCAGAC	657
OY	903	GCTCAACAGCCACCACACTGTGCATPACAACTCCCAAGGTGGGGCGACAGGTGTGACGG	962
Db	658	GCTCAACAGCCACCACACTGTGCATPACAACTCCCAAGGTGGGGCGACAGGTGTGACGG	717
OY	963	TGCTGCACTGTGTGCTGCTGCTTCTGCTGCGCTGCTGCTCATGGCTTACTGTATGCTC	1022
Db	718	TGCTGCACTGTGTGCTGCTGCTTCTGCTGCGCTGCTGCTCATGGCTTACTGTATGCTC	777
OY	1023	ACATCTCGGCGCGTCTGCTGTTTCCAGGGGGCAGGGGGGCGTGGGGGCGAATGGGGCGG	1082
Db	778	ACATCTCGGCGCGTCTGCTGTTTCCAGGGGGCAGGGGGGCGTGGGGGCGAATGGGGCGG	837
OY	1083	TGTGTGTGTGTGTGTGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1142
Db	838	TGTGTGTGTGTGTGTGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	897
OY	1143	TGAGCACTCTCATAGCACTGGGGGCTTTGGGCCCGCAACTGTGTGGCGAGAAAGCAGGTA	1202
Db	898	TGAGCACTCTCATAGCACTGGGGGCTTTGGGCCCGCAACTGTGTGGCGAGAAAGCAGGTA	957
OY	1203	ACGTGGCGCAAGTGTGCTACCTTCAGAGGCTGGGGCTACATGTGACTGTGCTCAACCGCTGC	1262
Db	958	ACGTGGCGCAAGTGTGCTACCTTCAGAGGCTGGGGCTACATGTGACTGTGCTCAACCGCTGC	1017
OY	1263	TCTATGCTTGTTAGAGGGGTAAAGTTCGCGGAGCGGATGTGATGCTGCTCTTGGCGCTGG	1322
Db	1018	TCTATGCTTGTTAGAGGGGTAAAGTTCGCGGAGCGGATGTGATGCTGCTCTTGGCGCTGG	1077
OY	1323	GCTAGCCCAACACAGAGAGGGCTCCAGAGGAGCAATGCTTCCCGCGGGGATTCATCT	1382
Db	1078	GCTAGCCCAACACAGAGAGGGCTCCAGAGGAGCAATGCTTCCCGCGGGGATTCATCT	1137
OY	1383	GGTGTGAGACCTCAGAGGCTCTCTACTGCGGCTTGTGAAGCGCGAATCGGGCTCCCTT	1442
Db	1138	GGTGTGAGACCTCAGAGGCTCTCTACTGCGGCTTGTGAAGCGCGAATCGGGCTCCCTT	1197
OY	1443	TGCGCCACAGCTGTACTTCCCGGCAATTCAGAGCTCTCCCTCTCTGTGCGGCTGTGGCT	1502
Db	1198	TGCGCCACAGCTGTACTTCCCGGCAATTCAGAGCTCTCCCTCTCTGTGCGGCTGTGGCT	1257

Qy	1503	CTCCCAATATCCGCGCTCCCGGGACCTGACAGCCGACACACACAGGTCTCCCG	1562
Db	1258	CTCCCAATATCTCGCTCCCGGACTCACTGGACACCCACACACAGGTCTCCCG	1317
Qy	1563	GAAGCCACCCCTCCAGCTCTGAGGACTGACACATTGCTCTTAAAGTGCACAGCCCA	1622
Db	1318	GAAGCCACCCCTCCAGCTCTGAGGACTGCACACTTGTCTCTTAAAGTGCACAGCCCA	1377
Qy	1673	TCTGTCCGCGCCGAGGTGGCTGCTGGAGCCCACTGCTCTTCATTGGAACTAAAC	1682
Db	1378	TCTGTCCGCGCCGAGGTGGCTGCTGGAGCCCACTGCTCTTCATTGGAACTAAAC	1437
Qy	1683	TTTCATCTTCCCAAGTCCGGGGAGTCAAGGCAATGGCGTGAAGGGTGTGCCCATAG	1742
Db	1438	TTTCATCTTCCCAAGTCCGGGGAGTCAAGGCAATGGCGTGAAGGGTGTGCCCATAG	1497
Qy	1743	CCACAGCCACAGGCTCCAGCTCAGCAGTGACTGTGGCATTGCTCCCAAGACCTTATAT	1802
Db	1498	CCACAGCCACAGGCTCCAGCTCAGCAGTGACTGTGGCATTGCTCCCAAGACCTTATAT	1557
Qy	1803	TTTGCTCTTTATTTTATATGTCTAAAAATCCTGCTTAAACCTTTCATTAACAGATGTC	1862
Db	1558	TTTGCTCTTTATTTTATATGTCTAAAAATCCTGCTTAAACCTTTCATTAACAGATGTC	1617
Qy	1863	AGGAAAAAATAAAA 1876	
Db	1618	AGGACAAAAAATAAAA 1631	

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1      RESULT 6
2      US-10-251-686-1
3      ; Sequence 1, Application US/10251686
4      ; GENERAL INFORMATION:
5      ; APPLICANT: Loetscher, Marcel
6      ; Moser, Bernhard
7      ; Qin, Shixin
8      ; Mackay, Charles R.
9      TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
10     ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
11     NUMBER OF SEQUENCES: 4
12     CORRESPONDENCE ADDRESS:
13     ADDRESSSEE: Hamilton, Brook, Smith & Reynolds, P.C.
14     STREET: Two Millitia Drive
15     CITY: Lexington
16     STATE: MA
17     COUNTRY: USA
18     ZIP: 02173
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: PatentIn Release #1.0, Version #1.30
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/10/251,686
26     FILING DATE: 20-SEP-2002
27     CLASSIFICATION: <Unknown>
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: US/08/829,839
30     FILING DATE: 31-MAR-1997
31     APPLICATION NUMBER: US 08/709,838
32     FILING DATE: 10-SEP-1996
33     ATTORNEY/AGENT INFORMATION:
34     NAME: Brook Esq., David E.
35     REGISTRATION NUMBER: 22,592
36     REFERENCE/DOCKET NUMBER: TK196-01A
37     TELECOMMUNICATION INFORMATION:
38     TELEPHONE: (617) 861-6240
39     TELEFAX: (617) 861-9540
40     INFORMATION FOR SEQ ID NO: 1:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 1670 base pairs
43     TYPE: nucleic acid
44     STRANDEDNESS: double
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TOPOLOGY: unknown
FEATURE:
NAME/KEY: CDS
LOCATION: 69..1172
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-251-686-1

Query Match 82.2%; Score 1541.6; DB 13; Length 1670;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 303 CCTCCCGCTTCCGCCCTACAGAGTGTAGACACCAAGTGTAAATGACGCCGAGTTG 362
Db 58 CCAGCCACCATGTGCTTGTAGTGTAGTACACCAAGTGTAAATGACGCCGAGTTG 117
Oy 363 CCGCCCTCTGTGAGAACTTACACTCTTCTATGACTATGAGAAAAAGAGTACTCT 422
Db 118 CCGCCCTCTGTGAGAACTTACACTCTTCTATGACTATGAGAAAAAGAGTACTCT 177
Oy 423 GCTGTACCTCCCGCCCTCCACAGAGTGTAGAGCTGAAGTTCGACCGGCTTCTGC 482
Db 178 GGTGTACCTCCCGCCCTCCACAGAGTGTAGAGCTGAAGTTCGACCGGCTTCTGC 237
Oy 483 CAGCCCTTACAGCCCTCTTCTGTGTGGGCTGTGGCAACGGCGGCTGGCAGCCG 542
Db 238 CAGCCCTTACAGCCCTCTTCTGTGTGGGCTGTGGCAACGGCGGCTGGCAGCCG 297
Oy 543 TGTCTGTAGCGGGGGGAGAGCCGTGAGAGACCGACACCTTCTGCTCCACTAGCTG 602
Db 298 TGTCTGTAGCGGGGGAGAGCCGTGAGAGACCGACACCTTCTGCTCCACTAGCTG 357
Oy 603 TAGCAGACACGCTGT 662
Db 358 TAGCAGACACGCTGT 417
Oy 663 GGGCTTTGT 722
Db 418 GGGCTTTGT 477
Oy 723 CAGGAGCCCTCTGT 782
Db 478 CAGGAGCCCTCTGT 537
Oy 783 CCCAGCTTACCGCGGG 842
Db 538 CCCAGCTTACCGCGGG 597
Oy 843 GGGCTGTCCCTTTTTCGCCCTCCAGAGTGTATCTTCTGTGTGTGTGTGTGTGTGT 902
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Oy 903 GCGTCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAG 962
Db 658 GCGTCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAG 717
Oy 963 TGTCTCAGCTGT 1022
Db 718 TGTCTCAGCTGT 777
Oy 1023 ACATCTTGCCGCTGT 1082
Db 778 ACATCTTGCCGCTGT 837
Oy 1083 TGT 1142
Db 838 TGT 897
Oy 1143 TGTGACATCTTATGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1202
Db 898 TGTGACATCTTATGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 957
Oy 1203 ACGTGGCAAGT 1262
Db 957 ACGTGGCAAGT

Db 958 ACGTGGCAAGT 1017
Oy 1263 TGTATGCTTTGTAGGGGTCAAGTTCGGGAGGGATGTGTGTGTGTGTGTGTGTGT 1322
Db 1018 TGTATGCTTTGTAGGGGTCAAGTTCGGGAGGGATGTGTGTGTGTGTGTGTGTGT 1077
Oy 1323 GGTGCCCAACAGAGAGGGGTTCAGAGGACAGCATGCTTCCCGCGGATTCATCTG 1382
Db 1078 GGTGCCCAACAGAGAGGGGTTCAGAGGACAGCATGCTTCCCGCGGATTCATCTG 1137
Oy 1383 GGTGTGAGACTTGTAGAGCCCTCTTACTGTGGGCTTGTGTAGGGCGGAATCCGGGCTCCCTT 1442
Db 1138 GGTGTGAGACTTGTAGAGCCCTCTTACTGTGGGCTTGTGTAGGGCGGAATCCGGGCTCCCTT 1197
Oy 1443 TGGCCCAAGT 1502
Db 1198 TGGCCCAAGT 1257
Oy 1503 CTGCCCAATATCTCTGCTCCCGGACTCACTGTGACGCCAGCAGCAGCAGTCTCCGG 1562
Db 1258 CTGCCCAATATCTCTGCTCCCGGACTCACTGTGACGCCAGCAGCAGCAGTCTCCGG 1317
Oy 1563 GAAGCCACCTCTCCAGCTGTGAGACTGCACATTTGCTGCTTGTAGTGTGCCAAGCCCA 1622
Db 1318 GAAGCCACCTCTCCAGCTGTGAGACTGCACATTTGCTGCTTGTAGTGTGCCAAGCCCA 1377
Oy 1623 TGTGTGCGCGCGAGGT 1682
Db 1378 TGTGTGCGCGCGAGGT 1437
Oy 1683 TTTCATTTCCCAAGT 1742
Db 1438 TTTCATTTCCCAAGT 1497
Oy 1743 CCACAGCCCAAGGCTCTACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1802
Db 1498 CCACAGCCCAAGGCTCTACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1557
Oy 1803 TTGTGCTTTTATTTTATGTCTTAAATCTGCTTAAACTTTTCAATTAACAGATCGTC 1862
Db 1558 TTGTGCTTTTATTTTATGTCTTAAATCTGCTTAAACTTTTCAATTAACAGATCGTC 1617
Oy 1863 AGGA 1866
Db 1618 AGGA 1621

RESULT 7
PCT-US02-30182-962
; Sequence 962, Application PC/TUS0230182
; GENERAL INFORMATION:
; APPLICANT: Gene Logic, Inc.
; APPLICANT: Mungier, William E.
; APPLICANT: Kulkarni, Prakash
; APPLICANT: Getzenberg, Robert H.
; APPLICANT: Waga, Iwao
; APPLICANT: Yamamoto, Jun
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperp
; TITLE OF INVENTION: Gene Expression Profiles
; FILE REFERENCE: 44921-5029-01-WO
; CURRENT APPLICATION NUMBER: PCT/US02/30182
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/960,706
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 962
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U32674
PCT-US02-30182-962


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Db 371 GCAAGTGGCAGGTGCCCCCTTTCACATCACTTCTACGAGGAGCCCTCCGTGSGCT 430
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Db 431 GCATAGCTTGGACCGGACCTGACATAGTTTCATGACCAACCGCTACGCGGGGGG 490
Qy 804 CCGCGCGCGGGTGACCTTCACCTGCTGCGTGTCTGCGGGGCTGCGCTGCTTTCGCGC 863
Db 491 CCGCGCGCGGGTGACCTTCACCTGCTGCGTGTCTGCGGGGCTGCGCTGCTTTCGCGC 550
Qy 864 TCCAGACTTCACTTCTGCTGCGGCGCACACAGACGAGCGCTCAAGCGCACCCACTGCC 923
Db 551 TCCAGACTTCACTTCTGCTGCGGCGCACACAGACGAGCGCTCAAGCGCACCCACTGCC 610
Qy 924 AATCAACTTGGCCACAGTGGGCGGCGACGCGCTGCGGGGCTGTGAGAGTGGTGGCTGCT 983
Db 611 AATCAACTTGGCCACAGTGGGCGGCGACGCGCTGCGGGGCTGTGAGAGTGGTGGCTGCT 670
Qy 984 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1043
Db 671 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 730
Qy 1044 TTTCCAGGGGCGACGCGCGCTGCGGGCGCATGCGGCTGGTGGTGGTGGTGGTGGCT 1103
Db 731 TTTCCAGGGGCGACGCGCGCTGCGGGCGCATGCGGCTGGTGGTGGTGGTGGTGGCT 790
Qy 1104 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1163
Db 791 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850
Qy 1164 GCGCTTTGGCGCGCAACTGTGGCGCGAGAAAGCAGAGGTAGAGCTGGCGCAAGTGGTCACT 1223
Db 851 GCGCTTTGGCGCGCAACTGTGGCGCGAGAAAGCAGAGGTAGAGCTGGCGCAAGTGGTCACT 910
Qy 1224 CAGGCTGGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1283
Db 911 CAGGCTGGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 970
Qy 1284 AGTTCGGGAGCGGATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1343
Db 971 AGTTCGGGAGCGGATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1030
Qy 1344 TCCAGAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1403
Db 1031 TCCAGAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1090
Qy 1404 CCTACTCGGGCTTGTA 1420
Db 1091 CCTACTCGGGCTTGTA 1107

RESULT 9
US-10-251-385-173
; Sequence 173, Application US/10251385
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-251-385-173
Query Match 58.4%; Score 1095.4; DB 11; Length 1107;
Best Local Similarity 99.9%; Pred. No. 3e-225;
Matches 1096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 324 AGGTAGTGAACCAAGTGTAAATGACGCGGAGTTGGCCGCTCGTGAAGAACTTCA 383
Db 11 AGGTAGTGAACCAAGTGTAAATGACGCGGAGTTGGCCGCTCGTGAAGAACTTCA 70
Qy 384 GCTTCTCTATGATGAGAGAAACAGAGTACTGCTGCTGATCTCCCGCTGCC 443
Db 71 GCTTCTCTATGATGAGAGAAACAGAGTACTGCTGCTGATCTCCCGCTGCC 130
Qy 444 CACAGAGCTTCAAGCTGAACTTCAGCGGGGCTTCTGCGACCGCTACAGCGCTCT 503
Db 131 CACAGAGCTTCAAGCTGAACTTCAGCGGGGCTTCTGCGACCGCTACAGCGCTCT 190
Qy 504 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563
Db 191 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 250
Qy 564 CCTAGACAGACACGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623
Db 251 CCTAGACAGACACGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
Qy 624 TGACACTGCGGCTGCGGAGTGAAGCGTGGCGCTGACAGTGGTCTTGGCTGSGCTCT 683
Db 311 TGACACTGCGGCTGCGGAGTGAAGCGTGGCGCTGACAGTGGTCTTGGCTGSGCTCT 370
Qy 684 GCAAGTGGCAGAGTCCCTCTTTCACATCACTTCTACGAGAGAGCCCTGCTGCGGCT 743
Db 371 GCAAGTGGCAGAGTCCCTCTTTCACATCACTTCTACGAGAGAGCCCTGCTGCGGCT 430
Qy 744 GCATAGCTTGGACCGCTACCTGAAATAGTTTCATGCCACCGAGCTTACCGCGGGGGC 803
Db 431 GCATAGCTTGGACCGCTACCTGAAATAGTTTCATGCCACCGAGCTTACCGCGGGGGC 490
Qy 804 CCGCGCGCGGCTGACCTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 863
Db 491 CCGCGCGCGGCTGACCTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
Qy 864 TCCAGACTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 923
Db 551 TCCAGACTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610
Qy 924 AATCAACTTCCACAGTGGGCGCGACGCGCTGCGGGGCTGTGAGAGTGGTGGCTGCT 983
Db 611 AATCAACTTCCACAGTGGGCGCGACGCGCTGCGGGGCTGTGAGAGTGGTGGCTGCT 670
Qy 984 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1043
Db 671 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 730
Qy 1044 TTTCCAGGGGCGACGCGCGCTGCGGGCGCATGCGGCTGGTGGTGGTGGTGGTGGCT 1103
Db 731 TTTCCAGGGGCGACGCGCGCTGCGGGCGCATGCGGCTGGTGGTGGTGGTGGTGGCT 790
Qy 1224 CAGGCTGGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1283
Db 911 CAGGCTGGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 970
Qy 1284 AGTTCGGGAGCGGATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1343
Db 971 AGTTCGGGAGCGGATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1030
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OY	823	CACGTGCTGGGTGTCGTGGGGCTCTGGCTGGTTTTCGGCCCTCCAGACTTATCTTCT	882
Db	588	CACGTGGGAGCAATCTTGCTGGGTGGGCTCTCTCTGGCTTGGCCAGAAATTTCTTGC	647
OY	883	GTCGGCCCAACAGCAGAGCGCTCAACGC-----CACCACTGGCAATACAA	930
Db	648	CAAGTACAGCAAGGCGCATACACAACTCCCTGGCACGTTGTGACCTTCTCCAGAGAA	707
OY	931	CTTCCACACA---GGTGGGCGCAGCGCTCTGGGGTGGCTGCAGCTGGTGGCTTCT	987
Db	708	CCAAACAGAAACGATGCTGGCTGGTTCCACTCCCGATTCTCTACATGTTGGCGGATTC	767
OY	988	GCTGCCCCGTGGTGGATGAGGCTACTGGCTATGGCTATGCCACATCCGAGCGCTGCTG	1044
Db	768	GCTGCCCCATGCTGGTGAATGGGCTGGTGTCTACCTGGGGGATGACACAGTTTCCGCGAG	827
OY	1045	TTCCAGGGGCGCCAGCGGCGCTGGCGGCCATGCGGGCTGGTGGTGGTGGTGGTGGCT	1104
Db	828	CCAGCGGGCGCCCTCAGCGGCGAGAAAGCAAGTACAGGGTGGGCAATCTGGTACAAAGCAT	887
OY	1105	TGCCCTCTGCTGATGACCCCTATCACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1164
Db	888	CTTCTCTGCTGGTGTACCCCTACACATGCTATCTTCTTCTGGTACACCTGGCAGGCTGA	947
OY	1165	GCCTTTGGCCCCGACACTGGGCGGAGAAAGCAGGGGATGACGAGGCGCAAGTGGTCACT	1224
Db	948	GCGCGTGGACATACCTCTGCACAGCTAATGGCTCTCTCCCGCTGGCGCATACCATGTGT	1007
OY	1225	AGCGCTGGGCTACATGACACTGCTGCCCTCAACCCGCTGCTATAGCTTTGTAAGGGTCA	1284
Db	1008	GTTCTGTGGGCTGGCGCCACTGCTGCTCAACCCCATGCTCTACACTTGTGGCGGGTGA	1067
OY	1285	GTTCCGGGAGCGGATGATGATGCTGCTCTGTGGGCTGGGGCTGCCCAAC	1334
Db	1068	GTTCCGACATGACTGTGCGGGCTCTGACGAAAGTGGGCTGTACCGGCC	1117
RESULT 12			
US-10-035-832-1412			
: Sequence 1412, Application US/10035832			
: GENERAL INFORMATION:			
: APPLICANT: Morris, David			
: APPLICANT: Engelhard, Eric			
: TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER			
: FILE REFERENCE: A-71249/RMS/DCF			
: CURRENT APPLICATION NUMBER: US/10/035,832			
: CURRENT FILING DATE: 2002-07-22			
: PRIOR APPLICATION NUMBER: US 09/747,377			
: PRIOR FILING DATE: 2000-12-22			
: PRIOR APPLICATION NUMBER: US 09/798,586			
: PRIOR FILING DATE: 2001-03-02			
: NUMBER OF SEQ ID NOS: 1613			
: SOFTWARE: PatentIn version 3.1			
: SEQ ID NO 1412			
: LENGTH: 32404			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: misc_feature			
: LOCATION: (384)..(403)			
: OTHER INFORMATION: "n" at positions 384 thru 403 can be any base			
US-10-035-832-1412			

	Query Match	13.8%	Score 240	DB 13	Length 32404
	Best Local Similarity	57.0%	Pred. No. 1.9e-41		
	Matches 507	Conservative 0	Mismatches 365	Indels 18	Gaps 3
Oy	463	CTTGCACCGGGCGCTTCTCTCCACGCCCTCTACAGCTCCTCTTTCTGCTGGGCTGCTGG	522		
Db	19830	CTTACAGGCGCGGTGTGCGCCGCGGCTACAGCTCTCTTCTCTGCGGGGTATCGG	19889		
Oy	533	CACGCGCGGTGCGAGCGCTGCTCTGAGCGCGGAGACGCCCTGAGCAGCAGCAGAC	582		

Db	19890	CAACGTCCTCGGTGCTGTGTGATCTCTGGAGCGGACCGCGAGACACCCAGTTCACGAGAC	19949
Qy	583	CTTCCCTGCTCCACCTAGCTGTAGCAGACAGCGTGCCTGTGCTGAGACTGCGCGCTTGGGC	642
Db	19950	CTTCCGTTTCCACACGTGGCGGTGGCGAGACTCTGCTGGTTCATCATTGTCCTTTGGCGT	20009
Qy	643	AGTGAAGCTGCGGCTTCCAGTGGGCTTTTGGCTGTGGCTCTGCAAAATGTGACAGTGGCCT	702
Db	20010	GGCCAGAGGCGCTTGTGGGGCTGGGTCTCTGGGGACCTTCTCCGCAAAACGTGTATTTGCCCT	20069
Qy	703	CTTCAACATCAACTCTATGCGAGAGAGCCCTCCTGCTGGCGTGCATCAGTTTGAACGGCTA	762
Db	20070	GCACAAAGTCAACTTCTATCTGTCAGAGAGCTGTCTCTGCTGCATGCGCTGTGACGGCTA	20129
Qy	763	CTGGAACATAGTTCATGTGCACACCACAGCTCTACCGCGCGGGGGCCCGCGCGCGGTAGCCT	822
Db	20130	CCTGGCGAATGTTCACAGCGGCTGTCAATGCTCACCGCACCGCGCGCTCTCTCATCCACAT	20189
Qy	823	CACGTGCTGCTGTCTGGGGGCTCTGCTGCTTTTGGCGCTCCAGACATTCCTCT	882
Db	20190	CACCTGTGGAGACATCTGTGCTGTGGGGCTCTCTCTGCTTGCACAGATTCCTTGGC	20249
Qy	883	GTGCGGCCACACAGACAGAGCGCTCAAGC-----CACCACCTGGCAATACAA	930
Db	20250	CAAAATGTACGCCAAGGSCATCAACAACACTCCCTGCCACAGTTGCACACTTCTCCCAAGACAA	20309
Qy	931	CTTCCACAC---GGTGGGCGCGACGCGCTCTGCGGGTGCAGCTGTGTGGGCTTCT	987
Db	20310	CCAAGCAGAAAGCATGCTGCTGTATCACTCCCGAATCTCTTCACTATGTGTGCGGGATTCT	20369
Qy	988	GCTGCCCCCTGCTGTATGGCCCTACTGCTATAGCCACATCTGCGCGTGTG--CTGAT	1044
Db	20370	GCTGCCCAATGTGTGATATGGGCTGTGGTACTGTGGGGAGTGCACAGATTTGCGCCAGGC	20429
Qy	1045	TTCACAGGGGCCAGCGGGCGCTCTGGGGCCATGCGGCTGTGTGTGTGTGTGTGTGTGTGTGT	1104
Db	20430	CCAGCGGGCGCCCTCAGCGGCAACAAAGGCAGTCAAGGGTGGCAATCCGTGTACAAAGCATTT	20489
Qy	1105	TGCGCTGTGCTGAGACCCCTATCAGCTGCTGTGTGTGTGTGTGGAGCATCTGCATGAGCTGGG	1164
Db	20490	CTTCTCTGTGTGTGTACCTTACCAATATGTCTATCTTCTGTGACACCTGTGGCAGGCTGAA	20549
Qy	1165	GCGTTTGGCCCAACTGTGTGGCGGAGAAAGCAGGGGTAGACGTGAGCGGCAAGTGGTCACTTC	1224
Db	20550	GGCGCGTGCATATCTGCAAGCTGAATAGGTCTCTCTCCCGTGGGCAATCAGCATGTGTGA	20609
Qy	1225	AGGCTGTGGCTATCATGCACTGCTGCTCAACCCGCTGCTCTATAGCTTTGTAGGGGTCAA	1284
Db	20610	GTTCCTGTGGGCGCTGAGCCACTGCTGCTCAAAACCCATGTGCTTCACTTTTGCAGCGGTGAA	20669
Qy	1285	GTTCGGGGAGCGGATGTGATCTGCTCTGTGGCGCTGGGCTGCCCAAC	1334
Db	20670	GTTCGCAAGTACCTGTGTGCGGCTCTCTTACGAAAGTGTGGGCTGTATCCGGCG	20719

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? RESULT 13
? US-10-251-385-65
? Sequence 65, Application US/10251385
? GENERAL INFORMATION:
? APPLICANT: Behan, Dominic P.
? APPLICANT: Chalmers, Derek T.
? APPLICANT: Liaw, Chen W.
? TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
? TITLE OF INVENTION: Protein-Coupled
? TITLE OF INVENTION: Receptors
? FILE REFERENCE: AREN-0040
? CURRENT APPLICATION NUMBER: US/10/251,385
? CURRENT FILING DATE: 2002-09-20
? PRIOR APPLICATION NUMBER: US/09/1170,496
? PRIOR FILING DATE: 1998-10-13
? NUMBER OF SEQ ID NOS: 294
? SOFTWARE: PatentIn version 3.1

```

SEQ ID NO 65
LENGTH: 1119
TYPE: DNA
ORGANISM: Homo sapiens
US-10-251-385-65

Query Match 12.7%; Score 238.4; DB 11; Length 1119;
Best Local Similarity 56.9%; Pred. No. 2.1e-41;
Matches 506; Conservative 0; Mismatches 366; Indels 18; Gaps 3;

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OY 463 CTTGACCGGGGCTTCCTCCAGCCCTCTACAGCCCTTCCTTCCTTCGTCGGGCTGTCGG 522
DB 144 CTTCAAGGCGCGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 203
OY 523 CAACGCGCGGTGGGAGCGGCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 582
DB 204 CAACGTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 263
OY 583 CTTGCTGCTCCAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 642
DB 264 CTTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 323
OY 643 AGTGACGCTGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 702
DB 324 GCGCGAGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG 383
OY 703 CTTCAACATCACTTCTACGAGAGCCCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 762
DB 384 GCACAAGTCACTTCTACGAGAGCCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 443
OY 763 CTTGAACATGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 822
DB 444 CTTGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 503
OY 823 CACTGCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 882
DB 504 CACTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 563
OY 883 GTGCGGCCACACGAGAGCGGCTCAAGC-----CACCCACTGCCAATACAA 930
DB 564 CAAAGTCAAGCCAGGCAATCAACACACTCCCTGCGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCG 623
OY 931 CTTCCACA---GTTGGGCGGAGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 987
DB 624 CCAGACAGAAAGCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 683
OY 988 GTGCGGCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1044
DB 684 GCTGCGCATGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 743
OY 1045 TTCCAGGGGCGGAGCGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1104
DB 744 CCAGGCGGGGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 803
OY 1105 TGCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1164
DB 804 CTTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 863
OY 1165 GCGTTTGGCCCGCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1224
DB 864 GCGCTGTGCAATACCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 923
OY 1225 AGGCTGTGAGCTACATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1284
DB 924 GTTCTGTGGGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 983
OY 1285 GTTCCGCGGAGCGAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1344
DB 984 GTTCCGCGAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1033
```

RESULT 14
US-10-251-385-199

Sequence 199, Application US/10251385
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
TITLE OF INVENTION: Protein-Coupled
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 199
LENGTH: 1119
TYPE: DNA
ORGANISM: Homo sapiens
US-10-251-385-199

Query Match 12.7%; Score 238.4; DB 11; Length 1119;
Best Local Similarity 56.9%; Pred. No. 2.1e-41;
Matches 506; Conservative 0; Mismatches 366; Indels 18; Gaps 3;

```
OY 463 CTTGACCGGGGCTTCCTCCAGCCCTCTACAGCCCTCTCTCTTCCTTCGTCGGGCTGTCGG 522
DB 144 CTTCAAGGCGCGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 203
OY 523 CAACGCGCGGTGGGAGCGGCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 582
DB 204 CAACGTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 263
OY 583 CTTGCTGCTCCAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 642
DB 264 CTTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 323
OY 643 AGTGACGCTGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 702
DB 324 GCGCGAGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGG 383
OY 703 CTTCAACATCACTTCTACGAGAGCCCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 762
DB 384 GCACAAGTCACTTCTACGAGAGCCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 443
OY 763 CTTGAACATGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 822
DB 444 CTTGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 503
OY 823 CACTGCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 882
DB 504 CACTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 563
OY 883 GTGCGGCCACACGAGAGCGGCTCAAGC-----CACCCACTGCCAATACAA 930
DB 564 CAAAGTCAAGCCAGGCAATCAACACACTCCCTGCGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCG 623
OY 931 CTTCCACA---GTTGGGCGGAGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 987
DB 624 CCAGACAGAAAGCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 683
OY 684 GCTGCGCATGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 743
DB 744 CCAGGCGGGGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 803
OY 744 CCAGGCGGGGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 863
OY 804 CTTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 923
OY 924 GTTCTGTGGGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 983
OY 983 GTTCCGCGGAGCGAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1044
DB 1045 TTCCAGGGGCGGAGCGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1104
OY 1105 TGCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1164
DB 1165 GCGTTTGGCCCGCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1224
OY 1225 AGGCTGTGAGCTACATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1284
DB 1285 GTTCCGCGGAGCGAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1344
OY 1344 GTTCCGCGAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1403
DB 1403 GTTCCGCGAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1462
```

QY 1165 CGCTTTGGCCGCACTGTGGCCGAGAAAGCAAGGATGAGCGGGCAATGGTCACTC 1224

Db 864 GGGCGTGGACAATACCTGGCAAGCTGAATGAGCTCTCCCGGGGCATCACCATTGTGGA 923

QY 1225 AGGCGCTGGCTACATGACATGCTGCGCTCAACCGCGCTGCTATGCTTTGTAGGGGTAA 1284

Db 924 GTTCTCTGGGCGCTGGCCCGACACTGCTGCTCTCAACCCCATGCTCTACACTTTGCGCGGGGTAA 983

QY 1285 GTTTCGGGAGCGGATGTGATGTGCTCTTTGGGCGCTGGGCTACCCCAAC 1334

Db 984 GTTCCGACATGACCTGTGCGGGGCTCTTGACCAACAGCTGGGCTGTACCGGCT 1033

RESULT 15

US-09-442-384B-424
; Sequence 424, Application US/09442384B
CURRENT INNOVATION.

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? GENERAL INFORMATION:
? APPLICANT: Chenchik, Alex
? APPLICANT: Lukashayev, Matvey
? TITLE OF INVENTION: Hematology/Immunology Array
? FILE REFERENCE: CLON-006CIP15
? CURRENT APPLICATION NUMBER: US/09/442,384B
? CURRENT FILING DATE: 1998-11-17
? PRIOR APPLICATION NUMBER: 09/053,375
? PRIOR FILING DATE: 1998-03-31
? NUMBER OF SEQ ID NOS: 830
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 424
? LENGTH: 2818
? TYPE: DNA
? ORGANISM: homo sapiens
? US-09-442-384B-424

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Query Match	12.7%	Score 238.4;	DB 9;	Length 2818;
Best Local Similarity	56.9%	Pred. No. 2.5e-41;		
Matches 506; Conservative	0;	Mismatches 366;	Indels 18;	Gaps 3;

OY	463	CTTGGACGGGCGCTTCCGTCGAGCGCCCTCTTACAGCCTCTCTTTTGTGGGGAGCGCTGGG	522
Db	228	CTTCAAGGCCCTGTTCGTGCGCCCGTGGCGCTACAGCCTATCTCTCTCTGGGGCTGATCGG	287
OY	523	CAACGGCGCGGTGGACGCCGTCTGCTGAGCGCGGCGGACACGCCCTGAGACGACACGAC	582
Db	288	CAACGCTCTGTGTGTGTGATCTCTGGAGCGGACACCGGACAGACACGCGATTTCCAGGGAGAC	347
OY	583	CTTCTGCTCCACCTACTACTGTAGAGACACAGCGCTCGTGCTGTGACACTGGCGCGCTGGGC	642
Db	348	CTTCTGCTGTCCACTGTGGCCGCTGGCGGACCTCTGCTGTCTTCACTCTTGGCCCTTTGGCGT	407
OY	643	AGTGGACGTGCGCTCCAGTGGGTCTTTTGGCTCTGGCCTCTGCACAACTGGCAGGTGGCCT	702
Db	408	GGCGGAGGGCTCTGTGGGCGTGGGCTCGGGGACCTCTCTGCACAACTGTGATTTGGCCT	467
OY	703	CTTCAACATCAACTTTTACGAGGAGGCGCCCTCTGCTGGCGCTGCATTCAGCTTACCGCTA	765
Db	468	GCACAAAGTCAACTTCTACTACTGACAGCAGCTGTCTCTGTGGCTGCACTGCCGTGGACCGCTA	527
OY	763	CTTGAACATAGTTCTATGCCCAACCCAGCTCTACCGCGGGGGCCCCCGGCGCGGTGACCTT	822
Db	528	CTTGGCAATGTCTCCACGCCCGCTACGCTTACCGGCACCGCGCGCTCTCTTCATCCACAT	587
OY	823	CACCTGCGCTGGCTGTCTGAGGGGGCTCTGCCGTCTTTTGGCCCTCCCAAGACTTCACTTCTCT	882
Db	588	CACCTGTGGGACATCTGGGCTGTGGGCTTCTCTCTTGGCCCAAGATTTCTCTTGGC	647
OY	883	GTCGGCCACACAGACAGAGGCGCTTCAACGC-----CACCCATGCAATACAA	938
Db	648	CAAGTGCAGCCAAAGGCCATCAACAACACTCCGTGCAAGTTGGACACTTTTCCAAAGAA	707
OY	931	CTTCCCAACA---GGTGGGCGCCAGCGCTCTGCGGGTCTGCACTGGTGGCTGGCTTCT	987
Db	708	CCAAAGCAAAACGATCGATCTGTGTTCACCTCCCGATTTCTCTACCATGTGGCGGGATTTCT	767

[illegible]

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Job time : 507 secs

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